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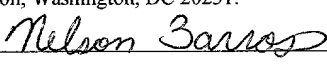
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Sir:

Transmitted herewith for filing is the patent application of:

Inventors: Markus Pompejus *et al.*

For: "Corynebacterium Glutamicum Genes Encoding Proteins Involved in
Membrane Synthesis and Membrane Transport"

Enclosed are:

- ☒ 61 pages of specification, 5 pages of claims and 1 page of abstract;
- ☒ 6 pages of Table 1;
- ☒ 16 pages of Table 2;
- ☒ 6 pages of Table 3;
- ☒ 18 pages of Table 4;
- ☒ 87 pages of Appendix A;
- ☒ 29 pages of Appendix B;
- ☒ 602 pages of Sequence Listing;
- ☒ Zip Disk Containing Sequence Listing;
- ☒ Transmittal Letter for Zip Disk Containing Sequence Listing;
- ☒ An *unexecuted* Declaration, Petition and Power of Attorney; and
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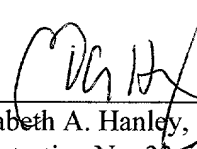
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***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING PROTEINS
INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT**

5 Related Applications

This application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application Serial No. 60/143262, filed July 9, 1999, and U.S. Provisional Patent Application Serial No. 60/151281, filed August 27, 1999. This application also claims priority to prior filed
10 German Patent Application No. 19930487.4, filed July 1, 1999, German Patent Application No. 19930489.0, filed July 1, 1999, German Patent Application No. 19931549.3, filed July 8, 1999, German Patent Application No. 19931550.7, filed July 8, 1999, German Patent Application No. 19932134.5, filed July 9, 1999, German Patent Application No. 19941379.7, filed August 31, 1999, German Patent Application
15 No. 19942088.2, filed September 3, 1999, and German Patent Application No. 19942097.1, filed September 3, 1999. The entire contents of all of the aforementioned applications are hereby expressly incorporated herein by this reference.

Background of the Invention

20 Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic
25 compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have
30 been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

35 The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C.*

glutamicum or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as membrane construction and membrane transport (MCT) proteins.

5 *C. glutamicum* is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The MCT nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by
10 fermentation processes. Modulation of the expression of the MCT nucleic acids of the invention, or modification of the sequence of the MCT nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

15 The MCT nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or
20 mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of
25 significant clinical relevance.

 The MCT nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

30 The MCT proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function involved in the metabolism (*e.g.*, the biosynthesis or degradation) of compounds necessary for membrane biosynthesis, or of assisting in the transmembrane transport of one or more compounds either into or out of the cell. Given the availability of cloning vectors for use in *Corynebacterium*
35 *glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985);

Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or efficiency of
5 production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

There are a number of mechanisms by which the alteration of an MCT protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein.

10 Those MCT proteins involved in the export of fine chemical molecules from the cell may be increased in number or activity such that greater quantities of these compounds are secreted to the extracellular medium, from which they are more readily recovered. Similarly, those MCT proteins involved in the import of nutrients necessary for the biosynthesis of one or more fine chemicals (*e.g.*, phosphate, sulfate, nitrogen
15 compounds, etc.) may be increased in number or activity such that these precursors, cofactors, or intermediate compounds are increased in concentration within the cell. Further, fatty acids and lipids themselves are desirable fine chemicals; by optimizing the activity or increasing the number of one or more MCT proteins of the invention which participate in the biosynthesis of these compounds, or by impairing the activity of one or
20 more MCT proteins which are involved in the degradation of these compounds, it may be possible to increase the yield, production, and/or efficiency of production of fatty acid and lipid molecules from *C. glutamicum*.

The mutagenesis of one or more MCT genes of the invention may also result in MCT proteins having altered activities which indirectly impact the production of one or
25 more desired fine chemicals from *C. glutamicum*. For example, MCT proteins of the invention involved in the export of waste products may be increased in number or activity such that the normal metabolic wastes of the cell (possibly increased in quantity due to the overproduction of the desired fine chemical) are efficiently exported before they are able to damage nucleotides and proteins within the cell (which would decrease
30 the viability of the cell) or to interfere with fine chemical biosynthetic pathways (which would decrease the yield, production, or efficiency of production of the desired fine chemical). Further, the relatively large intracellular quantities of the desired fine chemical may in itself be toxic to the cell, so by increasing the activity or number of transporters able to export this compound from the cell, one may increase the viability of
35 the cell in culture, in turn leading to a greater number of cells in the culture producing the desired fine chemical. The MCT proteins of the invention may also be manipulated such that the relative amounts of different lipid and fatty acid molecules are produced.

This may have a profound effect on the lipid composition of the membrane of the cell. Since each type of lipid has different physical properties, an alteration in the lipid composition of a membrane may significantly alter membrane fluidity. Changes in membrane fluidity can impact the transport of molecules across the membrane, as well as the integrity of the cell, both of which have a profound effect on the production of fine chemicals from *C. glutamicum* in large-scale fermentative culture.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as MCT proteins, which are capable of, for example, participating in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. Nucleic acid molecules encoding an MCT protein are referred to herein as MCT nucleic acid molecules. In a preferred embodiment, the MCT protein participates in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an MCT protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of MCT-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth in Appendix A or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth in Appendix A, or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth in Appendix B. The preferred MCT proteins of the present invention also preferably possess at least one of the MCT activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B, *e.g.*, sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains an MCT activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to participate in the

metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of Appendix B (e.g., an entire amino acid sequence selected from those sequences set forth in Appendix B). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (e.g., an MCT fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or has one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of Appendix A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* MCT protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, e.g., recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an MCT protein by culturing the host cell in a suitable medium. The MCT protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an MCT gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated MCT sequence as a transgene. In another embodiment, an endogenous MCT gene within the genome of the microorganism has been altered, e.g., functionally disrupted, by homologous recombination with an altered MCT gene. In another embodiment, an endogenous or introduced MCT gene in a microorganism has been altered by one or more point

mutations, deletions, or inversions, but still encodes a functional MCT protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MCT gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MCT gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

10 In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

15 Still another aspect of the invention pertains to an isolated MCT protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated MCT protein or portion thereof can participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. In another preferred embodiment, the isolated MCT protein or portion thereof is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes.

25 The invention also provides an isolated preparation of an MCT protein. In preferred embodiments, the MCT protein comprises an amino acid sequence of Appendix B. In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame set forth in Appendix A). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of Appendix B. In other embodiments, the isolated MCT protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated MCT protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 5 95%, 96%, 97%, 98,%, or 99% or more homologous, to a nucleotide sequence of Appendix B. It is also preferred that the preferred forms of MCT proteins also have one or more of the MCT bioactivities described herein.

The MCT polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MCT polypeptide to form a fusion protein. In preferred 10 embodiments, this fusion protein has an activity which differs from that of the MCT protein alone. In other preferred embodiments, this fusion protein participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates 15 production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an MCT protein, either by interacting with the protein itself or a substrate or binding partner of the MCT protein, or by modulating the transcription or translation of an MCT nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine 20 chemical. This method involves the culturing of a cell containing a vector directing the expression of an MCT nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector 25 directing the expression of an MCT nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of 30 a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates MCT protein activity or MCT nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* metabolic pathways for cell membrane components or is modulated for the transport of 35 compounds across such membranes, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates MCT protein activity can be an agent which stimulates MCT protein activity or MCT

nucleic acid expression. Examples of agents which stimulate MCT protein activity or MCT nucleic acid expression include small molecules, active MCT proteins, and nucleic acids encoding MCT proteins that have been introduced into the cell. Examples of agents which inhibit MCT activity or expression include small molecules and antisense
5 MCT nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant MCT gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can
10 take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino
15 acid is L-lysine.

Detailed Description of the Invention

The present invention provides MCT nucleic acid and protein molecules which are involved in the metabolism of cellular membrane components in *C. glutamicum* or
20 in the transport of compounds across such membranes. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where overexpression or optimization of a fatty acid biosynthesis protein has a direct impact on the yield, production, and/or efficiency of production of the fatty acid from modified *C. glutamicum*), or may have an
25 indirect impact which nonetheless results in an increase of yield, production, and/or efficiency of production of the desired compound (*e.g.*, where modulation of the metabolism of cell membrane components results in alterations in the yield, production, and/or efficiency of production or the composition of the cell membrane, which in turn may impact the production of one or more fine chemicals). Aspects of the invention are
30 further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to,
35 the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases,

nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in *Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (5 *e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and 10 Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) *Chemicals by Fermentation*, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine 15 chemicals are further explicated below.

A. Amino Acid Metabolism and Uses

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art- 20 recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ullmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L- 25 amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. *Biochemistry*, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, 30 and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino 35 acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various

applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) *Amino acids – technical production and use*, p. 466-502 in Rehm *et al.* (eds.) *Biotechnology* vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's *Encyclopedia of Industrial Chemistry*, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (e.g., polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley

& Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

5 Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B₆' (e.g., pyridoxine, pyridoxamine, pyridoxa-
10 5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)-β-alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β-alanine and pantoic acid. The
15 enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β-alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of
20 pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B₅), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in
25 Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α-ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which in turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-
30 methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system.
35 The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are

also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for

several medicinal applications (see, for example, Kuninaka, A. (1996) Nucleotides and Related Compounds in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) “*de novo* purine nucleotide biosynthesis”, in: Progress in Nucleic Acid Research and Molecular Biology, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) “Nucleotides and Nucleosides”, Chapter 8 in: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α, α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Membrane Biosynthesis and Transmembrane Transport

Cellular membranes serve a variety of functions in a cell. First and foremost, a membrane differentiates the contents of a cell from the surrounding environment, thus giving integrity to the cell. Membranes may also serve as barriers to the influx of

5 hazardous or unwanted compounds, and also to the efflux of desired compounds.

Cellular membranes are by nature impervious to the unfacilitated diffusion of hydrophilic compounds such as proteins, water molecules and ions due to their structure: a bilayer of lipid molecules in which the polar head groups face outwards (towards the exterior and interior of the cell, respectively) and the nonpolar tails face inwards at the center of the bilayer, forming a hydrophobic core (for a general review of membrane structure and function, see Gennis, R.B. (1989) Biomembranes, Molecular Structure and Function, Springer: Heidelberg). This barrier enables cells to maintain a relatively higher concentration of desired compounds and a relatively lower concentration of undesired compounds than are contained within the surrounding medium, since the

10 center of the bilayer, forming a hydrophobic core (for a general review of membrane structure and function, see Gennis, R.B. (1989) Biomembranes, Molecular Structure and Function, Springer: Heidelberg). This barrier enables cells to maintain a relatively higher concentration of desired compounds and a relatively lower concentration of undesired compounds than are contained within the surrounding medium, since the

15 diffusion of these compounds is effectively blocked by the membrane.

However, the membrane also presents an effective barrier to the import of desired compounds and the export of waste molecules. To overcome this difficulty, cellular membranes incorporate many kinds of transporter proteins which are able to facilitate the transmembrane transport of different kinds of compounds. There are two general

20 classes of these transport proteins: pores or channels and transporters. The former are integral membrane proteins, sometimes complexes of proteins, which form a regulated hole through the membrane. This regulation, or 'gating' is generally specific to the molecules to be transported by the pore or channel, rendering these transmembrane constructs selectively permeable to a specific class of substrates; for example, a

25 potassium channel is constructed such that only ions having a like charge and size to that of potassium may pass through. Channel and pore proteins tend to have discrete hydrophobic and hydrophilic domains, such that the hydrophobic face of the protein may associate with the interior of the membrane while the hydrophilic face lines the interior of the channel, thus providing a sheltered hydrophilic environment through

30 which the selected hydrophilic molecule may pass. Many such pores/channels are known in the art, including those for potassium, calcium, sodium, and chloride ions.

This pore and channel-mediated system of facilitated diffusion is limited to very small molecules, such as ions, because pores or channels large enough to permit the passage of whole proteins by facilitated diffusion would be unable to prevent the

35 passage of smaller hydrophilic molecules as well. Transport of molecules by this process is sometimes termed 'facilitated diffusion' since the driving force of a concentration gradient is required for the transport to occur. Permeases also permit facilitated

diffusion of larger molecules, such as glucose or other sugars, into the cell when the concentration of these molecules on one side of the membrane is greater than that on the other (also called 'uniport'). In contrast to pores or channels, these integral membrane proteins (often having between 6-14 membrane-spanning α -helices) do not form open channels through the membrane, but rather bind to the target molecule at the surface of the membrane and then undergo a conformational shift such that the target molecule is released on the opposite side of the membrane.

However, cells frequently require the import or export of molecules against the existing concentration gradient ('active transport'), a situation in which facilitated diffusion cannot occur. There are two general mechanisms used by cells for such membrane transport: symport or antiport, and energy-coupled transport such as that mediated by the ABC transporters. Symport and antiport systems couple the movement of two different molecules across the membrane (via permeases having two separate binding sites for the two different molecules); in symport, both molecules are transported in the same direction, while in antiport, one molecule is imported while the other is exported. This is possible energetically because one of the two molecules moves in accordance with a concentration gradient, and this energetically favorable event is permitted only upon concomitant movement of a desired compound against the prevailing concentration gradient. Single molecules may be transported across the membrane against the concentration gradient in an energy-driven process, such as that utilized by the ABC transporters. In this system, the transport protein located in the membrane has an ATP-binding cassette; upon binding of the target molecule, the ATP is converted to ADP + Pi, and the resulting release of energy is used to drive the movement of the target molecule to the opposite face of the membrane, facilitated by the transporter. For more detailed descriptions of all of these transport systems, see: Bamberg, E. *et al.*, (1993) "Charge transport of ion pumps on lipid bilayer membranes", *Q. Rev. Biophys.* 26: 1-25; Findlay, J.B.C. (1991) "Structure and function in membrane transport systems", *Curr. Opin. Struct. Biol.* 1:804-810; Higgins, C.F. (1992) "ABC transporters from microorganisms to man", *Ann. Rev. Cell Biol.* 8: 67-113; Gennis, R.B. (1989) "Pores, Channels and Transporters", in: *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 270-322; and Nikaido, H. and Saier, H. (1992) "Transport proteins in bacteria: common themes in their design", *Science* 258: 936-942, and references contained within each of these references.

The synthesis of membranes is a well-characterized process involving a number of components, the most important of which are lipid molecules. Lipid synthesis may be divided into two parts: the synthesis of fatty acids and their attachment to sn-glycerol-3-phosphate, and the addition or modification of a polar head group. Typical

lipids utilized in bacterial membranes include phospholipids, glycolipids, sphingolipids, and phosphoglycerides. Fatty acid synthesis begins with the conversion of acetyl CoA either to malonyl CoA by acetyl CoA carboxylase, or to acetyl-ACP by acetyltransacylase. Following a condensation reaction, these two product molecules

5 together form acetoacetyl-ACP, which is converted by a series of condensation, reduction and dehydration reactions to yield a saturated fatty acid molecule having a desired chain length. The production of unsaturated fatty acids from such molecules is catalyzed by specific desaturases either aerobically, with the help of molecular oxygen, or anaerobically (for reference on fatty acid synthesis, see F.C. Neidhardt *et al.* (1996)

10 *E. coli* and *Salmonella*. ASM Press: Washington, D.C., p. 612-636 and references contained therein; Lengeler *et al.* (eds) (1999) *Biology of Prokaryotes*. Thieme: Stuttgart, New York, and references contained therein; and Magnuson, K. *et al.*, (1993) *Microbiological Reviews* 57: 522-542, and references contained therein). The cyclopropane fatty acids (CFA) are synthesized by a specific CFA-synthase using SAM

15 as a cosubstrate. Branched chain fatty acids are synthesized from branched chain amino acids that are deaminated to yield branched chain 2-oxo-acids (see Lengeler *et al.*, eds. (1999) *Biology of Prokaryotes*. Thieme: Stuttgart, New York, and references contained therein). Another essential step in lipid synthesis is the transfer of fatty acids onto the polar head groups by, for example, glycerol-phosphate-acyltransferases. The

20 combination of various precursor molecules and biosynthetic enzymes results in the production of different fatty acid molecules, which has a profound effect on the composition of the membrane.

III. Elements and Methods of the Invention

25 The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as MCT nucleic acid and protein molecules, which control the production of cellular membranes in *C. glutamicum* and govern the movement of molecules across such membranes. In one embodiment, the MCT molecules participate in the metabolism of compounds necessary for the construction of cellular membranes in

30 *C. glutamicum*, or in the transport of molecules across these membranes. In a preferred embodiment, the activity of the MCT molecules of the present invention to regulate membrane component production and membrane transport has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the MCT molecules of the invention are modulated in activity, such that

35 the *C. glutamicum* metabolic pathways which the MCT proteins of the invention regulate are modulated in yield, production, and/or efficiency of production and the transport of compounds through the membranes is altered in efficiency, which either

directly or indirectly modulates the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "MCT protein" or "MCT polypeptide" includes proteins which participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. Examples of MCT proteins include those encoded by the MCT genes set forth in Table 1 and Appendix A. The terms "MCT gene" or "MCT nucleic acid sequence" include nucleic acid sequences encoding an MCT protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of MCT genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (e.g., kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (i.e., fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (e.g., the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

In another embodiment, the MCT molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an MCT protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. Those MCT proteins involved in the export

of fine chemical molecules from the cell may be increased in number or activity such that greater quantities of these compounds are secreted to the extracellular medium, from which they are more readily recovered. Similarly, those MCT proteins involved in the import of nutrients necessary for the biosynthesis of one or more fine chemicals
5 (e.g., phosphate, sulfate, nitrogen compounds, etc.) may be increased in number or activity such that these precursor, cofactor, or intermediate compounds are increased in concentration within the cell. Further, fatty acids and lipids themselves are desirable fine chemicals; by optimizing the activity or increasing the number of one or more MCT proteins of the invention which participate in the biosynthesis of these compounds, or by
10 impairing the activity of one or more MCT proteins which are involved in the degradation of these compounds, it may be possible to increase the yield, production, and/or efficiency of production of fatty acid and lipid molecules from *C. glutamicum*.

The mutagenesis of one or more MCT genes of the invention may also result in MCT proteins having altered activities which indirectly impact the production of one or
15 more desired fine chemicals from *C. glutamicum*. For example, MCT proteins of the invention involved in the export of waste products may be increased in number or activity such that the normal metabolic wastes of the cell (possibly increased in quantity due to the overproduction of the desired fine chemical) are efficiently exported before they are able to damage nucleotides and proteins within the cell (which would decrease
20 the viability of the cell) or to interfere with fine chemical biosynthetic pathways (which would decrease the yield, production, or efficiency of production of the desired fine chemical). Further, the relatively large intracellular quantities of the desired fine chemical may in itself be toxic to the cell, so by increasing the activity or number of transporters able to export this compound from the cell, one may increase the viability of
25 the cell in culture, in turn leading to a greater number of cells in the culture producing the desired fine chemical. The MCT proteins of the invention may also be manipulated such that the relative amounts of different lipid and fatty acid molecules are produced. This may have a profound effect on the lipid composition of the membrane of the cell. Since each type of lipid has different physical properties, an alteration in the lipid
30 composition of a membrane may significantly alter membrane fluidity. Changes in membrane fluidity can impact the transport of molecules across the membrane, as well as the integrity of the cell, both of which have a profound effect on the production of fine chemicals from *C. glutamicum* in large-scale fermentative culture.

The isolated nucleic acid sequences of the invention are contained within the
35 genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* MCT DNAs and the predicted amino acid sequences of the *C.*

glutamicum MCT proteins are shown in Appendices A and B, respectively.

Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode proteins involved in the metabolism of cellular membrane components or proteins involved in the transport of compounds across such membranes.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of Appendix B. As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

The MCT protein or a biologically active portion or fragment thereof of the invention can participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode MCT polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of MCT-encoding nucleic acid (*e.g.*, MCT DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank

the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MCT nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

10 A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of Appendix A, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* MCT DNA can be isolated from a *C. glutamicum* library using all or portion of one of the sequences of Appendix A as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence of Appendix A). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in Appendix A. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an MCT nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in Appendix A. The sequences of

Appendix A correspond to the *Corynebacterium glutamicum* MCT DNAs of the invention. This DNA comprises sequences encoding MCT proteins (*i.e.*, the "coding region", indicated in each sequence in Appendix A), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in Appendix A. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in Appendix A.

For the purposes of this application, it will be understood that each of the sequences set forth in Appendix A has an identifying RXA, RXN, or RXS number having the designation "RXA", "RXN", or "RXS" followed by 5 digits (*i.e.*, RXA00775, RXN02994, or RXS03221). Each of these sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation "one of the sequences in Appendix A", then, refers to any of the sequences in Appendix A, which may be distinguished by their differing RXA, RXN, or RXS designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is set forth in Appendix B. The sequences of Appendix B are identified by the same RXA, RXN, or RXS designations as Appendix A, such that they can be readily correlated. For example, the amino acid sequences in Appendix B designated RXA00775, RXN02994, and RXS03221 are translations of the coding regions of the nucleotide sequence of nucleic acid molecules RXA00775, RXN02994, and RXS03221, respectively, in Appendix A. Each of the RXA, RXN, and RXS nucleotide and amino acid sequences of the invention has also been assigned a SEQ ID NO, as indicated in Table 1. For example, as set forth in Table 1, the nucleic acid sequence of RXA00774 is SEQ ID NO:7, and the amino acid sequence of RXA00774 is SEQ ID NO:8.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, or RXS designation. For example, SEQ ID NO:21, designated, as indicated on Table 1, as "F RXA01245", is an F-designated gene, as are SEQ ID NOs: 35, 39, and 43 (designated on Table 1 as "F RXA01164", "F RXA01168", and "F RXA02062", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the *dapD* gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version

relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences shown in Appendix A, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in Appendix A is one which is sufficiently complementary to one of the nucleotide sequences shown in Appendix A such that it can hybridize to one of the nucleotide sequences shown in Appendix A, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence shown in Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to one of the nucleotide sequences shown in Appendix A, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences in Appendix A, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an MCT protein. The nucleotide sequences determined from the cloning of the MCT genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning MCT homologues in other cell types and organisms, as well as MCT homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the sequences set forth in Appendix A, an anti-sense sequence of one of the sequences set forth in Appendix A, or naturally occurring mutants thereof. Primers based on a nucleotide

sequence of Appendix A can be used in PCR reactions to clone MCT homologues. Probes based on the MCT nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an MCT protein, such as by measuring a level of an MCT-encoding nucleic acid in a sample of cells, *e.g.*, detecting MCT mRNA levels or determining whether a genomic MCT gene has been mutated or deleted.

10 In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in one of the sequences of Appendix B) amino acid residues to an amino acid sequence of Appendix B such that the protein or portion thereof is able to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. Protein members of such membrane component metabolic pathways or membrane transport systems, as described herein, may play a role in the production and secretion of one or more fine chemicals. Examples of such activities are also described herein. Thus, "the function of an MCT protein" contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of MCT protein activities are set forth in Table 1.

30 In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B.

35 Portions of proteins encoded by the MCT nucleic acid molecules of the invention are preferably biologically active portions of one of the MCT proteins. As used herein, the term "biologically active portion of an MCT protein" is intended to include a portion, *e.g.*, a domain/motif, of an MCT protein that participates in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in

the transport of molecules across these membranes, or has an activity as set forth in Table 1. To determine whether an MCT protein or a biologically active portion thereof can participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an MCT protein can be prepared by isolating a portion of one of the sequences in Appendix B, expressing the encoded portion of the MCT protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MCT protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Appendix A (and portions thereof) due to degeneracy of the genetic code and thus encode the same MCT protein as that encoded by the nucleotide sequences shown in Appendix A. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in Appendix B. In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 50% identical to the nucleotide sequence designated RXA00777 (SEQ ID NO:5), a nucleotide sequence which is greater than and/or at least 40% identical to the nucleotide sequence designated RXA02439 (SEQ ID NO:17), and a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00002 (SEQ ID NO:23). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated

percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* MCT nucleotide sequences shown in Appendix A, it will be appreciated by one of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of MCT proteins may exist within a population (*e.g.*, the *C. glutamicum* population). Such genetic polymorphism in the MCT gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an MCT protein, preferably a *C. glutamicum* MCT protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the MCT gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in MCT that are the result of natural variation and that do not alter the functional activity of MCT proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* MCT DNA of the invention can be isolated based on their homology to the *C. glutamicum* MCT nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of Appendix A. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent

hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a sequence of Appendix A corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* MCT protein.

In addition to naturally-occurring variants of the MCT sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of Appendix A, thereby leading to changes in the amino acid sequence of the encoded MCT protein, without altering the functional ability of the MCT protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Appendix A. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the MCT proteins (Appendix B) without altering the activity of said MCT protein, whereas an "essential" amino acid residue is required for MCT protein activity. Other amino acid residues, however, (e.g., those that are not conserved or only semi-conserved in the domain having MCT activity) may not be essential for activity and thus are likely to be amenable to alteration without altering MCT activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MCT proteins that contain changes in amino acid residues that are not essential for MCT activity. Such MCT proteins differ in amino acid sequence from a sequence contained in Appendix B yet retain at least one of the MCT activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of Appendix B and is capable of participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences in Appendix B, more preferably at least about 60-70% homologous to one of the sequences in Appendix B, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of the sequences in Appendix B, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the sequences in Appendix B.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the sequences of Appendix B and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the sequences of Appendix B) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the sequence selected from Appendix B), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an MCT protein homologous to a protein sequence of Appendix B can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Appendix A such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the sequences of Appendix A by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an MCT protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MCT coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an MCT activity described herein to identify mutants that retain MCT activity. Following mutagenesis of one of the sequences of Appendix A, the encoded protein can be expressed recombinantly and the activity of the

protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding MCT proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire MCT coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MCT protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of NO. 3 (RXA00777) comprises nucleotides 1 to 1065). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding MCT. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding MCT disclosed herein (*e.g.*, the sequences set forth in Appendix A), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MCT mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MCT mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MCT mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-

carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MCT protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are

capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave MCT mRNA transcripts to thereby inhibit translation of MCT mRNA. A ribozyme having specificity for an MCT-encoding nucleic acid can be designed based upon the nucleotide sequence of an MCT DNA disclosed herein (*i.e.*, NO. 3 (RXA00777 in Appendix A)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MCT-encoding mRNA.

See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, MCT mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, MCT gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MCT nucleotide sequence (*e.g.*, an MCT promoter and/or enhancers) to form triple helical structures that prevent transcription of an MCT gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MCT protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector.

However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

5 The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of
10 interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185,
15 Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI^q*-, *T7*-, *T5*-, *T3*-, *gal*-, *trc*-, *ara*-, *SP6*-, *amy*, *SPO2*, λ -*P_R*- or λ *P_L*, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as *ADC1*, *MF α* , *AC*, *P-60*, *CYC1*, *GAPDH*, *TEF*, *rp28*, *ADH*, promoters from plants such as *CaMV/35S*, *SSU*, *OCS*, *lib4*, *usp*, *STLS1*, *B33*, *nos* or *ubiquitin*- or *phaseolin*-promoters. It is also possible to use
20 artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described
25 herein (*e.g.*, MCT proteins, mutant forms of MCT proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of MCT proteins in prokaryotic or eukaryotic cells. For example, MCT genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.*
35 (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic

Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* –mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the MCT protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant MCT protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89 ; and

Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the MCT protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (IBSN 0 444 904018).

Alternatively, the MCT proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.*

(1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the MCT proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the
5 spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHIac+,
10 pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York IBSN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC
15 (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F.,
20 and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed.*, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type
25 (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and
30 Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddie (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and
35 European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990)

Science 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to MCT mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an MCT protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to one of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid,

transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an MCT protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an MCT gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MCT gene. Preferably, this MCT gene is a *Corynebacterium glutamicum* MCT gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous MCT gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a “knock out” vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MCT gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous MCT protein). In the homologous recombination vector, the altered portion of the MCT gene is flanked at its 5’ and 3’ ends by additional nucleic acid of the MCT gene to allow for homologous recombination to occur between the exogenous MCT gene carried by the vector and an endogenous MCT gene in a microorganism. The additional flanking MCT nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5’ and 3’ ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and

cells in which the introduced MCT gene has homologously recombined with the endogenous MCT gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene.

- 5 For example, inclusion of an MCT gene on a vector placing it under control of the lac operon permits expression of the MCT gene only in the presence of IPTG. Such regulatory systems are well known in the art.

- In another embodiment, an endogenous MCT gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that
10 expression of its protein product does not occur. In another embodiment, an endogenous or introduced MCT gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MCT protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MCT gene in a microorganism has been altered (*e.g.*, by deletion,
15 truncation, inversion, or point mutation) such that the expression of the MCT gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described MCT gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

- 20 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an MCT protein. Accordingly, the invention further provides methods for producing MCT proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an MCT protein has
25 been introduced, or into which genome has been introduced a gene encoding a wild-type or altered MCT protein) in a suitable medium until MCT protein is produced. In another embodiment, the method further comprises isolating MCT proteins from the medium or the host cell.

30 *C. Isolated MCT Proteins*

- Another aspect of the invention pertains to isolated MCT proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when
35 chemically synthesized. The language "substantially free of cellular material" includes preparations of MCT protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the

language "substantially free of cellular material" includes preparations of MCT protein having less than about 30% (by dry weight) of non-MCT protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-MCT protein, still more preferably less than about 10% of non-MCT protein, and most preferably less than about 5% non-MCT protein. When the MCT protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of MCT protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of MCT protein having less than about 30% (by dry weight) of chemical precursors or non-MCT chemicals, more preferably less than about 20% chemical precursors or non-MCT chemicals, still more preferably less than about 10% chemical precursors or non-MCT chemicals, and most preferably less than about 5% chemical precursors or non-MCT chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the MCT protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* MCT protein in a microorganism such as *C. glutamicum*.

An isolated MCT protein or a portion thereof of the invention can participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an MCT protein of the invention has an amino acid sequence shown in Appendix B. In yet another preferred embodiment, the MCT protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A. In still another preferred embodiment, the MCT protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably

at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more

- 5 homologous to one of the nucleic acid sequences of Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The
- 10 preferred MCT proteins of the present invention also preferably possess at least one of the MCT activities described herein. For example, a preferred MCT protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A, and which can participate in the metabolism of compounds necessary for
- 15 the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or which has one or more of the activities set forth in Table 1.

- In other embodiments, the MCT protein is substantially homologous to an amino acid sequence of Appendix B and retains the functional activity of the protein of one of
- 20 the sequences of Appendix B yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the MCT protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or
- 25 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B and which has at least one of the MCT activities described herein. Ranges and identity values intermediate to the
- 30 above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence
- 35 of Appendix B.

Biologically active portions of an MCT protein include peptides comprising amino acid sequences derived from the amino acid sequence of an MCT protein, *e.g.*,

the an amino acid sequence shown in Appendix B or the amino acid sequence of a protein homologous to an MCT protein, which include fewer amino acids than a full length MCT protein or the full length protein which is homologous to an MCT protein, and exhibit at least one activity of an MCT protein. Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an MCT protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an MCT protein include one or more selected domains/motifs or portions thereof having biological activity.

MCT proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the MCT protein is expressed in the host cell. The MCT protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MCT protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MCT protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-MCT antibody, which can be produced by standard techniques utilizing an MCT protein or fragment thereof of this invention.

The invention also provides MCT chimeric or fusion proteins. As used herein, an MCT "chimeric protein" or "fusion protein" comprises an MCT polypeptide operatively linked to a non-MCT polypeptide. An "MCT polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an MCT protein, whereas a "non-MCT polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the MCT protein, *e.g.*, a protein which is different from the MCT protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the MCT polypeptide and the non-MCT polypeptide are fused in-frame to each other. The non-MCT polypeptide can be fused to the N-terminus or C-terminus of the MCT polypeptide. For example, in one embodiment the fusion protein is a GST-MCT fusion protein in which the MCT sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant MCT proteins. In another embodiment, the fusion protein is an MCT protein containing a heterologous signal sequence at its N-terminus. In certain host cells

(e.g., mammalian host cells), expression and/or secretion of an MCT protein can be increased through use of a heterologous signal sequence.

Preferably, an MCT chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). An MCT-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MCT protein.

Homologues of the MCT protein can be generated by mutagenesis, e.g., discrete point mutation or truncation of the MCT protein. As used herein, the term "homologue" refers to a variant form of the MCT protein which acts as an agonist or antagonist of the activity of the MCT protein. An agonist of the MCT protein can retain substantially the same, or a subset, of the biological activities of the MCT protein. An antagonist of the MCT protein can inhibit one or more of the activities of the naturally occurring form of the MCT protein, by, for example, competitively binding to a downstream or upstream member of the cell membrane component metabolic cascade which includes the MCT protein, or by binding to an MCT protein which mediates transport of compounds across such membranes, thereby preventing translocation from taking place.

In an alternative embodiment, homologues of the MCT protein can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of the MCT protein for MCT protein agonist or antagonist activity. In one embodiment, a variegated library of MCT variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MCT variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MCT sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display) containing the set of MCT sequences therein.

There are a variety of methods which can be used to produce libraries of potential MCT homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential MCT sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the MCT protein coding can be used to generate a variegated population of MCT fragments for screening and subsequent selection of homologues of an MCT protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MCT coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the MCT protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of MCT homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MCT homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated MCT library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of
 5 genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of MCT protein regions required for function; modulation of an MCT protein activity; modulation of the metabolism of one or more cell membrane components; modulation of the transmembrane transport of one or more compounds; and modulation of cellular
 10 production of a desired compound, such as a fine chemical.

The MCT nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides
 15 the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.

Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to
 20 pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the
 25 body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria
 30 in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the
 35 presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules

in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The MCT nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic and transport processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the MCT nucleic acid molecules of the invention may result in the production of MCT proteins having functional differences from the wild-type MCT proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an MCT protein, either by interacting with the protein itself or a substrate or binding partner of the MCT protein, or by modulating the transcription or translation of an MCT nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more MCT proteins of the invention is contacted with one or more test

compounds, and the effect of each test compound on the activity or level of expression of the MCT protein is assessed.

There are a number of mechanisms by which the alteration of an MCT protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. Recovery of fine chemical compounds from large-scale cultures of *C. glutamicum* is significantly improved if *C. glutamicum* secretes the desired compounds, since such compounds may be readily purified from the culture medium (as opposed to extracted from the mass of *C. glutamicum* cells). By either increasing the number or the activity of transporter molecules which export fine chemicals from the cell, it may be possible to increase the amount of the produced fine chemical which is present in the extracellular medium, thus permitting greater ease of harvesting and purification. Conversely, in order to efficiently overproduce one or more fine chemicals, increased amounts of the cofactors, precursor molecules, and intermediate compounds for the appropriate biosynthetic pathways are required. Therefore, by increasing the number and/or activity of transporter proteins involved in the import of nutrients, such as carbon sources (*i.e.*, sugars), nitrogen sources (*i.e.*, amino acids, ammonium salts), phosphate, and sulfur, it may be possible to improve the production of a fine chemical, due to the removal of any nutrient supply limitations on the biosynthetic process. Further, fatty acids and lipids are themselves desirable fine chemicals, so by optimizing the activity or increasing the number of one or more MCT proteins of the invention which participate in the biosynthesis of these compounds, or by impairing the activity of one or more MCT proteins which are involved in the degradation of these compounds, it may be possible to increase the yield, production, and/or efficiency of production of fatty acid and lipid molecules from *C. glutamicum*.

The engineering of one or more MCT genes of the invention may also result in MCT proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, the normal biochemical processes of metabolism result in the production of a variety of waste products (*e.g.*, hydrogen peroxide and other reactive oxygen species) which may actively interfere with these same metabolic processes (for example, peroxynitrite is known to nitrate tyrosine side chains, thereby inactivating some enzymes having tyrosine in the active site (Groves, J.T. (1999) *Curr. Opin. Chem. Biol.* 3(2): 226-235). While these waste products are typically excreted, the *C. glutamicum* strains utilized for large-scale fermentative production are optimized for the overproduction of one or more fine chemicals, and thus may produce more waste products than is typical for a wild-type *C. glutamicum*. By optimizing the activity of one or more MCT proteins of the invention

which are involved in the export of waste molecules, it may be possible to improve the viability of the cell and to maintain efficient metabolic activity. Also, the presence of high intracellular levels of the desired fine chemical may actually be toxic to the cell, so by increasing the ability of the cell to secrete these compounds, one may improve the viability of the cell.

Further, the MCT proteins of the invention may be manipulated such that the relative amounts of various lipid and fatty acid molecules produced are altered. This may have a profound effect on the lipid composition of the membrane of the cell. Since each type of lipid has different physical properties, an alteration in the lipid composition of a membrane may significantly alter membrane fluidity. Changes in membrane fluidity can impact the transport of molecules across the membrane, which, as previously explicated, may modify the export of waste products or the produced fine chemical or the import of necessary nutrients. Such membrane fluidity changes may also profoundly affect the integrity of the cell; cells with relatively weaker membranes are more vulnerable in the large-scale fermentor environment to mechanical stresses which may damage or kill the cell. By manipulating MCT proteins involved in the production of fatty acids and lipids for membrane construction such that the resulting membrane has a membrane composition more amenable to the environmental conditions extant in the cultures utilized to produce fine chemicals, a greater proportion of the *C. glutamicum* cells should survive and multiply. Greater numbers of *C. glutamicum* cells in a culture should translate into greater yields, production, or efficiency of production of the fine chemical from the culture.

The aforementioned mutagenesis strategies for MCT proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MCT nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, Appendices, and the sequence listing cited throughout this application are hereby incorporated by reference.

5

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

10 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,
15 2.46 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l NaCl, 2 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 0.2 g/l CaCl_2 , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $\text{FeSO}_4 \times \text{H}_2\text{O}$, 10 mg/l $\text{ZnSO}_4 \times 7 \text{H}_2\text{O}$, 3 mg/l $\text{MnCl}_2 \times 4 \text{H}_2\text{O}$, 30 mg/l H_3BO_3 , 20 mg/l $\text{CoCl}_2 \times 6 \text{H}_2\text{O}$, 1 mg/l $\text{NiCl}_2 \times 6 \text{H}_2\text{O}$, 3 mg/l $\text{Na}_2\text{MoO}_4 \times 2 \text{H}_2\text{O}$, 500 mg/l complexing agent
20 (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
25 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by
30 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20
35 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

5

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.*, Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

20

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (*see e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

25

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g.* *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

30

35

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous
5 plasmids (as e.g., pHM1519 or pBL1) which replicate autonomously (for review see, e.g.,
Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli*
and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for
E. coli (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold
Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in
10 Molecular Biology", John Wiley & Sons) to which a origin or replication for and a
suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication
are preferably taken from endogenous plasmids isolated from *Corynebacterium* and
Brevibacterium species. Of particular use as transformation markers for these species are
genes for kanamycin resistance (such as those derived from the Tn5 or Tn903
15 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones —
Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the
literature of the construction of a wide variety of shuttle vectors which replicate in both *E.*
coli and *C. glutamicum*, and which can be used for several purposes, including gene over-
expression (for reference, see e.g., Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597,
20 Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*,
102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle
vectors described above and to introduce such a hybrid vectors into strains of
Corynebacterium glutamicum. Transformation of *C. glutamicum* can be achieved by
25 protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311),
electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in
cases where special vectors are used, also by conjugation (as described e.g. in Schäfer,
A *et al.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle
vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum*
30 (using standard methods well-known in the art) and transforming it into *E. coli*. This
transformation step can be performed using standard methods, but it is advantageous to
use an Mcr-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol.*
Biol. 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which
35 comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the
gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980)
Proc. Natl. Acad. Sci. USA 77(12): 7176-7180). In addition, genes may be

overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other
5 *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by
10 sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in
15 Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on
20 the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York), in which a primer
25 designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the
30 mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel
35 *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which

specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

5

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) “The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook “Applied Microbiol. Physiology, A

Practical Approach (eds. P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

5 All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or 15 NH₄OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the microorganisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This 20 time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 25 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

30 If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 35 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*. Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) *Enzymkinetik*, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of Enzymatic Analysis*, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining

- methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example, Ullman, *Encyclopedia of Industrial Chemistry*, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in:
- 5 Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) *Biotechnology*, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) *Bioseparations: downstream processing for biotechnology*, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) *Recovery processes for biological materials*, John Wiley and Sons;
- 10 J.A. and Henry, J.D. (1988) *Biochemical separations*, in: *Ullmann's Encyclopedia of Industrial Chemistry*, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) *Separation and purification techniques in biotechnology*, Noyes Publications.)

- In addition to the measurement of the final product of fermentation, it is also
- 15 possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (e.g., sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and
- 20 growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in *Applied Microbial Physiology, A Practical Approach*, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

25

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

- Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the
- 30 culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum* cells, then the cells are removed from the culture by low-speed centrifugation, and the
- 35 supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on

a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to MCT nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MCT protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped

BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM, described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins*. John Wiley and Sons: New York). The gene sequences of the invention were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP

(global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the

synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

5 The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

15 The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

25 The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing

35

polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (e.g., ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, e.g., Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (e.g., different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (e.g., metabolic)

situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

- 5 Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an
5 MCT protein, or a portion thereof, provided that the nucleic acid molecule does not
consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule
10 encodes an MCT protein involved in the production of a fine chemical.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the
group consisting of those sequences set forth in Appendix A, or a portion thereof,
provided that the nucleic acid molecule does not consist of any of the F-designated
15 genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected
from the group consisting of those sequences set forth in Appendix B, provided that
the nucleic acid molecule does not consist of any of the F-designated genes set forth
20 in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant
of a polypeptide selected from the group of amino acid sequences consisting of those
sequences set forth in Appendix B, provided that the nucleic acid molecule does not
25 consist of any of the F-designated genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least
50% homologous to a nucleotide sequence selected from the group consisting of
those sequences set forth in Appendix A, or a portion thereof, provided that the
30 nucleic acid molecule does not consist of any of the F-designated genes set forth in
Table 1.
7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides
of a nucleic acid comprising a nucleotide sequence selected from the group
35 consisting of those sequences set forth in Appendix A, provided that the nucleic acid
molecule does not consist of any of the F-designated genes set forth in Table 1.

8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1
5 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of claim 1.
11. The vector of claim 10, which is an expression vector.
10
12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium*
15 or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule
20 results in the modulation in production of a fine chemical from said cell.
16. The host cell of claim 15, wherein said fine chemical is selected from the group
consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine
and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated
fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors,
25 polyketides, and enzymes.
17. A method of producing a polypeptide comprising culturing the host cell of claim 12
in an appropriate culture medium to, thereby, produce the polypeptide.
18. An isolated MCT polypeptide from *Corynebacterium glutamicum*, or a portion
30 thereof.
19. The polypeptide of claim 18, wherein said polypeptide is involved in the production
of a fine chemical production.
35

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 5 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 10 22. The isolated polypeptide of claim 18, further comprising heterologous amino acid sequences.
- 15 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.
- 20 24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 25 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 30 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
- 35 28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.

29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*, *Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*, *Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*, *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of the sequences set forth in Appendix A or Appendix B in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule is disrupted.

5 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth in Appendix A.

10 38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

15

***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING PROTEINS INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT**

Abstract of the Disclosure

5

Isolated nucleic acid molecules, designated MCT nucleic acid molecules, which encode novel MCT proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MCT nucleic acid molecules, and host cells into which the expression
10 vectors have been introduced. The invention still further provides isolated MCT proteins, mutated MCT proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MCT genes in this organism.

Customer Number: 000959

Attorney's
Docket No. BGI-131CP

DECLARATION, PETITION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

**CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED
IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT**

X is attached hereto.

— was filed on _____ as

Application Serial No. _____

and was amended on _____
(if applicable)

I do not know and do not believe that the subject matter of this application was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date of this application, or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date of this application on an application filed more than twelve months (six months if this application is for a design) before the filing of this application; and I acknowledge my duty to disclose information of which I am aware which is material to the examination of this application, that no application for patent or inventor's certificate on the subject matter of this application has been filed by me or my representatives or assigns in any country foreign to the United States, except those identified below, and that I have reviewed and understand the contents of the specification, including the claims as amended by any amendment referred to herein.

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

CLAIM OF BENEFIT OF EARLIER FOREIGN APPLICATION(S)

I hereby claim priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below, and have also identified below any foreign application(s) for patent or inventor's certificate filed by me on the same subject matter having a filing date before that of the application(s) from which priority is claimed.

Check one:

☐ no such applications have been filed.

☒ such applications have been filed as follows

EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED WITHIN 12 MONTHS (6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION

Country	Application Number	Date of Filing (month,day,year)	Priority Claimed Under 35 USC 119
DE	19930487.4	07/01/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19930489.0	07/01/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931549.3	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931550.7	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19932134.5	07/09/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19941379.7	08/31/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19942088.2	09/03/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19942097.1	09/03/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>

ALL FOREIGN APPLICATION(S), IF ANY FILED MORE THAN 12 MONTHS (6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION

CLAIM FOR BENEFIT OF U.S. PROVISIONAL APPLICATION(S)

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

60/141,031
(Application Serial No.)

June 25, 1999
(Filing Date)

60/143,262
(Application Serial No.)

July 9, 1999
(Filing Date)

60/151,281
(Application Serial No.)

August 27, 1999
(Filing Date)

CLAIM FOR BENEFIT OF EARLIER U.S./PCT APPLICATION(S)

I hereby claim the benefit under Title 35, United States Code, §120 of any earlier United States application(s) or PCT international application(s) designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the earlier application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date(s) of the earlier application(s) and the national or PCT international filing date of this application. As to subject matter of this application which is common to my earlier application(s), if any, described below, I do not know and do not believe that the same was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date(s) of said earlier application(s), or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date(s) of said earlier application(s) on an application filed more than twelve months (six months if this application is for a design) before the filing of said earlier application(s); and I acknowledge that no application for patent or inventor's certificate on said subject matter has been filed by me or my representatives or assigns in any country foreign to the United States except those identified herein.

_____ (Application Serial No.)	_____ (Filing Date)	_____ (Status) (patented,pending,aband.)
_____ (Application Serial No.)	_____ (Filing Date)	_____ (Status) (patented,pending,aband.)

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

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Direct Telephone Calls to: (name and telephone number)

Giulio A. DeConti, Jr., Esq., (617) 227-7400

Wherefore I petition that letters patent be granted to me for the invention or discovery described and claimed in the attached specification and claims, and hereby subscribe my name to said specification and claims and to the foregoing declaration, power of attorney, and this petition.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the application of: Markus Pompejus *et al.*

Serial No.: Not Yet Assigned

Filed: Herewith

For: "*Corynebacterium Glutamicum Genes Encoding Proteins Involved in Membrane Synthesis and Membrane Transport*"

Attorney Docket No.: BGI-131CP

Group Art Unit: Not Yet Assigned

Examiner: Not Yet Assigned

Assistant Commissioner for Patents

BOX SEQUENCE LISTING

Washington, DC 20231

TRANSMITTAL LETTER FOR ZIP DISK OF SEQUENCE LISTING

Dear Sir:

Enclosed is a Zip disk which contains a computer readable form of the Sequence Listing for the patent application filed herewith. The Sequence Listing complies with the requirements of 37 C.F.R. §1.821. The material on this Zip disk is identical in substance to the paper copy of the Sequence Listing appearing on pages 1-602 which is submitted herewith, as required by 37 CFR §1.821(f). The computer readable form of the Sequence Listing contained on the enclosed Zip disk is understood to comply with the requirements of §1.824(d).

"Express Mail" mailing label number EL 373 207 273 US

Date of Deposit June 23, 2000

I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 on the date indicated above and is addressed to: Box Sequence Listing, Assistant Commissioner For Patents, Washington, D.C. 20231

Nelson Barros
Signature

Nelson Barros
Please Print Name of Person Signing

LAHIVE & COCKFIELD, LLP

Attorneys at Law

By:

Elizabeth A. Hanley
Registration No. 33, 505
28 State Street
Boston, MA 02109

Date: **June 23, 2000**

TABLE 1: GENES IN THE APPLICATION

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1	2	RXA00775	GR00205	6057	5287	PHOSPHATE TRANSPORT ATP-BINDING PROTEIN PSTB
3	4	RXA00776	GR00205	7016	6096	PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN PSTA
5	6	RXA00777	GR00205	8098	7034	PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN PSTC
7	8	RXA00774	GR00205	4546	5199	PHOSPHATE TRANSPORT SYSTEM REGULATORY PROTEIN
9	10	RXA00204	GR00032	3783	2212	RIBOSE TRANSPORT ATP-BINDING PROTEIN RBSA
11	12	RXA02438	GR00709	3236	2478	RIBOSE TRANSPORT ATP-BINDING PROTEIN RBAA
13	14	RXA00203	GR00032	2152	1241	RIBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RBSC
15	16	RXA00270	GR00041	2720	1833	RIBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RBSC
17	18	RXA02439	GR00709	4258	3236	RIBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RBSC
19	20	RXN02994	VV0070	2	724	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
21	22	F RXA01245	GR00360	2	1768	COPPER/POTASSIUM-TRANSPORTING ATPASE B (EC 3.6.1.36)

Lipoprotein and Lipopolysaccharide synthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
23	24	RXA00002	GR00001	2278	1595	DOLICHOL-PHOSPHATE MANNOSYL TRANSFERASE (EC 2.4.1.83) / APOLIPROTEIN N-ACYL TRANSFERASE (EC 2.3.1.-)
25	26	RXA00160	GR00024	4044	4616	LIPOPROTEIN NLPd/LPB HOMOLOG PRECURSOR
27	28	RXA00345	GR00064	90	1040	Zn-binding lipoprotein
29	30	RXA00413	GR00092	3859	2963	OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR
31	32	RXA00482	GR00119	18891	18244	OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR
33	34	RXN01164	VV0117	15894	14260	DOLICHOL-PHOSPHATE MANNOSYL TRANSFERASE (EC 2.4.1.83) / APOLIPROTEIN N-ACYL TRANSFERASE (EC 2.3.1.-)
35	36	F RXA01164	GR00332	1579	5	DOLICHOL-PHOSPHATE MANNOSYL TRANSFERASE (EC 2.4.1.83) / APOLIPROTEIN N-ACYL TRANSFERASE (EC 2.3.1.-)
37	38	RXN01168	VV0117	14224	13415	DOLICHOL-PHOSPHATE MANNOSYL TRANSFERASE (EC 2.4.1.83) / APOLIPROTEIN N-ACYL TRANSFERASE (EC 2.3.1.-)
39	40	F RXA01168	GR00333	1285	566	DOLICHOL-PHOSPHATE MANNOSYL TRANSFERASE (EC 2.4.1.83) / APOLIPROTEIN N-ACYL TRANSFERASE (EC 2.3.1.-)
41	42	RXN02062	VV0222	3159	1990	Lipopolysaccharide N-acetylglucosaminyltransferase
43	44	F RXA02062	GR00626	3159	1990	Lipopolysaccharide N-acetylglucosaminyltransferase
45	46	RXA02222	GR00651	9420	9794	PUTATIVE HOST CELL SURFACE-EXPOSED LIPOPROTEIN
47	48	RXA02313	GR00665	5812	4592	Lipopolysaccharide N-acetylglucosaminyltransferase
49	50	RXA02491	GR00720	902	2155	Lipopolysaccharide N-acetylglucosaminyltransferase
51	52	RXN02595	VV0098	11098	9935	Lipopolysaccharide N-acetylglucosaminyltransferase
53	54	F RXA02595	GR00741	19052	19702	Lipopolysaccharide N-acetylglucosaminyltransferase
55	56	RXA02616	GR00745	598	1308	LIPOPROTEIN NLPD PRECURSOR
57	58	RXA02627	GR00747	2981	2139	DTXR/IRON-REGULATED LIPOPROTEIN PRECURSOR
59	60	RXA02650	GR00752	1460	2038	LIPOPROTEIN SIGNAL PEPTIDASE (EC 3.4.23.36)
61	62	RXA01094	GR00306	2703	1756	PROLIPROTEIN DIACYLGLYCERYL TRANSFERASE (EC 2.4.99.-)

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
63	64	RXN00934	VV0171	15181	14099	(AE000805) LPS biosynthesis RfbU related protein [Methanobacterium thermoautotrophicum]
65	66	F RXA00934	GR00253	6835	6047	(AE000805) LPS biosynthesis RfbU related protein [Methanobacterium thermoautotrophicum]
67	68	RXA02605	GR00742	11557	12051	ANTIGEN 85-B PRECURSOR

ABC-Transporter

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
69	70	RXN00525	VV0079	26304	27566	Hypothetical ABC Transporter Permease Protein
71	72	F RXA00525	GR00136	664	5	Hypothetical ABC Transporter Permease Protein
73	74	F RXA00556	GR00146	1	594	Hypothetical ABC Transporter Permease Protein
75	76	RXA02750	GR00764	5079	5894	Hypothetical ABC Transporter Permease Protein
77	78	RXN02096	VV0126	20444	22135	Hypothetical ABC Transporter Permease Protein
79	80	F RXA02096	GR00629	15458	16774	Hypothetical ABC Transporter Permease Protein
81	82	RXA02562	GR00732	796	1515	PUTATIVE ABC TRANSPORTER
83	84	RXA00950	GR00260	173	1078	similar to ABC transporter (ATP-binding protein) START CODON GTG
85	86	RXA02119	GR00636	4222	2582	similar to ABC transporter (ATP-binding protein)
87	88	RXA01185	GR00338	2451	1594	ATP-BINDING PROTEIN
89	90	RXN00412	VV0086	53923	52844	Hypothetical Amino Acid ABC Transporter ATP-Binding Protein
91	92	F RXA00412	GR00092	2764	1685	ATP-BINDING PROTEIN ABC
93	94	RXN02925	VV0104	543	2759	COPPER/POTASSIUM-TRANSPORTING ATPASE B (EC 3.6.1.36)
95	96	RXN00939	VV0079	45152	43917	COPPER/POTASSIUM-TRANSPORTING ATPASE B (EC 3.6.1.36)
97	98	F RXA00939	GR00256	1501	1334	COPPER/POTASSIUM-TRANSPORTING ATPASE B (EC 3.6.1.36)
99	100	RXN01323	VV0082	4321	6585	COPPER/POTASSIUM-TRANSPORTING ATPASE B (EC 3.6.1.36)
101	102	F RXA01323	GR00385	1175	3439	similar to heavy metal-transporting ATPase
103	104	RXN00702	VV0005	12478	10772	COBAL T TRANSPORT ATP-BINDING PROTEIN CBIO
105	106	F RXA00702	GR00182	2165	846	COBAL T TRANSPORT ATP-BINDING PROTEIN CBIO
107	108	RXN00828	VV0180	1376	1828	COBAL T TRANSPORT ATP-BINDING PROTEIN CBIO
109	110	F RXA00828	GR00223	1687	1319	COBAL T TRANSPORT ATP-BINDING PROTEIN CBIO
111	112	RXN03020	VV0139	606	4	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
113	114	RXN00726	VV0188	1	591	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
115	116	RXN02570	VV0101	11699	12340	MALTOSE TRANSPORT SYSTEM PERMEASE PROTEIN MALF
117	118	RXN02354	VV0095	473	1306	MALTOSE TRANSPORT SYSTEM PERMEASE PROTEIN MALG
119	120	F RXA02354	GR00682	4023	1261	MALTOSE TRANSPORT SYSTEM PERMEASE PROTEIN MALG
121	122	RXN00001	VV0196	4023	2896	MALTOSE/MALTODEXTRIN TRANSPORT ATP-BINDING PROTEIN MALK
123	124	F RXA00001	GR00001	1386	259	SN-GLYCEROL-3-PHOSPHATE TRANSPORT ATP-BINDING PROTEIN MALK
125	126	RXN02356	VV0051	1868	873	MALTOSE/MALTODEXTRIN TRANSPORT ATP-BINDING PROTEIN MALK
127	128	RXN02455	VV0196	1273	5	MALTOSE-BINDING PROTEIN PRECURSOR
129	130	RXN02795	VV0176	29237	27801	OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN APPF
131	132	F RXA02795	GR00778	3	1097	OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN APPF
133	134	RXN01939	VV0139	22695	20965	OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN OPDP
135	136	F RXA00761	GR00203	8530	9120	OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN OPDP
137	138	F RXA01939	GR00556	2042	1440	OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN OPDP

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
139	140	RXN00759	VV0139	24645	23722	OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPB
141	142	F RXA00759	GR00203	6580	7503	OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPB
143	144	RXN00431	VV0112	8987	8199	O-ANTIGEN EXPORT SYSTEM ATP-BINDING PROTEIN RFB
145	146	F RXA00431	GR00099	119	793	ABCA PROTEIN two-component ABC transporter involved in the metabolism of two wall leishic acids
147	148	RXN00732	VV0132	1	1647	PROBABLE TRANSPORT ATP-BINDING PROTEIN MSBA
149	150	F RXA00732	GR00196	826	5	PROBABLE TRANSPORT ATP-BINDING PROTEIN MSBA
151	152	F RXA00734	GR00197	863	411	Hypothetical ABC Transporter ATP-Binding Protein
153	154	RXN01808	VV0216	3	1151	PUTATIVE ABC TRANSPORTER
155	156	F RXA01808	GR00509	8993	7875	PUTATIVE ABC TRANSPORTER
157	158	RXN02975	VV0231	252	4	Hypothetical ABC Transporter ATP-Binding Protein
159	160	RXN03116	VV0090	38067	38675	MALTOSE/MALTODEXTRIN TRANSPORT ATP-BINDING PROTEIN MALK
161	162	RXN03108	VV0077	5535	5801	NITRATE TRANSPORT ATP-BINDING PROTEIN NRTD
163	164	RXN03129	VV0122	24042	22819	SN-GLYCEROL-3-PHOSPHATE TRANSPORT ATP-BINDING PROTEIN UGPC
165	166	F RXA01890	GR00541	874	155	SN-GLYCEROL-3-PHOSPHATE TRANSPORT ATP-BINDING PROTEIN UGPC
167	168	RXN02945	VV0180	492	1424	COBALT TRANSPORT ATP-BINDING PROTEIN CBIO

Other transporters

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
169	170	RXA01247	GR00361	256	489	COPPER/POTASSIUM-TRANSPORTING ATPASE B (EC 3.6.1.36)
171	172	RXN00099	VV0129	18876	17704	CYANATE TRANSPORT PROTEIN CYNX
173	174	F RXA00099	GR00014	8172	9344	CYANATE TRANSPORT PROTEIN CYNX
175	176	RXA00634	GR00166	3732	5114	DI-TRYPEPTIDE TRANSPORTER
177	178	RXA02451	GR00710	3484	5007	DI-TRYPEPTIDE TRANSPORTER
179	180	RXA02394	GR00697	1895	585	DICARBOXYLATE TRANSPORTER
181	182	RXA01012	GR00288	3748	2108	DIPEPTIDE TRANSPORT ATP-BINDING PROTEIN DPPD
183	184	RXA02660	GR00753	548	1186	DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPB
185	186	RXA02661	GR00753	1239	1457	DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPB
187	188	RXA02034	GR00619	1787	822	DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC
189	190	RXA01013	GR00288	4549	3765	DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC
191	192	RXN02933	VV0176	30042	29233	DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC
193	194	F RXA02033	GR00619	800	12	DIPEPTIDE TRANSPORTER PROTEIN DPPB
195	196	RXA01006	GR00287	862	5	D-SERINE/D-ALANINE/GLYCINE TRANSPORTER
197	198	RXA02312	GR00665	4459	3101	FERRIC ANGUINACTIN TRANSPORT SYSTEM PERMEASE PROTEIN FATC
199	200	RXA00090	GR00013	6644	7762	FERRIC ANGUINACTIN TRANSPORT SYSTEM PERMEASE PROTEIN FATD
201	202	RXA00089	GR00013	5656	6654	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
203	204	RXN01285	VV0215	1780	1055	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
205	206	F RXA01285	GR00371	3	545	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
207	208	RXA02728	GR00761	184	996	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
209	210	RXN03080	VV0045	1670	2449	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
211	212	F RXA02864	GR10007	2806	2027	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
213	214	RXN00523	VV0194	1363	338	FERRIC ENTEROBACTIN TRANSPORT PROTEIN FEPC
215	216	F RXA00523	GR00135	30	779	FERRIC ENTEROBACTIN TRANSPORT PROTEIN FEPC

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
217	218	RXA01289	GR00372	2376	3419	FERRIC ENTEROBACTIN TRANSPORT PROTEIN FEPG
219	220	RXA01290	GR00372	3412	4575	FERRIC ENTEROBACTIN TRANSPORT PROTEIN FEPG
221	222	RXA01822	GR00516	6	587	FERRIC ENTEROBACTIN TRANSPORT PROTEIN FEPG
223	224	RXN00466	VV0086	63271	64266	Ferrichrome transport proteins
225	226	F RXA00466	GR00117	947	1933	Ferrichrome transport proteins
227	228	RXN03081	VV0045	2476	2934	FERRIENTEROBACTIN-BINDING PERIPLASMIC PROTEIN PRECURSOR
229	230	F RXA02863	GR10007	2000	1026	Ferrichrome transport proteins
231	232	RXS03221	GR00575	622	5	GALACTOSE-PROTON SYMPORT
233	234	F RXA01986	VV0107	14297	13203	GALACTOSE-PROTON SYMPORT
235	236	RXN02447	GR00710	1	270	GALACTOSE-PROTON SYMPORT
237	238	F RXA02447	GR00771	1	711	GALACTOSE-PROTON SYMPORT
239	240	F RXA02769				D-XYLOSE-PROTON SYMPORT
241	242	RXS03220				D-XYLOSE-PROTON-SYMPORTER
243	244	F RXA02762	GR00768	346	630	GALACTOSE-PROTON SYMPORT
245	246	F RXA02761	GR00768	153	353	GALACTOSE-PROTON SYMPORT
247	248	RXA00123	GR00019	7029	5911	MAGNESIUM AND COBALT TRANSPORT PROTEIN CORA
249	250	RXA02441	GR00709	5940	5284	MANGANESE TRANSPORT SYSTEM ATP-BINDING PROTEIN MNTA
251	252	RXN02442	VV0217	5970	6818	zinc transport system membrane protein
253	254	F RXA02442	GR00709	5970	6818	MANGANESE TRANSPORT SYSTEM MEMBRANE PROTEIN MNTB
255	256	RXA01756	GR00498	2069	762	MG2+ TRANSPORTER MGTE
257	258	RXA02068	GR00627	2	1120	MG2+ TRANSPORTER MGTE
259	260	RXA00665	GR00174	135	572	MG2+/CITRATE COMPLEX SECONDARY TRANSPORTER
261	262	RXA02808	GR00789	1	258	MG2+/CITRATE COMPLEX SECONDARY TRANSPORTER
263	264	RXN00444	VV0112	20785	19949	MOLYBDENUM TRANSPORT SYSTEM PERMEASE PROTEIN MODB
265	266	F RXA00444	GR00106	626	1402	MOLYBDENUM TRANSPORT SYSTEM PERMEASE PROTEIN MODB
267	268	RXN02614	VV0313	5964	5236	TAURINE TRANSPORT ATP-BINDING PROTEIN TAUB
269	270	F RXA02614	GR00743	5964	5236	NITRATE TRANSPORT ATP-BINDING PROTEIN NRTC
271	272	RXN01142	VV0077	5805	6302	NITRATE TRANSPORT ATP-BINDING PROTEIN NRTD
273	274	F RXA01142	GR00320	721	302	NITRATE TRANSPORT ATP-BINDING PROTEIN NRTD
275	276	RXN01141	VV0077	4644	5468	NITRATE TRANSPORT PROTEIN NRTA
277	278	F RXA01135	GR00318	327	4	NITRATE TRANSPORT PROTEIN NRTA
279	280	F RXA01141	GR00319	636	175	NITRATE TRANSPORT PROTEIN NRTA
281	282	RXA00728	GR00193	1658	2449	NOPALINE TRANSPORT SYSTEM PERMEASE PROTEIN NOCM
283	284	RXA02663	GR00753	2059	3453	OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN OPD
285	286	RXA02664	GR00753	3611	4270	OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN OPF
287	288	RXA00760	GR00203	7499	8530	OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPFC
289	290	RXA02035	GR00619	3295	1787	PERIPLASMIC DIPEPTIDE TRANSPORT PROTEIN PRECURSOR
291	292	RXN01002	VV0106	8858	8055	PHOSPHONATES TRANSPORT ATP-BINDING PROTEIN PHNC
293	294	F RXA01002	GR00285	3	419	PHOSPHONATES TRANSPORT ATP-BINDING PROTEIN PHNC
295	296	RXN01000	VV0106	7252	6407	PHOSPHONATES TRANSPORT SYSTEM PERMEASE PROTEIN PHNE
297	298	F RXA01000	GR00284	2	541	PHOSPHONATES TRANSPORT SYSTEM PERMEASE PROTEIN PHNE
299	300	RXA01003	GR00285	419	1222	PHOSPHONATES TRANSPORT SYSTEM PERMEASE PROTEIN PHNE
301	302	RXN00193	VV0371	1	594	POTENTIAL STARCH DEGRADATION PRODUCTS TRANSPORT SYSTEM
303	304	F RXA00193	GR00029	10101	9259	PERMEASE PROTEIN AMYD
						POTENTIAL STARCH DEGRADATION PRODUCTS TRANSPORT SYSTEM
						PERMEASE PROTEIN AMYD

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
305	306	RXN01298	VV0116	2071	1142	POTENTIAL STARCH DEGRADATION PRODUCTS TRANSPORT SYSTEM
307	308	F RXA01298	GR00374	1254	862	PERMEASE PROTEIN AMYD
309	310	F RXA02422	GR00705	8200	8634	POTENTIAL STARCH DEGRADATION PRODUCTS TRANSPORT SYSTEM
311	312	RXN02515	VV0087	962	1717	PERMEASE PROTEIN AMYD
313	314	F RXA02515	GR00723	964	1719	Hypothetical ABC Transporter ATP-Binding Protein
315	316	RXN01995	VV0182	2139	3476	PROBABLE ATP-DEPENDENT TRANSPORTER YCF16
317	318	F RXA01995	GR00584	1362	2015	PUTATIVE 3-(3-HYDROXYPHENYL) PROPIONATE TRANSPORT PROTEIN
319	320	RXA01188	GR00339	1585	482	PUTATIVE 3-(3-HYDROXYPHENYL) PROPIONATE TRANSPORT PROTEIN
321	322	RXA01972	GR00569	2116	1523	PUTATIVE TRANSPORT PROTEIN SGAT
323	324	RXA00311	GR00053	1592	738	QUATERNARY AMINE TRANSPORTER
325	326	RXA00312	GR00053	2066	1641	SHIKIMATE TRANSPORTER
327	328	RXN01411	VV0050	26015	26779	SHIKIMATE TRANSPORTER
329	330	F RXA01411	GR00412	1	327	SHIKIMATE TRANSPORTER
331	332	RXA01900	GR00544	2822	4120	SHIKIMATE TRANSPORTER
333	334	RXA02507	GR00720	19760	21160	SHIKIMATE TRANSPORTER
335	336	RXA00445	GR00107	21	932	SHIKIMATE TRANSPORTER
337	338	RXA02353	GR00682	6	473	SHIKIMATE TRANSPORTER
339	340	RXA01297	GR00374	826	29	SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN
341	342	RXS00088	VV0027	2	877	UGPA
343	344	RXS00372	VV0226	3456	2380	SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN
345	346	RXS02590	VV0098	15313	16248	UGPE
347	348	RXS00758	VV0139	24827	26827	FERRIC ANGUIBACTIN-BINDING PROTEIN PRECURSOR
349	350	RXS01346	VV0123	5120	6694	PERIPLASMIC-IRON-BINDING PROTEIN SHIB
351	352	RXS00912	VV0339	552	280	MALIC ACID TRANSPORT PROTEIN
353	354	RXS00453	VV0076	1173	3521	PERIPLASMIC OLIGOPEPTIDE-BINDING PROTEIN PRECURSOR
355	356	RXS00932	VV0171	13120	13593	potassium efflux system protein phaF
357	358	RXS00479	VV0086	42008	39819	Drug Transporter
359	360	RXS02586	VV0098	19854	20123	Drug Transporter
361	362	RXS02587	VV0098	17807	19897	Drug Transporter
363	364	RXS03042	VV0018	2440	1835	Drug Transporter
365	366	RXS03075	VV0042	2491	3216	Drug Transporter
367	368	RXS03124	VV0108	4	963	Drug Transporter
369	370	RXS03125	VV0108	972	1142	Drug Transporter

Channel Proteins

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
371	372	RXA00596	GR00159	335	787	potassium efflux system protein phaE
373	374	RXA02079	GR00628	9034	9648	CATION EFFLUX SYSTEM PROTEIN CZCD

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<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
375	376	RXA01303	GR00376	1724	390	NITRITE EXTRUSION PROTEIN
377	378	RXA02079	GR00628	9034	9648	CATION EFFLUX SYSTEM PROTEIN CZCD
379	380	RXN00832	VV0180	3133	4182	CALCIUM/PROTON ANTIPORTER
381	382	F RXA00832	GR00224	2239	1685	CALCIUM/PROTON ANTIPORTER
383	384	RXN00378	VV0223	8027	5418	Cation transport ATPases
385	386	F RXA00378	GR00081	3271	1499	Cation transport ATPases
387	388	RXA00942	GR00257	2406	2203	CATION-TRANSPORTING ATPASE PACS (EC 3.6.1.-)
389	390	RXN01338	VV0032	2	1903	CATION-TRANSPORTING ATPASE PACS (EC 3.6.1.-)
391	392	F RXA01338	GR00389	6964	5087	CATION-TRANSPORTING ATPASE PACS (EC 3.6.1.-)
393	394	RXA01625	GR00452	3850	3650	CATION-TRANSPORTING ATPASE PACS (EC 3.6.1.-)
395	396	RXA02220	GR00651	3205	5880	CATION-TRANSPORTING ATPASE PACS (EC 3.6.1.-)
397	398	RXN00980	VV0149	2635	4428	CATION-TRANSPORTING P-TYPE ATPASE PMA1 (EC 3.6.1.-)
399	400	F RXA00980	GR00276	2648	3286	CATION-TRANSPORTING P-TYPE ATPASE B (EC 3.6.1.-)
401	402	RXN02348	VV0078	6027	7910	CUP SYSTEM POTASSIUM UPTAKE PROTEIN
403	404	F RXA02348	GR00677	1719	586	CUP SYSTEM POTASSIUM UPTAKE PROTEIN
405	406	F RXA02344	GR00676	682	5	CUP SYSTEM POTASSIUM UPTAKE PROTEIN
407	408	RXN00960	VV0075	1139	105	PROTON/SODIUM-GLUTAMATE SYMPORT PROTEIN
409	410	F RXA00960	GR00266	563	105	PROTON/SODIUM-GLUTAMATE SYMPORT PROTEIN
411	412	RXA01070	GR00299	2089	704	PROTON/SODIUM-GLUTAMATE SYMPORT PROTEIN
413	414	RXA02628	GR00748	6	410	LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL
415	416	RXN03164	VV0277	1586	2455	POTASSIUM CHANNEL BETA SUBUNIT
417	418	F RXA01395	GR00408	6106	5021	POTASSIUM CHANNEL BETA SUBUNIT

Other membrane proteins

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
419	420	RXA02597	GR00742	2329	542	OUTER MEMBRANE USHER PROTEIN FIMC PRECURSOR
421	422	RXA01454	GR00420	270	4	integral membrane protein
423	424	RXA01455	GR00420	745	284	integral membrane protein
425	426	RXA02684	GR00754	8923	8060	MEMBRANE-BOUND PROTEIN L YTR
427	428	RXN02391	VV0176	3525	3923	(U59457) Pseudomonas aeruginosa ankYrn (ankB) gene, complete cds
429	430	RXN02549	VV0098	3165	5867	[Pseudomonas aeruginosa]
431	432	RXN00808	VV0009	63243	64700	PUTATIVE INTEGRAL MEMBRANE PROTEIN
433	434	RXS01425	VV0050	2679	3563	60 KD INNER-MEMBRANE PROTEIN
435	436	RXS01658	VV0010	44183	42351	membrane protein
437	438	RXS01677	VV0179	12923	12180	membrane protein
439	440	RXS02932	VV0176	23391	24362	Membrane Spanning Protein
441	442	F RXA02402	GR00700	747	4	(AF027868) putative transporter [Bacillus subtilis]
443	444	RXS00654	VV0109	6289	5024	60 KD INNER-MEMBRANE PROTEIN

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	glbB; glbD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenylyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	gluA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	
AF038651	deiAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolyase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	pand	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum pand gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4)1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AI001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP." <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AI004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AI007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AI010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AI132968	cat	Chloramphenicol acetyl transferase	
AI224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AI238250	ndh	NADH dehydrogenase	
AI238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
DI7429		Transposable element IS31831	Veres, A.A. et al. "Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) <i>odhA</i> gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
F01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
F04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and deshydrobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
F04041		Deshydrobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and deshydrobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
L04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isoctiric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isoctiric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
F05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
H05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 199334481-A 1 12/27/93
F06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 199334481-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Homo, N. et al. "Gene DNA participating in integration of membranous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
F08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95

GenBank™ Accession No.	Gene Name	Gene Function	Reference
F08649		Aspartase	Kohama, K. et al "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydropicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydropicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
F12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydropicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydropicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomerase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in <i>Escherichia coli</i> and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the <i>Corynebacterium glutamicum</i> mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in <i>Corynebacterium glutamicum</i> ," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from <i>Corynebacterium glutamicum</i> ," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxR	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the <i>Corynebacterium diphtheriae</i> dtxR from <i>Brevibacterium lactofermentum</i> ," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follette, M.T. et al. "Molecular cloning and nucleotide sequence of the <i>Corynebacterium glutamicum</i> pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthraniolate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	aecD; bmq; yhbw	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbw	Rossol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethyleysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the bmq gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	tpdD	Anthraniolate phosphoribosyltransferase	O'Garra, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 tpd gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIM; cglIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cgIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?;gamma glutamyl kinase;similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thrR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5"-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	copI	PsI protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of PS1 is similar to the <i>Mycobacterium</i> antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GdHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mttA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinyl/diaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascal, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of <i>Corynebacterium glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE, lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahn, H. et al. "D-pantothenate synthesis in <i>Corynebacterium glutamicum</i> and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer <i>Brevibacterium lactofermentum</i> (<i>Corynebacterium glutamicum</i> ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the <i>Corynebacterium glutamicum</i> hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC;ftsQ/divD;ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from <i>Brevibacterium lactofermentum</i> ," <i>Mol. Gen. Gene.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of <i>Corynebacterium glutamicum</i> proline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from <i>Corynebacterium glutamicum</i> : characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from <i>Corynebacterium glutamicum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP." <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynephage 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisbarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmndR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?, SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)

¹ A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniogenes	21054							
Brevibacterium	ammoniogenes	19350							
Brevibacterium	ammoniogenes	19351							
Brevibacterium	ammoniogenes	19352							
Brevibacterium	ammoniogenes	19353							
Brevibacterium	ammoniogenes	19354							
Brevibacterium	ammoniogenes	19355							
Brevibacterium	ammoniogenes	19356							
Brevibacterium	ammoniogenes	21055							
Brevibacterium	ammoniogenes	21077							
Brevibacterium	ammoniogenes	21553							
Brevibacterium	ammoniogenes	21580							
Brevibacterium	ammoniogenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							

Brevibacterium	flavum			B11477						
Brevibacterium	flavum			B11478						
Brevibacterium	flavum	21127								
Brevibacterium	flavum			B11474						
Brevibacterium	heali	15527								
Brevibacterium	ketoglutamicum	21004								
Brevibacterium	ketoglutamicum	21089								
Brevibacterium	ketosoreductum	21914								
Brevibacterium	lactofermentum				70					
Brevibacterium	lactofermentum				74					
Brevibacterium	lactofermentum				77					
Brevibacterium	lactofermentum	21798								
Brevibacterium	lactofermentum	21799								
Brevibacterium	lactofermentum	21800								
Brevibacterium	lactofermentum	21801								
Brevibacterium	lactofermentum			B11470						
Brevibacterium	lactofermentum			B11471						
Brevibacterium	lactofermentum	21086								
Brevibacterium	lactofermentum	21420								
Brevibacterium	lactofermentum	21086								
Brevibacterium	lactofermentum	31269								
Brevibacterium	linens	9174								
Brevibacterium	linens	19391								
Brevibacterium	linens	8377								
Brevibacterium	paraffinolyticum					11160				
Brevibacterium	spec.						717.73			
Brevibacterium	spec.						717.73			
Brevibacterium	spec.	14604								
Brevibacterium	spec.	21860								
Brevibacterium	spec.	21864								
Brevibacterium	spec.	21865								

Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							

Corynebacterium	spec.	31090								
Corynebacterium	spec.	15954							20145	
Corynebacterium	spec.	21857								
Corynebacterium	spec.	21862								
Corynebacterium	spec.	21863								

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saitama, Japan.

<u>ID #</u>	<u>length</u>	<u>Genbank Hit</u>	<u>(NT)</u>
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23-Sep-99

TABLE 4: ALIGNMENT RESULTS

rxa00193	594	GB_PR3:AC005826	177585	AC005826	Homo sapiens clone UWGC rg041403 from 7p14-15, complete sequence.	Homo sapiens	37,012	16-OCT-1998
		GB_HTG2:AC007076	95477	AC007076	Homo sapiens clone DU0698F07, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	Homo sapiens	37,012	5-Jun-99
		GB_HTG2 AC007076	95477	AC007076	Homo sapiens clone DU0698F07, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	Homo sapiens	37,012	5-Jun-99
rxa00203	1035	GB_GSS3:B88972	699	B88972	CIT-HSP-2173C11, TR CIT-HSP Homo sapiens genomic clone 2173C11, genomic survey sequence.	Homo sapiens	41,411	25-Jun-98
		GB_GSS11:AQ290299	642	AQ290299	nbxb0036N17r, genomic survey sequence.	Oryza sativa	38,245	03-DEC-1998
		GB_EST20:AA843374	479	AA843374	aj16e10.s1 Soares,parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1390506 3', mRNA sequence	Homo sapiens	34,874	31-DEC-1998
rxa00204	1695	GB_BA1:SC3F9	19830	AL023862	Streptomyces coelicolor cosmid 3F9.	Streptomyces coelicolor	49,556	10-Feb-99
		GB_BA2:AF160811	10671	AF160811	Bacillus steaerothermophilus L-arabinose transport, ATP binding protein (araG), L-arabinose membrane permease (araH), AraR (araR), L-ribulose 5-steaerothermophilus phosphate 4-epimerase (araD), L-ribulokinase (araB), L-arabinose isomerase (araA), and IS5377 transposase genes, complete cds.	Bacillus	51,004	28-Jul-99
		GB_BA2:MPAE000056	16213	AEO00056	Mycoplasma pneumoniae section 56 of 63 of the complete genome.	Mycoplasma pneumoniae	34,895	18-Nov-96
rxa00270	1011	GB_BA1:MLCB1770	37821	Z70722	Mycobacterium leprae cosmid B1770.	Mycobacterium leprae	37,089	29-Aug-97
		GB_GSS4:AQ681972	452	AQ681972	HS_5503_B2_C02_T7A RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=1079 Col=4 Row=F, genomic survey sequence.	Homo sapiens	40,099	28-Jun-99
		GB_VI:IVU47137	986	U47137	Inkoo virus Prototype KN3641 nucleocapsid protein and non-structural protein genes, complete cds.	Inkoo virus	37,061	22-Aug-96
rxa00311	978	GB_VI:VMVY16780	186986	Y16780	varola minor virus complete genome.	varola minor virus	37,722	2-Sep-99
		GB_VI:VARGC	186103	L22579	Varola major virus (strain Banglades-1975) complete genome.	Varola major virus	38,558	12-Jan-95
		GB_VI:VVCGA	185578	X69198	Varola virus DNA complete genome.	Varola virus	39,518	13-DEC-1996
rxa00312	549	GB_HTG4:AC011190	164409	AC011190	Homo sapiens clone hRRK24_A_1, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces.	Homo sapiens	34,741	19-OCT-1999
		GB_HTG4:AC011190	164409	AC011190	Homo sapiens clone hRRK24_A_1, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces.	Homo sapiens	34,741	19-OCT-1999
		GB_HTG4:AC011190	164409	AC011190	Homo sapiens clone hRRK24_A_1, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces.	Homo sapiens	34,807	19-OCT-1999
rxa00345	1074	GB_HTG2:AC007356	185382	AC007356	Drosophila melanogaster chromosome 2 clone BACR24H09 (D595) RPCI-98 24.H.9 map 49A-49B strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces.	Drosophila melanogaster	36,364	2-Aug-99
		GB_HTG2:AC007356	185382	AC007356	Drosophila melanogaster chromosome 2 clone BACR24H09 (D595) RPCI-98 24.H.9 map 49A-49B strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces.	Drosophila melanogaster	36,364	2-Aug-99
		GB_HTG2:AC005814	183922	AC005814	Drosophila melanogaster chromosome 3 clone BACR48M07 (D471) RPCI-98 48.M.7 map 64A6-64B6 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces	Drosophila melanogaster	38,031	30-Jul-99

TABLE 4: ALIGNMENT RESULTS

rx00378	2733	GB_BA2:ALW243431	26953	AJ243431	Acinetobacter lwofii wzc, wzb, wza, weeA, weeb, wecC, wzx, wzy, weeD, weeE, weef, weeG, weeh, weel, weej, week, galU, ugd, pgi, galE, pgm (partial) and mip (partial) genes (emusan biosynthetic gene cluster), strain RAG-1.	Acinetobacter lwofii	36,717	01-OCT-1999
		GB_BA2:ALW243431	26953	AJ243431	Acinetobacter lwofii wzc, wzb, wza, weeA, weeb, wecC, wzx, wzy, weeD, weeE, weef, weeG, weeh, weel, weej, week, galU, ugd, pgi, galE, pgm (partial) and mip (partial) genes (emusan biosynthetic gene cluster), strain RAG-1.	Acinetobacter lwofii	36,394	01-OCT-1999
rx00412	1203	GB_RO:MMCOI.3A1	43601	X52046	M.musculus COL3A1 gene for collagen alpha-1	Mus musculus	35,159	8-Nov-94
		GB_BA1:ECU70214	123171	U70214	Escherichia coli chromosome minutes 4-6.	Escherichia coli	39,914	21-Sep-96
		GB_BA1:ECOTSF	91430	D83536	Escherichia coli genomic DNA. (4.1 - 6.1 min).	Escherichia coli	39,828	28-MAY-1999
		GB_HTG3:AC011366	177590	AC011366	Homo sapiens chromosome 5 clone CIT-HSPC_568L21, ***	Homo sapiens	46,212	06-OCT-1999
rx00413	1020	GB_PR3:AC005209	184130	AC005209	SEQUENCING IN PROGRESS *** , 82 unordered pieces.			
		GB_PR3:AC005209	184130	AC005209	Homo sapiens chromosome 17, clone hRPK.628_O_18, complete sequence.	Homo sapiens	34,028	24-Jul-98
		GB_PR3:HUMIL8R	13089	M99412	Human interleukin-8 receptor (IL8RB) gene, complete cds.	Homo sapiens	37,934	22-Apr-98
		GB_PR4:AC006974	90241	AC006974	Homo sapiens PAC clone DJ0958B11 from 7q33-q36, complete sequence.	Homo sapiens	37,948	29-Jul-99
rx00431	912	GB_BA1:MSGY126	37164	AD000012	Mycobacterium tuberculosis sequence from clone y126.	Mycobacterium tuberculosis	66,776	10-DEC-1996
		GB_BA1:MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162.	Mycobacterium tuberculosis	66,776	17-Jun-98
rx00444	960	GB_BA1:MSGB971CS	37566	L78821	Mycobacterium leprae cosmid B971 DNA sequence.	Mycobacterium leprae	39,429	15-Jun-96
		GB_PR4:AC007564	194058	AC007564	Homo sapiens 12q22 BAC RPC111-513P18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	35,220	3-Jul-99
		GB_HTG4:AC007553	271496	AC007553	Homo sapiens chromosome 12q22-102.7-103.4 clone RPC111-557K11, ***	Homo sapiens	35,408	21-OCT-1999
		GB_HTG4:AC007553	271496	AC007553	SEQUENCING IN PROGRESS *** , 70 unordered pieces			
		GB_HTG4:AC007553	271496	AC007553	Homo sapiens chromosome 12q22-102.7-103.4 clone RPC111-557K11, ***	Homo sapiens	35,408	21-OCT-1999
		GB_HTG4:AC007553	271496	AC007553	SEQUENCING IN PROGRESS *** , 70 unordered pieces.			
rx00445	1035	GB_HTG3:AC011455_0244238	AC011455		SEQUENCING IN PROGRESS *** , 287 unordered pieces.	Homo sapiens	35,455	19-Dec-99
		GB_HTG3:AC011455_0244238	AC011455		SEQUENCING IN PROGRESS *** , 287 unordered pieces.			
		GB_HTG3:AC011455_0244238	AC011455		Homo sapiens chromosome 19 clone CIT-HSPC_360G5, ***	Homo sapiens	35,455	19-Dec-99
		GB_HTG3:AC011455_0244238	AC011455		SEQUENCING IN PROGRESS *** , 287 unordered pieces.			
		GB_HTG3:AC011455_0244238	AC011455		Homo sapiens chromosome 19 clone CIT-HSPC_360G5, ***	Homo sapiens	41,511	19-Dec-99
rx00466					SEQUENCING IN PROGRESS *** , 287 unordered pieces.			
rx00482	771	GB_PR4:AF119709	43566	AF119709	Homo sapiens chromosome 8q24 BAC clone H103, complete sequence.	Homo sapiens	36,724	28-Feb-99
		GB_RO:AC005960	158414	AC005960	Mus musculus chromosome 17 BAC clb20h22 from the MHC region, complete sequence.	Mus musculus	39,836	01-DEC-1998
		GB_RO:MUSMH2M4X3994	L14278		Mouse MHC class I H2-M4 gene, exons 1-5.	Mus musculus	32,713	11-Aug-93

TABLE 4: ALIGNMENT RESULTS

rx005623	1149	GB_BA2:AF176902	3032	AF176902	Corynebacterium diphtheriae IRP1B (irp1B), IRP1C (irp1C), and IRP1D (irp1D) genes, complete cds.	Corynebacterium diphtheriae	58,781	5-Sep-99
		GB_HTG3:AC002489	91638	AC002489	Mus musculus chromosome X clone 592 map X, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	Mus musculus	37,819	3-Aug-99
		GB_HTG3:AC002489	91638	AC002489	Mus musculus chromosome X clone 592 map X, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	Mus musculus	37,819	3-Aug-99
rx005625	1386	GB_BA1:D90917	154619	D90917	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470.	Synechocystis sp.	46,966	7-Feb-99
		GB_PL1:AOF132610	477	AJ132610	Asparagus officinalis mRNA for intracellular pathogenesis-related protein, isoform 4.	Asparagus officinalis	38,819	1-Feb-99
		GB_PAT:A26571	737	A26571	A. officinalis AoPR1 gene.	Asparagus officinalis	37,620	28-Sep-95
rx005696	576	GB_PR3:AC004659	129577	AC004659	Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence.	Homo sapiens	34,321	02-MAY-1998
		GB_PR3:AC004659	129577	AC004659	Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence.	Homo sapiens	35,739	02-MAY-1998
		GB_PR1:HUMCBP2	2047	D83174	Human mRNA for collagen binding protein 2, complete cds.	Homo sapiens	40,404	6-Feb-99
rx006634	1506	GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dehydrobiotin synthetase, complete cds.	Corynebacterium glutamicum	39,111	3-Feb-99
		GB_PAT:E08643	285	E08643	Base sequence having the promoter function in Corynebacterium microorganism.	Corynebacterium glutamicum	39,111	29-Sep-97
		GB_HTG2:AC006174	203407	AC006174	Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, *** SEQUENCING IN PROGRESS ***; 6 unordered pieces.	Homo sapiens	37,517	09-DEC-1998
rx00665	601	GB_BA1:SCI30A	35033	AL096811	Streptomyces coelicolor cosmid 130A.	Streptomyces coelicolor A3(2)	38,095	22-Jul-99
		GB_PR3:AC002366	259202	AC002366	Human Xp22 BAC CT-285115 (from CalTech/Research Genetics), PAC RPC1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.	Homo sapiens	33,045	11-Jun-98
		GB_PR3:AC002366	259202	AC002366	Human Xp22 BAC CT-285115 (from CalTech/Research Genetics), PAC RPC1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.	Homo sapiens	35,214	11-Jun-98
rx00702	1830	GB_BA1:PLNRTABC	6449	Z19598	P. lamiosum nrtA-Phi, nrtB-Phi and nrtC-Phi genes.	Phormidium lamiosum	40,550	7-Feb-96
		GB_GSS10:AQ256518	704	AQ256518	nbxb0016M14r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0016M14r, genomic survey sequence.	Oryza sativa	41,477	23-OCT-1998
		GB_BA1:AAC243194	1720	AJ243194	Alicyclobacillus acidocaldarius kdpA gene.	Alicyclobacillus acidocaldarius	39,740	21-Jun-99
rx00728	892	GB_EST21:AA974252	426	AA974252	oq14a01.s1 NC1_CGAP GC4 Homo sapiens cDNA clone IMAGE:1586280 3' similar to SWLIPA_ECOLI_P25845 LIPOIC ACID SYNTHETASE, contains MER22.12 MER22 repetitive element; mRNA sequence.	Homo sapiens	42,236	7-Jul-98
		GB_HTG2:AC004060	124000	AC004060	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***; 10 unordered pieces.	Homo sapiens	38,106	21-Jul-98
		GB_HTG2:AC004060	124000	AC004060	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***; 10 unordered pieces.	Homo sapiens	38,106	21-Jul-98

TABLE 4: ALIGNMENT RESULTS

rx00732	1670	GB_BA2:AE000241	10160	AE000241	Escherichia coli K-12 MG1655 section 131 of 400 of the complete genome.	Escherichia coli	40,024	12-Nov-98
		GB_HITG3:AC010073	121859	AC010073	Homo sapiens chromosome 15 clone BAC 16E3 map 15q25, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	39,001	11-Sep-99
		GB_BA1:D90783	15399	D90783	E.coli genomic DNA, Kohara clone #272(32.4-32.7 min.).	Escherichia coli	40,024	29-MAY-1997
rx00759	1047	GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome, segment 155/162.	Mycobacterium tuberculosis	39,960	24-Jun-99
		GB_PL1:BPNIIR1	2472	X60093	B. pendula mRNA for nitrite reductase.	Betula pendula	38,106	19-MAR-1992
		GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome, segment 155/162.	Mycobacterium tuberculosis	41,618	24-Jun-99
rx00760	1155	GB_BA2:AF092918	20758	AF092918	Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster.	Pseudomonas alcaligenes	40,450	06-DEC-1998
		GB_BA1:SC17	34893	AL096743	Streptomyces coelicolor cosmid 17.	Streptomyces coelicolor	40,352	1-Jul-99
		GB_BA1:D90763	18199	D90763	E. coli genomic DNA, Kohara clone #252(28.1-28.4 min.).	Escherichia coli	38,747	29-MAY-1997
rx00774	777	GB_EST8:AA020814	419	AA020814	ze63h10.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363715 3' similar to PIR.A35715 A35715 fodrin alpha chain - human ; mRNA sequence.	Homo sapiens	37,500	30-Jan-97
		GB_PL2:ATAC004521	104797	AC004521	Arabidopsis thaliana chromosome II BAC F411 genomic sequence, complete sequence.	Arabidopsis thaliana	36,411	12-MAY-1998
		GB_PL2:ATAC004521	104797	AC004521	Arabidopsis thaliana chromosome II BAC F411 genomic sequence, complete sequence.	Arabidopsis thaliana	38,589	12-MAY-1998
rx00775	894	GB_BA1:MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	Mycobacterium tuberculosis	66,107	24-Jun-99
		GB_BA2:AF045938	777	AF045938	Mycobacterium smegmatis putative ABC transporter nucleotide binding subunit (mnp1) gene, complete cds.	Mycobacterium smegmatis	73,454	02-MAY-1998
		GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266	Mycobacterium leprae	63,494	09-MAR-1995
rx00776	1044	GB_PR3:HS453C12	147620	AL021578	Human DNA sequence from clone 453C12 on chromosome 20q12-13.12, complete sequence	Homo sapiens	35,833	23-Nov-99
		GB_PR3:AC004877	128361	AC004877	Homo sapiens PAC clone DJ0751H13 from 7q35-qter, complete sequence.	Homo sapiens	38,754	19-Sep-98
		GB_PR3:HS30012	63796	AL035660	Human DNA sequence from clone 30012 on chromosome 20q12-13.12, complete sequence.	Homo sapiens	32,233	23-Nov-99
rx00777	1188	GB_BA1:ASAJ187	6213	AJ000187	Arthrobacter sp. catA gene.	Arthrobacter sp.	49,694	5-Jul-99
		GB_IN1:CEL120D4	42052	U80029	Caenorhabditis elegans cosmid T20D4.	Caenorhabditis elegans	36,457	04-DEC-1996
		GB_GSS4:AG693388	531	AC693388	HS_5458_A2_D10_T7A RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=1034 Col=20 Row=G, genomic survey sequence.	Homo sapiens	38,123	6-Jul-99
rx00828	576	GB_GSS1:CNS00ZMZ	796	AL097877	Drosophila melanogaster genome survey sequence SP6 end of BAC BACN02F13 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.	Drosophila melanogaster	39,286	26-Jul-99
		GB_BA1:PSEBPH	4169	D16407	Pseudomonas sp. bphE,bphG,bphF and ORF4 genes.	Pseudomonas sp.	36,364	4-Feb-99
		GB_GSS9:AG156606	668	AG156606	nbxb0008K19r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0008K19r, genomic survey sequence.	Oryza sativa	36,364	12-Sep-98

TABLE 4: ALIGNMENT RESULTS

rx00832	1173	GB_PR4:AC006504	210137	AC006504	Homo sapiens chromosome 19, BAC 326584 (CIT-B-459F4), complete sequence.	Homo sapiens	40,545	4-Feb-99
		GB_GSS12:AQ417775	642	AQ417775	RPC1-11-197B9, TV RPC1-11 Homo sapiens genomic clone RPC1-11-197B9, genomic survey sequence.	Homo sapiens	44,286	23-MAR-1999
		GB_PR4:AC006504	210137	AC006504	Homo sapiens chromosome 19, BAC 326584 (CIT-B-459F4), complete sequence.	Homo sapiens	35,886	4-Feb-99
rx00934	1206	GB_BA1:MLCL581	36225	Z96801	Mycobacterium leprae cosmid L581.	Mycobacterium leprae	38,243	24-Jun-97
		GB_BA1:MTCY1A10	25949	Z96387	Mycobacterium tuberculosis H37Rv complete genome, segment 117/162.	Mycobacterium tuberculosis	38,350	17-Jun-98
		GB_PR3:HS434O14	135928	AL022398	Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.	Homo sapiens	36,788	23-Nov-99
rx00939	1308	GB_BA1:MTCY251	38380	Z74410	Mycobacterium tuberculosis H37Rv complete genome, segment 5/162.	Mycobacterium tuberculosis	49,462	17-Jun-98
		GB_PAT1:26656	3250	I26656	Sequence 1 from patent US 5559011.	Unknown.	49,462	07-OCT-1996
		GB_BA2:SCJ1	36925	AL109962	Streptomyces coelicolor cosmid J1.	Streptomyces coelicolor A3(2)	49,228	24-Sep-99
rx00942	327	GB_JN1:CELLT19D2	28406	U42846	Caenorhabditis elegans cosmid T19D2.	Caenorhabditis elegans	43,910	19-DEC-1995
		GB_PR4:AC004905	134350	AC004905	Homo sapiens PAC clone DJ0845121 from 7q11.21-q11.23, complete sequence	Homo sapiens	35,505	12-Jan-99
rx00950	1029	GB_JN1:CELLF18C5	29095	U29097	Caenorhabditis elegans cosmid F18C5.	Caenorhabditis elegans	37,107	15-Jun-95
		GB_BA1:SLTNRB	2849	X73633	S.lorigisporoflavus TrnB gene.	Streptomyces longisporoflavus	52,255	9-Aug-94
		GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome, segment 52/162.	Mycobacterium tuberculosis	38,872	17-Jun-98
		GB_BA1:MSGY367	36336	AD000008	Mycobacterium tuberculosis sequence from clone y367	Mycobacterium tuberculosis	39,921	03-DEC-1996
rx00960	1058	GB_PL2:ATAC009325	105543	AC009325	Arabidopsis thaliana chromosome III BAC F4P13 genomic sequence, complete sequence.	Arabidopsis thaliana	36,074	08-OCT-1999
		GB_BA2:U59485	29078	U59485	Agrobacterium tumefaciens AtnC (atnC) gene, partial cds; AtnB (atnB), AtnA (atnA), AtnA1 (atnA1), AtnA2 (atnA2), AtnB (atnB), AtnC (atnC), AtnD (atnD), AtnE (atnE), and AtnF (atnF) genes, complete cds; AtnC (atnC) gene, alternative splice products, complete cds; AtnH (atnH), AtnI (atnI), AtnJ (atnJ), AtnK (atnK), AtnL (atnL), AtnM (atnM), AtnO (atnO), AtnP (atnP), AtnR (atnR), AtnS (atnS), AtnT (atnT), AtnU (atnU), AtnV (atnV), AtnW (atnW), AtnX (atnX), AtnY (atnY), AtnZ (atnZ), AtnA (atnA), AtnB (atnB), AtnC (atnC), and AtnD (atnD) genes, complete cds; and AtnE (atnE) gene, partial cds	Agrobacterium tumefaciens	39,884	16-Jul-99
		GB_PL2:ATAC009325	105543	AC009325	Arabidopsis thaliana chromosome III BAC F4P13 genomic sequence, complete sequence.	Arabidopsis thaliana	36,162	08-OCT-1999
rx00980	1917	GB_BA1:MTCY10D7	39800	Z79700	Mycobacterium tuberculosis H37Rv complete genome, segment 44/162.	Mycobacterium tuberculosis	48,176	17-Jun-98

TABLE 4: ALIGNMENT RESULTS

		GB_GSS10:AQ265373	639	AQ265373	mgxb0012D24: CUGI Rice Blast BAC Library Magnaporthe grisea genomic survey sequence.	38,624	23-OCT-1998
		GB_EST26:AU004809	728	AU004809	clone mgxb0012D24: genomic survey sequence.	38,223	19-Jan-99
rxa01000					AU004809 Bombyx mori p50(Daizo) Bombyx mori cDNA clone ws20873, mRNA sequence.		
rxa01002	927	GB_BA2:AE001197	10039	AE001197	Treponema pallidum section 13 of 87 of the complete genome.	37,161	16-Jul-98
		GB_PL1:HVPGLYH	3790	Y10099	H vulgare mRNA for novel P-glycoprotein homologue.	42,239	24-OCT-1997
		GB_JN1:AB003329	4328	AB003329	Leishmania amazonensis LamDR1 multidrug resistance gene, complete cds.	40,176	24-MAR-1999
rxa01003	927	GB_HTG2:HSJ168B21	67973	AL118518	Homo sapiens chromosome 6 clone RP1-168B21 map q26-27, *** SEQUENCING IN PROGRESS *** in unordered pieces.	35,159	03-DEC-1999
		GB_HTG2:HSJ168B21	67973	AL118518	Homo sapiens chromosome 6 clone RP1-168B21 map q26-27, *** SEQUENCING IN PROGRESS *** in unordered pieces.	35,159	03-DEC-1999
		GB_HTG2:HSJ168B21	67973	AL118518	Homo sapiens chromosome 6 clone RP1-168B21 map q26-27, *** SEQUENCING IN PROGRESS *** in unordered pieces.	39,956	03-DEC-1999
rxa01006	958	GB_JN2:S74163	2630	S74163	Drosophila sp. T-related protein (Trig) mRNA, complete cds.	37,131	06-OCT-1999
		GB_PR4:AF130343	292721	AF130343	Homo sapiens chromosome 8 clone PAC 87.2 map 8q24.1, complete sequence.	34,398	9-Jul-99
		GB_HTG3:AC009415	186991	AC009415	Homo sapiens clone NH0576H09, *** SEQUENCING IN PROGRESS *** , 5 unordered pieces.	36,325	21-Aug-99
rxa01012	1764	GB_BA1:SYOATPBP	2883	D14438	Synechococcus elongatus genes for ATP-binding protein and Mn-stabilizing protein.	50,346	3-Feb-99
		GB_BA1:BSU20909	6404	U20909	Bacillus subtilis permease system App operon AppD (appD), AppF (appF), AppA (appA), AppB (appB), and AppC (appC) genes, complete cds.	50,376	23-Feb-95
		GB_BA2:ECOPOTABCD385	41284	M64519	E. coli transport protein (potA, potB, potC, and potD) genes, complete cds.	42,881	17-Jun-96
rxa01013	818	GB_JN2:AC005930	41284	AC005930	Leishmania major chromosome 3 clone L712 strain Friedlin, complete sequence.	40,444	13-Nov-99
		GB_PR2:HS1110P6	40033	AL049175	Human DNA sequence from clone 1110P6 on chromosome Xq21.1-22.3. Contains a putative CpG island, complete sequence	36,981	23-Nov-99
rxa01070	1509	GB_JN2:AC005930	41284	AC005930	Leishmania major chromosome 3 clone L712 strain Friedlin, complete sequence.	44,121	13-Nov-99
		GB_BA2:U32795	10038	U32795	Haemophilus influenzae Rd section 110 of 163 of the complete genome.	44,668	29-MAY-1998
		GB_PR4:AC004985	159607	AC004985	Homo sapiens clone DJ1165K10, complete sequence	37,508	7-Aug-99
		GB_PR3:AC005244	127506	AC005244	Homo sapiens chromosome 17, clone hRPK.471_L_13, complete sequence.	33,176	7-Aug-98
rxa01094	736	GB_BA1:CORPYKI	2795	L27126	Corynebacterium pyruvate kinase gene, complete cds.	99,558	07-DEC-1994
		GB_BA1:SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	37,569	23-Jul-99

Treponema pallidum	37,161	16-Jul-98
Hordeum vulgare	42,239	24-OCT-1997
Leishmania amazonensis	40,176	24-MAR-1999
Homo sapiens	35,159	03-DEC-1999
Homo sapiens	35,159	03-DEC-1999
Homo sapiens	35,159	03-DEC-1999
Homo sapiens	39,956	03-DEC-1999
Drosophila sp.	37,131	06-OCT-1999
Homo sapiens	34,398	9-Jul-99
Homo sapiens	36,325	21-Aug-99
Synechococcus elongatus	50,346	3-Feb-99
Bacillus subtilis	50,376	23-Feb-95
Escherichia coli	42,881	17-Jun-96
Leishmania major	40,444	13-Nov-99
Homo sapiens	36,981	23-Nov-99
Leishmania major	44,121	13-Nov-99
Haemophilus influenzae Rd	44,668	29-MAY-1998
Homo sapiens	37,508	7-Aug-99
Homo sapiens	33,176	7-Aug-98
Corynebacterium glutamicum	99,558	07-DEC-1994
Streptomyces coelicolor A3(2)	37,569	23-Jul-99

TABLE 4: ALIGNMENT RESULTS

rxa01141	948	GB_HTG2:HSJ395C13	150336	AL117344	Homo sapiens chromosome 6 clone RP3-395C13 map q25.2-26. *** PROGRESS *** in unordered pieces.	Homo sapiens	38,577	15-OCT-1999
		GB_HTG2:HSJ395C13	150336	AL117344	Homo sapiens chromosome 6 clone RP3-395C13 map q25.2-26. *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	36,538	03-DEC-1999
		GB_HTG2:HSJ395C13	150336	AL117344	Homo sapiens chromosome 6 clone RP3-395C13 map q25.2-26. *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	36,538	03-DEC-1999
		GB_HTG2:HSJ395C13	150336	AL117344	Homo sapiens chromosome 6 clone RP3-395C13 map q25.2-26. *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	37,908	03-DEC-1999
rxa01142	621	GB_BA1:CORAI A	4705	L09232	Corynebacterium glutamicum acetohydroxy acid synthase (ilvB) and (ilvN) genes, and acetohydroxy acid isomerase (ilvC) gene, complete cds.	Corynebacterium glutamicum	35,897	23-Feb-95
		GB_BA1:SCH35	45396	AL078610	Streptomyces coelicolor cosmid H35.	Streptomyces coelicolor	52,295	4-Jun-99
		GB_BA2:AFACHRRA	7390	J05278	Ralstonia eutropha Chrb (chrB), Chra (chrA), Chrc (chrC), Chrd (chrd), YbbB (ybbB), pirl, and heat shock protein sigma-32 (RP32) genes, complete cds.	Ralstonia eutropha	54,589	26-MAR-1999
rxa01164	1758	GB_GSS14:AQ555104	609	AQ555104	RPC1-11-415H1. TJ RPC1-11 Homo sapiens genomic clone RPC1-11-415H1, genomic survey sequence	Homo sapiens	40,000	28-MAY-1999
		GB_BA2:AE000309	13453	AE000309	Escherichia coli K-12 MG1655 section 199 of 400 of the complete genome.	Escherichia coli	39,261	12-Nov-98
		GB_GSS14:AQ548213	668	AQ548213	RPC1-11-415H4. TV RPC1-11 Homo sapiens genomic clone RPC1-11-415H4, genomic survey sequence.	Homo sapiens	41,176	28-MAY-1999
rxa01168	933	GB_BA1:MTV018	53450	AL021899	Mycobacterium tuberculosis H37Rv complete genome; segment 90/162.	Mycobacterium tuberculosis	38,033	18-Jun-98
		GB_PL2:ATAC003033	84254	AC003033	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence.	Arabidopsis thaliana	37,486	19-DEC-1997
		GB_PL2:ATAC003033	84254	AC003033	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence.	Arabidopsis thaliana	38,142	19-DEC-1997
rxa01185	667	GB_BA2:AF013987	3150	AF013987	Vibrio cholerae strain 0395 putative ABC transporter ATP-binding protein, regulatory IIA protein (ptsN) genes, complete cds.	Vibrio cholerae	44,128	21-MAY-1998
		GB_BA1:SASTPSMP	1848	Z30588	S. aureus (RNA220) genes for potential ABC transporter and potential membrane spanning protein.	Staphylococcus aureus	43,402	25-MAY-1995
		GB_PR3:HS357116	134506	AL021921	Homo sapiens DNA sequence from PAC 357116 on chromosome 1p36.13. Contains GSSs, genomic marker D1S449 and a CA repeat polymorphism, complete sequence.	Homo sapiens	38,957	23-Nov-99
rxa01188	1227	GB_PR3:HSN21F1	39212	Z94162	Human DNA sequence from cosmid N21F1 on chromosome 22. Contains exon trap and STS, complete sequence.	Homo sapiens	37,277	23-Nov-99
		GB_EST38:AW066174	455	AW066174	687007C06.y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA	Zea mays	42,439	12-OCT-1999
		GB_GSS4:AQ719542	493	AQ719542	HS_5529_B2_A02_SP6E RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=1105 Col=4 Row=B, genomic survey sequence.	Homo sapiens	39,837	14-Jul-99

TABLE 4: ALIGNMENT RESULTS

rx01247	357	GB_BA2:AF127374	63734	AF127374	Streptomyces lavendulae LinA homolog, cytochrome P450 hydroxylase ORF4, cytochrome P450 hydroxylase ORF3, MitT (mitT), MITS (mitS), MitR (mitR), MitQ (mitQ), MitP (mitP), MitO (mitO), MitN (mitN), MitM (mitM), MitL (mitL), MitK (mitK), MitJ (mitJ), MitI (mitI), MitH (mitH), MitG (mitG), MitF (mitF), MitE (mitE), MitD (mitD), MitC (mitC), MitB (mitB), MitA (mitA), MimcA (mimcA), MimcB (mimcB), MimcC (mimcC), MimcD (mimcD), MimcE (mimcE), MimcF (mimcF), MimcG (mimcG), MimcH (mimcH), MimcI (mimcI), MimcJ (mimcJ), MimcK (mimcK), MimcL (mimcL), MimcM (mimcM), MimcN (mimcN), MimcO (mimcO), Mird (mird), MimcP (mimcP), MimcQ (mimcQ), MimcR (mimcR), MimcS (mimcS), MimcT (mimcT), MimcU (mimcU), MimcV (mimcV), Mct (mct), MimcW (mimcW), MimcX (mimcX), and MimcY (mimcY) genes, complete cds, and unknown genes	Streptomyces lavendulae	38,592	27-MAY-1999
rx01285	749	GB_PR4:AC006039 GB_BA1:SCI51	176257 40745	AC006039 AL109848	Homo sapiens clone NH0319F03, complete sequence. Streptomyces coelicolor cosmid I51.	Homo sapiens Streptomyces coelicolor A3(2)	30,899 38,627	05-MAY-1999 16-Aug-99
		GB_BA2:SCF34	38995	AL109974	Streptomyces coelicolor cosmid F34.	Streptomyces coelicolor A3(2)	38,586	24-Sep-99
		GB_BA2:MSU10425	4261	U10425	Mycobacterium smegmatis ferric exochelatin uptake proteins FxuB (fxuB), FxuD (fxuD) genes, complete cds, FxuC (fxuC) gene, partial cds, and ferric exochelatin biosynthesis protein FxuD (fxuD) gene, complete cds.	Mycobacterium smegmatis	61,230	07-DEC-1994
rx01289	1167	GB_BA1:SCI51 GB_BA1:SCI51	40745 40745	AL109848 AL109848	Streptomyces coelicolor cosmid I51. Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2) Streptomyces coelicolor A3(2)	35,456 37,576	16-Aug-99 16-Aug-99
		GB_EST31:A1704930	227	A1704930	UI-R-AB1-y6-c-07-0-UI-s1 UI-R-AB1 Rattus norvegicus cDNA clone UI-R-AB1-y6-c-07-0-UI-3', mRNA sequence.	Rattus norvegicus A3(2)	38,326	3-Jun-99
rx01290	1287	GB_HTG2:AC006892	299081	AC006892	Caenorhabditis elegans clone Y69A2, *** SEQUENCING IN PROGRESS *** ***, 10 unordered pieces.	Caenorhabditis elegans	33,727	26-Feb-99

TABLE 4: ALIGNMENT RESULTS

rxa01297	921	GB_BA1:MTCY16B7	43430	Z81331	Myco bacterium tuberculosis sequence from clone y414a.	Myco bacterium tuberculosis	38,133	17-Jun-98
		GB_BA1:MSGY414A	40121	AD000007	Myco bacterium tuberculosis sequence from clone y414a.	Myco bacterium tuberculosis	61,716	03-DEC-1996
		GB_HTG4:AC010181	185244	AC010181	Homo sapiens chromosome 3 seeders clone RPC111-68L1, *** SEQUENCING IN PROGRESS *** , 26 unordered pieces.	Homo sapiens	34,807	21-OCT-1999
rxa01298	1053	GB_BA1:MTCY16B7	43430	Z81331	Myco bacterium tuberculosis H37Rv complete genome; segment 123/162.	Myco bacterium tuberculosis	38,160	17-Jun-98
		GB_BA1:MSGY414A	40121	AD000007	Myco bacterium tuberculosis sequence from clone y414a	Myco bacterium tuberculosis	58,611	03-DEC-1996
		GB_PL1:SCYJL013C	2289	Z49288	S. cerevisiae chromosome X reading frame ORF YJL013C.	Saccharomyces cerevisiae	36,180	11-Aug-97
rxa01303	1458	GB_BA1:TTA5043	837	AJ225043	Thermus thermophilus partial narX gene.	Thermus thermophilus	55,245	18-Jun-98
		GB_PL2:AC010675	84723	AC010675	Arabidopsis thaliana chromosome I BAC T17F3 genomic sequence, complete sequence.	Arabidopsis thaliana	37,058	11-Nov-99
		GB_GSS9:AQ170862	518	AQ170862	HS_3165_B2_F03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3165 Col=6 Row=L, genomic survey sequence.	Homo sapiens	38,610	17-OCT-1998
rxa01323	2388	GB_BA1:MTCY10D7	39800	Z79700	Myco bacterium tuberculosis H37Rv complete genome, segment 44/162.	Myco bacterium tuberculosis	53,376	17-Jun-98
		GB_BA1:MTCY39	38500	Z74025	Myco bacterium tuberculosis H37Rv complete genome, segment 89/162.	Myco bacterium tuberculosis	39,197	17-Jun-98
		GB_BA1:MTCY251	38380	Z74410	Myco bacterium tuberculosis H37Rv complete genome, segment 5/162.	Myco bacterium tuberculosis	52,698	17-Jun-98
rxa01338	1925	GB_IN1:DROPROS	6422	M81389	D.melanogaster Pros protein (prospero) mRNA, complete cds.	Drosophila melanogaster	37,229	26-Apr-93
		GB_EST9:AA060074	688	AA060074	mi7307.r1 Soares mouse p3NM1F19.5 Mus musculus cDNA clone IMAGE:481765.5 similar to gb:X00246 Mouse mRNA with a Set 1 repetitive element for a class I (MOUSE); mRNA sequence.	Mus musculus	39,919	23-Sep-96
		GB_EST16:AA560009	437	AA560009	vi16a01.r1 Stragene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:972360.5, mRNA sequence.	Mus musculus	37,071	18-Aug-97
rxa01395	294	GB_BA1:CGLYSEG	2374	X96471	C. glutamicum lysE and lysG genes.	Corynebacterium glutamicum	38,462	24-Feb-97
		GB_IN1:CELLF28B3	36262	AF003136	Caenorhabditis elegans cosmid F28B3.	Caenorhabditis elegans	37,241	31-DEC-1997
		GB_GSS13:AQ486324	573	AQ486324	RPC1-11-264E18 TJ RPC1-11 Homo sapiens genomic clone RPC1-11-264E18, genomic survey sequence.	Homo sapiens	39,785	24-Apr-99

rxa01411	888	GB_EST124:AU035428	756	AU035428	AU035428 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-0438, mRNA sequence.	Mus musculus	37,112	06-MAR-1990
		GB_GSS12:ACQ399225	621	ACQ399225	mgxb0019C11f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0019C11f, genomic survey sequence.	Magnaporthe grisea	36,430	
		GB_EST18:T42211	337	T42211	5474 Lambda-PRL2 Arabidopsis thaliana cDNA clone 111C20T7, mRNA sequence.	Arabidopsis thaliana	42,433	7-Jan-98
rxa01454	367	GB_GSS5:AQ818876	486	AQ818876	HS_5297_B1_E12_SF6E RPCL-11 Human Male BAC Library Homo sapiens genomic clone Plate=873 Col=23 Row=J, genomic survey sequence.	Homo sapiens	36,585	26-Aug-99
		GB_EST19:AA778691	650	AA778691	at87h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1049045 3' similar to contains L1.12 L1 repetitive element ;, mRNA sequence	Homo sapiens	32,344	5-Feb-98
		GB_GSS15:AQ599724	543	AQ599724	HS_5354_B1_B01_T7A RPCL-11 Human Male BAC Library Homo sapiens genomic clone Plate=930 Col=1 Row=D, genomic survey sequence.	Homo sapiens	39,773	10-Jun-99
rxa01455	585	GB_PL2:AF002169	5217	AF002169	Neurospora crassa coxI translation protein CYA5 (cyA5) gene, complete cds.	Neurospora crassa	39,161	24-MAR-1999
		GB_PL2:AF002169	5217	AF002169	Neurospora crassa coxI translation protein CYA5 (cyA5) gene, complete cds.	Neurospora crassa	37,565	24-MAR-1999
rxa01625	324	GB_EST36:AV200593	300	AV200593	AV200593 Yujii Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk577f10 3', mRNA sequence.	Caenorhabditis elegans	43,284	26-Jul-99
		GB_PL1:S48358	414	S48358	tRNA Trp [Saccharomyces cerevisiae, Genomic, 414 nt].	Saccharomyces cerevisiae	37,143	08-MAY-1993
		GB_GSS8:AQ005656	390	AQ005656	CIT-HSP-2292G20, TR CIT-HSP Homo sapiens genomic clone 2292G20, genomic survey sequence.	Homo sapiens	39,205	27-Jun-98
rxa01756	1431	GB_HTG4:AC009886	163668	AC009886	Homo sapiens chromosome 15 clone 437_N_14 map 15, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	35,865	19-OCT-1999
		GB_HTG4:AC009886	163668	AC009886	Homo sapiens chromosome 15 clone 437_N_14 map 15, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	35,865	19-OCT-1999
		GB_EST6:N47950	424	N47950	yy84d12.s1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:280247 3', mRNA sequence	Homo sapiens	38,261	14-Feb-96
rxa01808	1172	GB_BA1:SEABCT	1976	X80735	S erylthraea (NCIMB 8594) ertX gene for putative ABC transporter	Saccharopolyspora erythraea	63,607	07-DEC-1995
		GB_BA1:MTV047	10866	AL022002	Mycobacterium tuberculosis H37Rv complete genome; segment 75/162.	Mycobacterium tuberculosis	40,563	17-Jun-98
rxa01822	605	GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	35,112	17-Apr-96
		GB_HTG3:AC008480	106822	AC008480	Homo sapiens chromosome 5 clone CIT-HSPC_397O13, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces.	Homo sapiens	35,940	3-Aug-99
		GB_HTG3:AC008480	106822	AC008480	Homo sapiens chromosome 5 clone CIT-HSPC_397O13, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces.	Homo sapiens	35,940	3-Aug-99
		GB_PL2:CNS01B8L	660	AL113917	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.	Botryotinia fuckeliana	43,322	2-Sep-99
rxa01900	1422	GB_BA2:AF056309	4346	AF056309	Streptomyces aguilaceus membrane protein and mithramycin regulator MtmR (mtmR) genes, complete cds.	Streptomyces aguilaceus	39,199	27-Jan-99

TABLE 4: ALIGNMENT RESULTS

rxa01939	1854	GB_EST25:AU045582	273	AU045582	AU045582 Mouse sixteen-cell-embryo cDNA Mus musculus cDNA clone J0937H06 3', mRNA sequence.	Mus musculus	61,172	09-DEC-1998
		GB_EST15:AA458642	217	AA458642	aa16b10.st Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813403 3' similar to TR:G496330 G496330 (KBL MRNA .. mRNA sequence.	Homo sapiens	43,056	9-Jun-97
rxa01939	1854	GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	38,145	24-Jun-99
		GB_BA1:SC2A11	22789	AL031184	Streptomyces coelicolor cosmid 2A11.	Streptomyces coelicolor	45,783	5-Aug-98
		GB_BA2:AE000431	11575	AE000431	Escherichia coli K-12 MG1655 section 321 of 400 of the complete genome.	Escherichia coli	38,384	12-Nov-98
rxa01972	717	GB_HTG2:AC007650	166670	AC007650	Drosophila melanogaster chromosome 3 clone BACR30G22 (D688) RPCL-98 30.G.22 map 87F-87F strain y; cn bw sp. *** SEQUENCING IN PROGRESS *** , 101 unordered pieces.	Drosophila melanogaster	37,712	2-Aug-99
		GB_HTG2:AC007650	166670	AC007650	Drosophila melanogaster chromosome 3 clone BACR30G22 (D688) RPCL-98 30.G.22 map 87F-87F strain y; cn bw sp. *** SEQUENCING IN PROGRESS *** , 101 unordered pieces.	Drosophila melanogaster	37,712	2-Aug-99
		GB_HTG2:AC008204	138364	AC008204	Drosophila melanogaster chromosome 3 clone BACR04E17 (D762) RPCL-98 04.E.17 map 95E-95F strain y; cn bw sp. *** SEQUENCING IN PROGRESS*** , 96 unordered pieces.	Drosophila melanogaster	36,827	2-Aug-99
rxa01995	1461	GB_HTG7:AC008065	172383	AC008065	Homo sapiens clone RP11-284E18. *** SEQUENCING IN PROGRESS *** , Homo sapiens 4 unordered pieces.	Homo sapiens	37,213	09-DEC-1999
		GB_GSS5:AQ805794	426	AQ805794	HS_3192_A2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3192 Col=8 Row=E. genomic survey	Homo sapiens	41,148	9-Aug-99
		GB_GSS10:AQ173736	436	AQ173736	HS_3194_A1_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=7 Row=E. genomic survey	Homo sapiens	40,421	17-OCT-1998
rxa02034	1089	GB_PR4:AC002531	197900	AC002531	Homo sapiens chromosome Y, clone 486_O_8, complete sequence.	Homo sapiens	36,934	13-OCT-1999
		GB_PR2:HSB7L1C4	106710	AL078476	Homo sapiens chromosome 21 BAC B7L1C4, complete sequence.	Homo sapiens	34,454	9-Nov-99
rxa02035		GB_IN2:CELF26D11	36161	AF068716	Caenorhabditis elegans cosmid F26D11.	Caenorhabditis elegans	36,524	29-MAY-1998
rxa02062	1293	GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	38,606	17-Jun-98
		GB_EST34:AV153141	305	AV153141	AV153141 Mus musculus hippocampus C57BL/6J adult Mus musculus cDNA clone 290005B17, mRNA sequence	Mus musculus	37,705	7-Jul-99
		GB_BA1:PHU88400	3855	U88400	Prochlorotrix hollandica hoxUVH operon, hydrogenase diaphorase subunit (hoxU) gene, partial cds, and bidirectional hydrogenase small subunit (hoxY), unknown protein, and bidirectional hydrogenase large subunit (hoxH) genes, complete cds.	Prochlorotrix hollandica	38,712	05-MAY-1997

TABLE 4: ALIGNMENT RESULTS

rx02068	1230	GB_GSS13:AAQ488513	673	AQ488513	RPCI-11-243J24, TV RPCI-11 Homo sapiens genomic clone RPCI-11-243J24, genomic survey sequence.	Homo sapiens	36,567	24-Apr-99
		GB_GSS13:AAQ488513	673	AQ488513	RPCI-11-243J24, TV RPCI-11 Homo sapiens genomic clone RPCI-11-243J24, genomic survey sequence.	Homo sapiens	36,567	24-Apr-99
rx02079	738	GB_PR4:AC006531	167525	AC006531	Homo sapiens chromosome 16 clone 113K5, complete sequence.	Homo sapiens	37,870	7-Feb-99
		GB_BA1:DLARGD	1471	L42615	Deleya cupida 16S ribosomal RNA (16S rRNA) gene	Halomonas cupida	40,476	3-Jan-96
		GB_BA1:AF009342	1482	AF009342	Haemophilus ducreyi ribosomal protein L11 gene, partial cds, and ribosomal protein L1 gene, complete cds.	Haemophilus ducreyi	34,813	22-Jul-97
rx02096	1815	GB_BA1:MTV033	21620	AL021928	Mycobacterium tuberculosis H37Rv complete genome; segment 11/162.	Mycobacterium tuberculosis	48,302	17-Jun-98
		GB_BA2:MSU10425	4261	U10425	Mycobacterium smegmatis ferric exochelin uptake proteins FxuB (fxuB), FxuA (fxuA) genes, complete cds, FxuC (fxuC) gene, partial cds, and ferric exochelin biosynthesis protein FxhA (fxhA) gene, complete cds.	Mycobacterium tuberculosis	41,282	07-DEC-1994
rx02119	1764	GB_EST30:AV018477	249	AV018477	AV018477 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1190005G23, mRNA sequence.	Mus musculus	42,169	28-Aug-99
		GB_BA1:SCARD1GN	2321	X84374	S. capreolus ard1 gene.	Streptomyces capreolus	49,857	23-Aug-95
		GB_PL2:SPBC29A3	42770	AL022299	S pombe chromosome II cosmid c29A3	Schizosaccharomyces pombe	37,269	02-DEC-1999
		GB_HTG1:CEY47H10	296589	Z95311	Caenorhabditis elegans chromosome I clone Y47H10, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Caenorhabditis elegans	34,160	7-Sep-99
rx02200	1233	GB_PR3:HSA494O16	50502	AL117328	Human DNA sequence from clone 494O16 on chromosome 22, complete sequence.	Homo sapiens	38,648	23-Nov-99
		GB_HTG2:AC008161	158440	AC008161	Mus musculus clone 182_H_5, *** SEQUENCING IN PROGRESS *** , 29 unordered pieces.	Mus musculus	35,938	28-Jul-99
		GB_HTG2:AC008161	158440	AC008161	Mus musculus clone 182_H_5, *** SEQUENCING IN PROGRESS *** , 29 unordered pieces.	Mus musculus	35,938	28-Jul-99
rx02222								
rx02312	1482	GB_BA1:ECOUW93	338534	U114003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	60,729	17-Apr-96
		GB_BA2:AE000492	10181	AE000492	Escherichia coli K-12 MG1655 section 382 of 400 of the complete genome.	Escherichia coli	60,729	12-Nov-98
		GB_BA1:BSUB0004	213190	Z99107	Bacillus subtilis complete genome (section 4 of 21), from 600701 to 813890.	Bacillus subtilis	35,670	26-Nov-97
rx02313	1344	GB_EST30:AV013722	344	AV013722	AV013722 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1110049L02, mRNA sequence.	Mus musculus	39,941	25-Aug-99
		GB_EST29:A1596306	356	A1596306	ve20b05.y1 Soares mouse NblMH Mus musculus cDNA clone IMAGE:818673 5', mRNA sequence.	Mus musculus	40,395	21-Apr-99
		GB_EST29:A1596357	335	A1596357	ve20b05.x1 Soares mouse NblMH Mus musculus cDNA clone IMAGE:818673 3', mRNA sequence.	Mus musculus	35,821	21-Apr-99

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TABLE 4: ALIGNMENT RESULTS

	GB_BA1:MXENO201	390	X92571	M.xenopi gene for 32 kDa protein (partial).	Mycobacterium xenopi	59,233	15-Jan-98	
rx002614	852	GB_BA1:SCH35	45396	AL078610	Streptomyces coelicolor cosmid H35.	Streptomyces coelicolor	50,976	4-Jun-99
	GB_BA2:AF126201	12402	AF126201	Pseudomonas putida strain S-313 sulfate ester desulfurization gene locus, complete sequence.	Pseudomonas putida	46,763	12-OCT-1999	
	GB_BA1:SC8B7	14634	AL031225	Streptomyces coelicolor cosmid 8B7	Streptomyces coelicolor	38,026	7-Aug-98	
rx002616	834	GB_BA1:SCD78	36224	AL034355	Streptomyces coelicolor cosmid D78.	Streptomyces coelicolor	43,705	26-Nov-98
	GB_EST28:AI509984	534	AI509984	mj18e06.y1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:476482.5', mRNA sequence.	Mus musculus	38,653	12-MAR-1999	
	GB_EST8:AA050633	522	AA050633	mj18e06.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:476482.5', mRNA sequence	Mus musculus	41,602	9-Sep-96	
rx002627	866	GB_GSS6:AQ826046	427	AQ826046	HS_5311_B2_B01_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=887 Col=2 Row=D, genomic survey sequence.	Homo sapiens	38,095	27-Aug-99
	GB_PR2:HS329F2	24753	AL031710	Human DNA sequence from clone LA16-329F2 on chromosome 16, complete sequence	Homo sapiens	38,580	22-Nov-99	
	GB_GSS10:AQ255771	621	AQ255771	nbxb0014E22r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0014E22r, genomic survey sequence.	Oryza sativa	34,622	23-OCT-1998	
rx002628	528	GB_BA1:RCAHIMA	5403	M84030	Rhodobacter capsulatus integration host factor (ihmA) gene, complete cds.	Rhodobacter capsulatus	37,452	26-Apr-93
	GB_GSS13:ACQ476201	312	AQ476201	CITBI-E1-2592P3, TF CITBI-E1 Homo sapiens genomic clone 2592P3, genomic survey sequence.	Homo sapiens	43,182	23-Apr-99	
	GB_EST38:AW054154	648	AW054154	614079C04.x1 614 - root cDNA library from Walbot Lab Zea mays cDNA, mRNA sequence.	Zea mays	37,657	21-Sep-99	
rx002650	702	GB_EST19:AA803900	441	AA803900	GM14564, 5prime GM Drosophila melanogaster ovary POT2 Drosophila melanogaster cDNA clone GM14564 5prime, mRNA sequence.	Drosophila melanogaster	40,394	25-Nov-98
	GB_EST19:AA803900	441	AA803900	GM14564, 5prime GM Drosophila melanogaster ovary POT2 Drosophila melanogaster cDNA clone GM14564 5prime, mRNA sequence.	Drosophila melanogaster	37,757	25-Nov-98	
rx002660	762	GB_PR3:HS30801	166715	Z93403	Human genomic DNA sequence from clone 30801 on chromosome Xp11.3-Homo sapiens 11.4. Contains EST, CA repeat, STS, GSS, CpG island.	Homo sapiens	33,912	23-Nov-99
	GB_PR3:AC003669	159446	AC003669	Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human BAC library) contains Brnx gene, complete sequence.	Homo sapiens	35,734	24-MAR-1998	
	GB_HTG3:AC010923	152021	AC010923	Drosophila melanogaster chromosome X clone BACR19K15 (D897) RPCI-98 19.K.15 map 15B-15E strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 175 unordered pieces	Drosophila melanogaster	28,070	08-OCT-1999	
rx002661	342	GB_HTG2:AC007802	118569	AC007802	Drosophila melanogaster chromosome 2 clone BACR0711 (D648) RPCI-98 07.1.11 map 58A1-58A2 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces	Drosophila melanogaster	43,373	2-Aug-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG2:AC007802	118569	AC007802	Drosophila melanogaster chromosome 2 clone BACR07111 (D646) RPCI-98 07.1.11 map 58A1-58A2 strain y; cn bw sp. *** SEQUENCING IN PROGRESS *** , 70 unordered pieces.	Drosophila melanogaster	43,373	2-Aug-99
		GB_EST2:R04660	288	R04660	pk27b04.r1 Kuwabara Mixed stage C. briggsae Caenorhabditis briggsae cDNA, mRNA sequence.	Caenorhabditis briggsae	47,009	31-MAR-1995
rx02663	1518	GB_BA1:SC9F2	11908	AL035559	Streptomyces coelicolor cosmid 9F2.	Streptomyces coelicolor	45,964	25-Feb-99
		GB_BA1:MTCY50	36030	Z77137	Mycobacterium tuberculosis H37Rv complete genome, segment 55/162.	Mycobacterium tuberculosis	38,998	17-Jun-98
		GB_BA1:D90721	16578	D90721	Escherichia coli genomic DNA, (18.6 - 19.0 min)	Escherichia coli	44,325	7-Feb-99
rx02664	783	GB_BA2:U32798	10423	U32798	Haemophilus influenzae Rd section 113 of 163 of the complete genome.	Haemophilus influenzae Rd	39,868	29-MAY-1998
		GB_BA1:HIU17295	9424	U17295	Haemophilus influenzae dppB, dppC, dppD, dppF, isn, artP, artI/J, artQ, and artM genes, complete cds, and opa gene, partial cds	Haemophilus influenzae	49,298	4-Apr-96
		GB_BA2:U32792	11306	U32792	Haemophilus influenzae Rd section 107 of 163 of the complete genome.	Haemophilus influenzae Rd	39,764	29-MAY-1998
rx02684	987	GB_PR2:CNS00006	181433	AL049775	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-497E19 of RPCI-1 library from chromosome 14 of Homo sapiens (Human), complete sequence.	Homo sapiens	36,961	17-Jun-99
		GB_HTG3:AC009857	148241	AC009857	Homo sapiens clone 2_F_6, *** SEQUENCING IN PROGRESS *** , 9 unordered pieces.	Homo sapiens	35,380	3-Sep-99
		GB_HTG3:AC009857	148241	AC009857	Homo sapiens clone 2_F_6, *** SEQUENCING IN PROGRESS *** , 9 unordered pieces	Homo sapiens	35,380	3-Sep-99
rx02728	936	GB_BA1:YEHEMSTUV	3901	X77867	Y enterocolitica hemS, hemT, hemU and hemV genes.	Yersinia enterocolitica	48,253	11-OCT-1996
		GB_BA1:ECOUW76	225419	U00039	E. coli chromosomal region from 76.0 to 81.5 minutes.	Escherichia coli	39,177	7-Nov-96
		GB_HTG3:AC008616	112626	AC008616	Homo sapiens chromosome 19 clone CIT9785KB_144D21, *** SEQUENCING IN PROGRESS *** , 49 unordered pieces.	Homo sapiens	41,741	3-Sep-99
rx02750	939	GB_GSS15:AQ663436	430	AQ663436	HS_2160_B2_F10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2160 Col=20 Row=L, genomic survey sequence.	Homo sapiens	42,020	23-Jun-99
		GB_GSS15:AQ663436	430	AQ663436	HS_2160_B2_F10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2160 Col=20 Row=L, genomic survey sequence.	Homo sapiens	39,161	23-Jun-99
rx02795	1560	GB_HTG5:AC011134	192982	AC011134	Homo sapiens clone 1_A_23, *** SEQUENCING IN PROGRESS *** , 22 unordered pieces	Homo sapiens	35,630	5-Nov-99
		GB_HTG5:AC011134	192982	AC011134	Homo sapiens clone 1_A_23, *** SEQUENCING IN PROGRESS *** , 22 unordered pieces.	Homo sapiens	34,643	5-Nov-99
		GB_BA1:MTCY50	36030	Z77137	Mycobacterium tuberculosis H37Rv complete genome; segment 55/162.	Mycobacterium tuberculosis	39,934	17-Jun-98
rx02808	281	GB_PR4:AC004897	90731	AC004897	Homo sapiens PAC clone DJ0811N16 from 7q34-q36, complete sequence.	Homo sapiens	42,804	19-Aug-99
		GB_RO:AC002121	84056	AC002121	Genomic sequence from Mouse 11, complete sequence.	Mus musculus	39,130	10-Jul-97

TABLE 4: ALIGNMENT RESULTS

GB_PR4:AC005078	73231	AC005078	Homo sapiens BAC clone RG252K19 from 7p15.2-p21, complete sequence.	Homo sapiens	37,175	18-MAR-1999
GB_PL1:CKHUP2	2353	X66855	C.kessleri HUP2 mRNA.	Chlorella kessleri	45,328	17-Feb-97
GB_EST38:AW048153	383	AW048153	U1-M-BH1-alc-h-05-0-U1.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone U1-M-BH1-alc-h-05-0-U1 3' mRNA sequence.	Mus musculus	41,758	18-Sep-99
GB_PL1:CKHUP2	2353	X66855	C.kessleri HUP2 mRNA.	Chlorella kessleri	38,106	17-Feb-97
GB_BA1:BSUB0010	233780	Z99113	Bacillus subtilis complete genome (section 10 of 21): from 1781201 to 2014980.	Bacillus subtilis	52,282	26-Nov-97
GB_BA1:BSU66480	26114	U66480	Bacillus subtilis SpoVK (spovK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynab), YnaC (ynac), YnaD (ynad), YnaE (yneaE), YnaF (ynaF), YnaG (ynaG), YnaH (ynah), YnaI (ynai), YnaJ (ynaj), xylan beta-1,4-xylosidase (xynB), xylose repressor (xylR), xylose isomerase (xylA), xylose kinase (xylB), YncB (yncb), YncC (yncc), YncD (yncd) and YncE (ynce) genes, complete cds.	Bacillus subtilis	52,282	22-Jan-97
GB_BA1:BSUB0010	233780	Z99113	Bacillus subtilis complete genome (section 10 of 21): from 1781201 to 2014980.	Bacillus subtilis	36,983	26-Nov-97

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BGI-131CP

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 Ala Thr Ala Arg Glu Val Phe Ile Gln Thr Pro Lys Gly His Ile Glu
 230 235 240 245
 tct gct ctt gca ctt ggc gca acc cgc tgg gaa gtc gtt cgt ttg acg 883
 Ser Ala Leu Ala Leu Gly Ala Thr Arg Trp Glu Val Val Arg Leu Thr
 250 255 260
 gtt ctc cca ttc gga atg tcc ggc tac gtt tcc ggc gcg atg ctc ggc 931
 Val Leu Pro Phe Gly Met Ser Gly Tyr Val Ser Gly Ala Met Leu Gly
 265 270 275
 ctc ggc cgc gca ctg ggt gag acc atg gcg cta tac atg gtt gtt tct 979
 Leu Gly Arg Ala Leu Gly Glu Thr Met Ala Leu Tyr Met Val Val Ser
 280 285 290
 cca tcc tcg gcg ttc cgc ttc tcg ctt ttc gat ggc ggt acc acc ttc 1027
 Pro Ser Ser Ala Phe Arg Phe Ser Leu Phe Asp Gly Gly Thr Thr Phe
 295 300 305
 gca acg gcc atc gcc aat gcc gct cca gaa ttc aac gac aac acc cgc 1075
 Ala Thr Ala Ile Ala Asn Ala Ala Pro Glu Phe Asn Asp Asn Thr Arg
 310 315 320 325
 gca ggc gcg tac atc tcc gcc ggc ctc gtg ctg ttc gcc ctt acc ttc 1123
 Ala Gly Ala Tyr Ile Ser Ala Gly Leu Val Leu Phe Ala Leu Thr Phe
 330 335 340
 atc gtc aac gct ggc gct cgc gcc atg gtt aac cgc gga aag 1165
 Ile Val Asn Ala Gly Ala Arg Ala Met Val Asn Arg Gly Lys
 345 350 355
 tagaagggga caaaatcatg act 1188

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Arg	Val	Gln	Ala 20	His	Pro	Val	Ala	Val 25	Asn	Ala	Asn	Ser	Ser 30	Gln	Thr
Lys	Pro	Ser 35	Lys	Lys	Ile	Val	Ala 40	Glu	Gly	Gly	Gly	Ser 45	Val	Lys	Arg
Pro	Gly 50	Asp	Arg	Ile	Phe	Glu 55	Val	Leu	Ser	Thr	Ala 60	Ser	Ala	Ala	Ile
Ile 65	Thr	Ala	Ile	Ile	Ile 70	Ala	Ile	Ala	Ala	Phe 75	Leu	Ile	Trp	Arg	Ala 80
Val	Pro	Ala	Leu	Met 85	Arg	Asn	Ala	Glu	Gly 90	Ile	Gly	Gly	Phe	Phe 95	Thr
Tyr	Ser	Gly	Ala 100	Trp	Asn	Thr	Thr	Asp 105	Ile	Asp	Ala	Met	Tyr 110	Phe	Gly
Ile	Pro	Asn 115	Leu	Leu	Ala	Ala	Thr 120	Leu	Leu	Ile	Ser	Val 125	Ile	Ala	Leu
Ile 130	Ile	Ala	Met	Pro	Ile	Ala 135	Leu	Gly	Ile	Ala	Ile 140	Phe	Leu	Ser	Asn
Tyr 145	Ser	Pro	Lys	Arg	Leu 150	Val	Lys	Pro	Leu	Gly 155	Tyr	Met	Val	Asp	Met 160
Leu	Ala	Ala	Val	Pro 165	Ser	Ile	Val	Tyr	Gly 170	Leu	Trp	Gly	Trp	Gln 175	Val
Leu	Gly	Pro	Ala 180	Leu	Ser	Gly	Phe	Tyr 185	Thr	Trp	Ile	Glu	Ser 190	Trp	Gly
Gly	Ser	Phe 195	Phe	Leu	Phe	Ala	Thr 200	Tyr	Gln	Asn	Ser	Pro 205	Ser	Phe	Ala
Thr 210	Gly	Arg	Asn	Met	Leu	Thr 215	Gly	Gly	Ile	Val	Leu 220	Ala	Val	Met	Ile
Leu 225	Pro	Val	Ile	Glu 230	Ala	Thr	Ala	Arg	Glu	Val 235	Phe	Ile	Gln	Thr	Pro 240
Lys	Gly	His	Ile 245	Glu	Ser	Ala	Leu	Ala	Leu 250	Gly	Ala	Thr	Arg	Trp 255	Glu
Val	Val	Arg	Leu 260	Thr	Val	Leu	Pro	Phe 265	Gly	Met	Ser	Gly	Tyr 270	Val	Ser
Gly	Ala	Met 275	Leu	Gly	Leu	Gly	Arg 280	Ala	Leu	Gly	Glu 285	Thr	Met	Ala	Leu

Tyr Met Val Val Ser Pro Ser Ser Ala Phe Arg Phe Ser Leu Phe Asp
 290 295 300
 Gly Gly Thr Thr Phe Ala Thr Ala Ile Ala Asn Ala Ala Pro Glu Phe
 305 310 315 320
 Asn Asp Asn Thr Arg Ala Gly Ala Tyr Ile Ser Ala Gly Leu Val Leu
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 Phe Ala Leu Thr Phe Ile Val Asn Ala Gly Ala Arg Ala Met Val Asn
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 Arg Gly Lys
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 <223> RXA00774

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 Met Asp Lys Ala Thr
 1 5
 gat gcc ctc ctg cgc act tct ttg gca tcg gca gaa agc gct tta ggc 163
 Asp Ala Leu Leu Arg Thr Ser Leu Ala Ser Ala Glu Ser Ala Leu Gly
 10 15 20
 aat gca gaa aag ctt gaa gag ctt cgt act gga tgc gag tct caa gcc 211
 Asn Ala Glu Lys Leu Glu Glu Leu Arg Thr Gly Cys Glu Ser Gln Ala
 25 30 35
 gtc gaa ctt ttg gcg ctt gaa act cct gta gcc cgt gat ctt cgc cag 259
 Val Glu Leu Leu Ala Leu Glu Thr Pro Val Ala Arg Asp Leu Arg Gln
 40 45 50
 gtt gtc tcc tcc atc tac atc gtc gag gaa att acc cgt atg ggt gct 307
 Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile Thr Arg Met Gly Ala
 55 60 65
 ctg gca atg cac gtg gct aat tcc gtg cgc cgc cgt tac ccc gat ccg 355
 Leu Ala Met His Val Ala Asn Ser Val Arg Arg Arg Tyr Pro Asp Pro
 70 75 80 85
 gtg atc ccg gag gac atg cgt ggc tat ttc aag gag atg gcc cgc ctc 403
 Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys Glu Met Ala Arg Leu
 90 95 100
 gca gct gac atg aca gat cat att cgt cag atc ctc att gat cct gaa 451
 Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile Leu Ile Asp Pro Glu
 105 110 115

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cca gat ctt gcc cta gag atg gct aaa agc gat gac gcg gtg gat gat 499
Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp Asp Ala Val Asp Asp
      120              125              130

ctg cat cag cac atc atg cgt att ctc acg ctg cgt cct tgg cct cac 547
Leu His Gln His Ile Met Arg Ile Leu Thr Leu Arg Pro Trp Pro His
      135              140              145

gac acc aag agc gcg gtt gat ttg acg ctg ctt tcc cgc ttc tac gag 595
Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu Ser Arg Phe Tyr Glu
      150              155              160              165

cgt tac gcc gat cac acg gta aac gtg gcc gcc cgt atc att tac ctg 643
Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala Arg Ile Ile Tyr Leu
      170              175              180

tcc acc ggg ctg cac ccg gag gag tac atg gaa aag cgc gag caa caa 691
Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu Lys Arg Glu Gln Gln
      185              190              195

agg gcc gat gcc gac atg gag aag cgc tgg gcc gag ctg gag cgg cag 739
Arg Ala Asp Ala Asp Met Glu Lys Arg Trp Ala Glu Leu Glu Arg Gln
      200              205              210

ttc cgc acc agc gag taaaaagctg cttctcgacg cta 777
Phe Arg Thr Ser Glu
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<210> 8
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<212> PRT
<213> Corynebacterium glutamicum

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Glu Ser Ala Leu Gly Asn Ala Glu Lys Leu Glu Glu Leu Arg Thr Gly
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Cys Glu Ser Gln Ala Val Glu Leu Leu Ala Leu Glu Thr Pro Val Ala
      35              40              45

Arg Asp Leu Arg Gln Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile
      50              55              60

Thr Arg Met Gly Ala Leu Ala Met His Val Ala Asn Ser Val Arg Arg
      65              70              75              80

Arg Tyr Pro Asp Pro Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys
      85              90              95

Glu Met Ala Arg Leu Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile
      100              105              110

Leu Ile Asp Pro Glu Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp
      115              120              125

Asp Ala Val Asp Asp Leu His Gln His Ile Met Arg Ile Leu Thr Leu
      130              135              140

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Arg Pro Trp Pro His Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu
145                      150                      155                      160

Ser Arg Phe Tyr Glu Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala
                      165                      170                      175

Arg Ile Ile Tyr Leu Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu
                      180                      185                      190

Lys Arg Glu Gln Gln Arg Ala Asp Ala Asp Met Glu Lys Arg Trp Ala
                      195                      200                      205

Glu Leu Glu Arg Gln Phe Arg Thr Ser Glu
210                      215

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<210> 9
<211> 1695
<212> DNA
<213> Corynebacterium glutamicum

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<220>
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<222> (101)..(1672)
<223> RXA00204

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gcgaaagccg cacagaacac gcaacacgag gtgagcctag atg gtg aac tct gaa 115
                                   Met Val Asn Ser Glu
                                   1                      5

caa gcg ctt cat cag cat gat cct gca cca atc ctt cag ttg gat aaa 163
Gln Ala Leu His Gln His Asp Pro Ala Pro Ile Leu Gln Leu Asp Lys
                      10                      15                      20

gtc tcc aag tcg ttt ggc cca gtc aac gtc att aat caa gtg agc atc 211
Val Ser Lys Ser Phe Gly Pro Val Asn Val Ile Asn Gln Val Ser Ile
                      25                      30                      35

gat gtt cgc cct ggc agg gtg ctt gcg ctg ttg ggt gaa aat ggt gcg 259
Asp Val Arg Pro Gly Arg Val Leu Ala Leu Leu Gly Glu Asn Gly Ala
                      40                      45                      50

ggt aaa tct acg ctg atc aag atg atg tcg ggt gtg tat cag cct gat 307
Gly Lys Ser Thr Leu Ile Lys Met Met Ser Gly Val Tyr Gln Pro Asp
                      55                      60                      65

ggc ggg cag att ttg gtg gat gga aag ccc acg act ttg cct gat acg 355
Gly Gly Gln Ile Leu Val Asp Gly Lys Pro Thr Thr Leu Pro Asp Thr
                      70                      75                      80                      85

aaa act gct gag tct ttt ggc atc gct acg att cac cag gaa ttg aat 403
Lys Thr Ala Glu Ser Phe Gly Ile Ala Thr Ile His Gln Glu Leu Asn
                      90                      95                      100

ctg gtg ccc acg atg acg gtg gcg gaa aac gtc atg ctg ggc cgc act 451
Leu Val Pro Thr Met Thr Val Ala Glu Asn Val Met Leu Gly Arg Thr
                      105                      110                      115

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BGI-131CP

cct cgg aag tgg ggt ttg gtc aat ttc aaa cat ttg cgc agg cag gca	499
Pro Arg Lys Trp Gly Leu Val Asn Phe Lys His Leu Arg Arg Gln Ala	
120 125 130	
cag gcg gcg ctg gat ctc atc ggc gtg gat gtg gat ctg aat gct cag	547
Gln Ala Ala Leu Asp Leu Ile Gly Val Asp Val Asp Leu Asn Ala Gln	
135 140 145	
gtg ggt tct tta gga atc gct agg cag cag atg gtg gag atc gcc aag	595
Val Gly Ser Leu Gly Ile Ala Arg Gln Gln Met Val Glu Ile Ala Lys	
150 155 160 165	
gcg ttg tcc atg aat gcg cgg ata ttg att ttg gat gag ccc act gca	643
Ala Leu Ser Met Asn Ala Arg Ile Leu Ile Leu Asp Glu Pro Thr Ala	
170 175 180	
gcg ttg act ggt cgt gaa att gat cag tta ttc aaa gtg gtg gat cag	691
Ala Leu Thr Gly Arg Glu Ile Asp Gln Leu Phe Lys Val Val Asp Gln	
185 190 195	
ctg aaa gaa aaa ggc gtg gcc atg gtg ttt att tcg cac cac ttg gat	739
Leu Lys Glu Lys Gly Val Ala Met Val Phe Ile Ser His His Leu Asp	
200 205 210	
gag atc gcg cgc atc ggc gat acc gtc tct gtg ctg cgt gat ggc cag	787
Glu Ile Ala Arg Ile Gly Asp Thr Val Ser Val Leu Arg Asp Gly Gln	
215 220 225	
ttc atc gcg gag ctg cca gcg gat act gat gaa gat gag ctg gtg cgg	835
Phe Ile Ala Glu Leu Pro Ala Asp Thr Asp Glu Asp Glu Leu Val Arg	
230 235 240 245	
ctg atg gtg ggt cgt agc att gaa aac cag tat ccg cgt agt gcg cca	883
Leu Met Val Gly Arg Ser Ile Glu Asn Gln Tyr Pro Arg Ser Ala Pro	
250 255 260	
gag atc ggg cag cca ctg ttg gag gtg aaa aac ctc aac gcg gag ggc	931
Glu Ile Gly Gln Pro Leu Leu Glu Val Lys Asn Leu Asn Ala Glu Gly	
265 270 275	
cgg ttc acg gat att tcc ttg act gtt cgc gct ggt gaa gtc gta ggc	979
Arg Phe Thr Asp Ile Ser Leu Thr Val Arg Ala Gly Glu Val Val Gly	
280 285 290	
ctt gcc ggt ctt gtg ggt gct ggt cgc acg gaa gtg gtt cgc tcg att	1027
Leu Ala Gly Leu Val Gly Ala Gly Arg Thr Glu Val Val Arg Ser Ile	
295 300 305	
gct ggc gtg gac aaa gtt gat tcc ggt gag gtg atc gtt gct ggc aag	1075
Ala Gly Val Asp Lys Val Asp Ser Gly Glu Val Ile Val Ala Gly Lys	
310 315 320 325	
aaa ttg cgc ggc ggc gat att tcc gag gct att aaa aac ggc atc ggg	1123
Lys Leu Arg Gly Gly Asp Ile Ser Glu Ala Ile Lys Asn Gly Ile Gly	
330 335 340	
cac att ccg gaa gat cga aaa gcc cag ggc ctg gtg ctg ggg tcg tct	1171
His Ile Pro Glu Asp Arg Lys Ala Gln Gly Leu Val Leu Gly Ser Ser	
345 350 355	

gtg gag gac aac ctg gga ttg gcg act ttg gcg tcg aca gcc cgc gca 1219
 Val Glu Asp Asn Leu Gly Leu Ala Thr Leu Ala Ser Thr Ala Arg Ala
 360 365 370

ggt ttg gtc gat cga tca gga cag cac aaa cga gcc gcc gag gtc gcg 1267
 Gly Leu Val Asp Arg Ser Gly Gln His Lys Arg Ala Ala Glu Val Ala
 375 380 385

gaa aaa ctc cgc atc cgg atg gca agc ctc aaa caa ccg att agc gat 1315
 Glu Lys Leu Arg Ile Arg Met Ala Ser Leu Lys Gln Pro Ile Ser Asp
 390 395 400 405

tta tcg ggc ggc aat cag caa aag gcc gtg ttc ggc cgc tgg gtg ctt 1363
 Leu Ser Gly Gly Asn Gln Gln Lys Ala Val Phe Gly Arg Trp Val Leu
 410 415 420

gcc ggg tca aac gtg ctg ctt ctc gac gaa ccg acc cgt ggc gtt gac 1411
 Ala Gly Ser Asn Val Leu Leu Leu Asp Glu Pro Thr Arg Gly Val Asp
 425 430 435

gtc ggc gcg aag gtg gaa att tac aac atc att aat gag atg acg gaa 1459
 Val Gly Ala Lys Val Glu Ile Tyr Asn Ile Ile Asn Glu Met Thr Glu
 440 445 450

aaa ggt ggc gct gtg ctc atg gtg tca tcg gag ctt ccc gaa gtc ttg 1507
 Lys Gly Gly Ala Val Leu Met Val Ser Ser Glu Leu Pro Glu Val Leu
 455 460 465

ggc atg gct gat cgc att ttg gtc atg tct ggt gga cgc atc gca ggc 1555
 Gly Met Ala Asp Arg Ile Leu Val Met Ser Gly Gly Arg Ile Ala Gly
 470 475 480 485

gaa ctg cca gcg aag gga aca acc cag gac gat gtc atg gct cta gct 1603
 Glu Leu Pro Ala Lys Gly Thr Thr Gln Asp Asp Val Met Ala Leu Ala
 490 495 500

gtt tcc cag gtg gat gat tcc atc acc gag gaa gct gct gca gaa atc 1651
 Val Ser Gln Val Asp Asp Ser Ile Thr Glu Glu Ala Ala Glu Ile
 505 510 515

gaa aac aca aag gag gac cgt tgagcaccgc cgtagtttca cag 1695
 Glu Asn Thr Lys Glu Asp Arg
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<210> 10

<211> 524

<212> PRT

<213> Corynebacterium glutamicum

<400> 10

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 20 25 30

Asn Gln Val Ser Ile Asp Val Arg Pro Gly Arg Val Leu Ala Leu Leu
 35 40 45

Gly Glu Asn Gly Ala Gly Lys Ser Thr Leu Ile Lys Met Met Ser Gly

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Val Tyr Gln Pro Asp Gly Gly Gln Ile Leu Val Asp Gly Lys Pro Thr		
65	70	75 80
Thr Leu Pro Asp Thr Lys Thr Ala Glu Ser Phe Gly Ile Ala Thr Ile		
	85	90 95
His Gln Glu Leu Asn Leu Val Pro Thr Met Thr Val Ala Glu Asn Val		
	100	105 110
Met Leu Gly Arg Thr Pro Arg Lys Trp Gly Leu Val Asn Phe Lys His		
	115	120 125
Leu Arg Arg Gln Ala Gln Ala Ala Leu Asp Leu Ile Gly Val Asp Val		
	130	135 140
Asp Leu Asn Ala Gln Val Gly Ser Leu Gly Ile Ala Arg Gln Gln Met		
	145	150 155 160
Val Glu Ile Ala Lys Ala Leu Ser Met Asn Ala Arg Ile Leu Ile Leu		
	165	170 175
Asp Glu Pro Thr Ala Ala Leu Thr Gly Arg Glu Ile Asp Gln Leu Phe		
	180	185 190
Lys Val Val Asp Gln Leu Lys Glu Lys Gly Val Ala Met Val Phe Ile		
	195	200 205
Ser His His Leu Asp Glu Ile Ala Arg Ile Gly Asp Thr Val Ser Val		
	210	215 220
Leu Arg Asp Gly Gln Phe Ile Ala Glu Leu Pro Ala Asp Thr Asp Glu		
	225	230 235 240
Asp Glu Leu Val Arg Leu Met Val Gly Arg Ser Ile Glu Asn Gln Tyr		
	245	250 255
Pro Arg Ser Ala Pro Glu Ile Gly Gln Pro Leu Leu Glu Val Lys Asn		
	260	265 270
Leu Asn Ala Glu Gly Arg Phe Thr Asp Ile Ser Leu Thr Val Arg Ala		
	275	280 285
Gly Glu Val Val Gly Leu Ala Gly Leu Val Gly Ala Gly Arg Thr Glu		
	290	295 300
Val Val Arg Ser Ile Ala Gly Val Asp Lys Val Asp Ser Gly Glu Val		
	305	310 315 320
Ile Val Ala Gly Lys Lys Leu Arg Gly Gly Asp Ile Ser Glu Ala Ile		
	325	330 335
Lys Asn Gly Ile Gly His Ile Pro Glu Asp Arg Lys Ala Gln Gly Leu		
	340	345 350
Val Leu Gly Ser Ser Val Glu Asp Asn Leu Gly Leu Ala Thr Leu Ala		
	355	360 365
Ser Thr Ala Arg Ala Gly Leu Val Asp Arg Ser Gly Gln His Lys Arg		
	370	375 380

Ala Ala Glu Val Ala Glu Lys Leu Arg Ile Arg Met Ala Ser Leu Lys
385 390 395 400

Gln Pro Ile Ser Asp Leu Ser Gly Gly Asn Gln Gln Lys Ala Val Phe
405 410 415

Gly Arg Trp Val Leu Ala Gly Ser Asn Val Leu Leu Leu Asp Glu Pro
420 425 430

Thr Arg Gly Val Asp Val Gly Ala Lys Val Glu Ile Tyr Asn Ile Ile
435 440 445

Asn Glu Met Thr Glu Lys Gly Gly Ala Val Leu Met Val Ser Ser Glu
450 455 460

Leu Pro Glu Val Leu Gly Met Ala Asp Arg Ile Leu Val Met Ser Gly
465 470 475 480

Gly Arg Ile Ala Gly Glu Leu Pro Ala Lys Gly Thr Thr Gln Asp Asp
485 490 495

Val Met Ala Leu Ala Val Ser Gln Val Asp Asp Ser Ile Thr Glu Glu
500 505 510

Ala Ala Ala Glu Ile Glu Asn Thr Lys Glu Asp Arg
515 520

<210> 11

<211> 882

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(859)

<223> RXA02438

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tgctcaatca ccgattcgag cgtttcaaca aggagcgatc atg aca gac ctc att 115
Met Thr Asp Leu Ile
1 5

caa ctc cgc gaa gta tcc aaa aaa tac ggt gct ttc cag gcc ctc aac 163
Gln Leu Arg Glu Val Ser Lys Lys Tyr Gly Ala Phe Gln Ala Leu Asn
10 15 20

gac atc aat ttg aac gtc cgc gca ggc gaa gtc acc tgt gtt ctg ggt 211
Asp Ile Asn Leu Asn Val Arg Ala Gly Glu Val Thr Cys Val Leu Gly
25 30 35

gac aac ggc gcc gga aaa tcc acc ctc atc aag att ctc tcc ggc ctg 259
Asp Asn Gly Ala Gly Lys Ser Thr Leu Ile Lys Ile Leu Ser Gly Leu
40 45 50

cat ccc gcc acc tcc ggc gaa gta atc gtg gcc ggc gat gta gtg aat 307
His Pro Ala Thr Ser Gly Glu Val Ile Val Ala Gly Asp Val Val Asn
55 60 65

CCDS: C131CP.1

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ttt gga tcc ccc cgc gac gcc ctc gac gcc gga atc gcc acc gtc tac 355
Phe Gly Ser Pro Arg Asp Ala Leu Asp Ala Gly Ile Ala Thr Val Tyr
70 75 80 85

caa gac cta gca gtg gtc ggg cag atg agt gtg tgg cgc aac ttc ttc 403
Gln Asp Leu Ala Val Val Gly Gln Met Ser Val Trp Arg Asn Phe Phe
90 95 100

ctc ggc cag gaa ctc acc ggc cga ttt ggc gtt ctg aaa caa gaa gaa 451
Leu Gly Gln Glu Leu Thr Gly Arg Phe Gly Val Leu Lys Gln Glu Glu
105 110 115

atg cgc cgc atc acc gac gaa caa ctc cgc gaa atg ggc atc gaa ctc 499
Met Arg Arg Ile Thr Asp Glu Gln Leu Arg Glu Met Gly Ile Glu Leu
120 125 130

cgc gat gtc gac gtc cct gtg gcc tcc ctt tca ggt ggt caa cgc caa 547
Arg Asp Val Asp Val Pro Val Ala Ser Leu Ser Gly Gly Gln Arg Gln
135 140 145

gtt gtc gcc atc gcc cgc gcc atc tac ttc ggc gcg cgc gtc ctc att 595
Val Val Ala Ile Ala Arg Ala Ile Tyr Phe Gly Ala Arg Val Leu Ile
150 155 160 165

ttg gac gag ccc acc gca gcg ctg ggc gtg aaa caa tct ggc atg gtg 643
Leu Asp Glu Pro Thr Ala Ala Leu Gly Val Lys Gln Ser Gly Met Val
170 175 180

ctg cgc ttt att gcc gca gca cgc gac cgg ggg atc ggc gtc att ttc 691
Leu Arg Phe Ile Ala Ala Ala Arg Asp Arg Gly Ile Gly Val Ile Phe
185 190 195

atc acg cac aac ccc cac cac gcc tac ctt gtc ggt gat cac ttc atc 739
Ile Thr His Asn Pro His His Ala Tyr Leu Val Gly Asp His Phe Ile
200 205 210

ctg ctc aac tta ggc aag cag gtc atg gac aaa tcc cgc gca gaa gtc 787
Leu Leu Asn Leu Gly Lys Gln Val Met Asp Lys Ser Arg Ala Glu Val
215 220 225

gag ctg gaa gaa ctc acc ctc gcc atg tcc ggc ggc ggc gag ctc gac 835
Glu Leu Glu Glu Leu Thr Leu Ala Met Ser Gly Gly Gly Glu Leu Asp
230 235 240 245

tca ctc agc cac gaa ttg aag cgt taacctactt cttcttttcg ctc 882
Ser Leu Ser His Glu Leu Lys Arg
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<210> 12

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 12

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Phe Gln Ala Leu Asn Asp Ile Asn Leu Asn Val Arg Ala Gly Glu Val
20 25 30

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Thr	Cys	Val	Leu	Gly	Asp	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Ile	Lys
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Ile	Leu	Ser	Gly	Leu	His	Pro	Ala	Thr	Ser	Gly	Glu	Val	Ile	Val	Ala
	50					55					60				
Gly	Asp	Val	Val	Asn	Phe	Gly	Ser	Pro	Arg	Asp	Ala	Leu	Asp	Ala	Gly
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Ile	Ala	Thr	Val	Tyr	Gln	Asp	Leu	Ala	Val	Val	Gly	Gln	Met	Ser	Val
				85					90					95	
Trp	Arg	Asn	Phe	Phe	Leu	Gly	Gln	Glu	Leu	Thr	Gly	Arg	Phe	Gly	Val
			100					105					110		
Leu	Lys	Gln	Glu	Glu	Met	Arg	Arg	Ile	Thr	Asp	Glu	Gln	Leu	Arg	Glu
		115					120					125			
Met	Gly	Ile	Glu	Leu	Arg	Asp	Val	Asp	Val	Pro	Val	Ala	Ser	Leu	Ser
	130					135					140				
Gly	Gly	Gln	Arg	Gln	Val	Val	Ala	Ile	Ala	Arg	Ala	Ile	Tyr	Phe	Gly
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Ala	Arg	Val	Leu	Ile	Leu	Asp	Glu	Pro	Thr	Ala	Ala	Leu	Gly	Val	Lys
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Gln	Ser	Gly	Met	Val	Leu	Arg	Phe	Ile	Ala	Ala	Ala	Arg	Asp	Arg	Gly
			180					185					190		
Ile	Gly	Val	Ile	Phe	Ile	Thr	His	Asn	Pro	His	His	Ala	Tyr	Leu	Val
		195					200					205			
Gly	Asp	His	Phe	Ile	Leu	Leu	Asn	Leu	Gly	Lys	Gln	Val	Met	Asp	Lys
	210					215					220				
Ser	Arg	Ala	Glu	Val	Glu	Leu	Glu	Glu	Leu	Thr	Leu	Ala	Met	Ser	Gly
225					230					235					240
Gly	Gly	Glu	Leu	Asp	Ser	Leu	Ser	His	Glu	Leu	Lys	Arg			
				245					250						

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<210> 13
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101)..(1012)  
<223> RXA00203
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acagaagaag tccacaacgg catccaaaat tggacattgg atg ctc aat aac ggt 115
Met Leu Asn Asn Gly
      1           5
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gcg ttg gtg ggg ctg att gca ctg tgt gtt gga ctt ttt att gca aca 163
 Ala Leu Val Gly Leu Ile Ala Leu Cys Val Gly Leu Phe Ile Ala Thr
 10 15 20

ccc cac ttt ctc acc att cct aac ctg atc aac atc ggt atc caa tcg 211
 Pro His Phe Leu Thr Ile Pro Asn Leu Ile Asn Ile Gly Ile Gln Ser
 25 30 35

gcg acg gtg gcg atc ctg gcg ttc ggc atg acc ttc gtc atc gtt acc 259
 Ala Thr Val Ala Ile Leu Ala Phe Gly Met Thr Phe Val Ile Val Thr
 40 45 50

gca ggc att gat ttg tct gtg gga tca gtg gct gcg ttg ggt gcg atg 307
 Ala Gly Ile Asp Leu Ser Val Gly Ser Val Ala Ala Leu Gly Ala Met
 55 60 65

acc tcg gcg tat ttc ttc gcg gaa gtt ggt ttg ccg ggc tgg atc acg 355
 Thr Ser Ala Tyr Phe Phe Ala Glu Val Gly Leu Pro Gly Trp Ile Thr
 70 75 80 85

ctg ctg att ggc ctg ttc atc gga ttg ttg gcg ggt gcg atc tct ggc 403
 Leu Leu Ile Gly Leu Phe Ile Gly Leu Leu Ala Gly Ala Ile Ser Gly
 90 95 100

att tct att gct tat ggc aag ttg cct gcg ttt att gcc acc ttg gcc 451
 Ile Ser Ile Ala Tyr Gly Lys Leu Pro Ala Phe Ile Ala Thr Leu Ala
 105 110 115

atg atg tcg atc gcc agg gga atc acc ttg gtc att tcc caa ggc tca 499
 Met Met Ser Ile Ala Arg Gly Ile Thr Leu Val Ile Ser Gln Gly Ser
 120 125 130

cca att ccc agt gca cca gct gtg aac gct ttg ggg cgc acc tac ttt 547
 Pro Ile Pro Ser Ala Pro Ala Val Asn Ala Leu Gly Arg Thr Tyr Phe
 135 140 145

ggc atc ccg atg ccg att ctg atg atg gca ctg gct ggc att gtg tgt 595
 Gly Ile Pro Met Pro Ile Leu Met Met Ala Leu Ala Gly Ile Val Cys
 150 155 160 165

tgg ttt att ttg agc cgc acc gtg ctg gga cgg tcc atg tac gcc att 643
 Trp Phe Ile Leu Ser Arg Thr Val Leu Gly Arg Ser Met Tyr Ala Ile
 170 175 180

ggc gga aac atg gaa gca gcc cga cta tct ggt ctg cca gtg aag aaa 691
 Gly Gly Asn Met Glu Ala Ala Arg Leu Ser Gly Leu Pro Val Lys Lys
 185 190 195

atc ctg gtc atg gtc tat gca ctg gct ggt gtg tat gca gca ctt gcg 739
 Ile Leu Val Met Val Tyr Ala Leu Ala Gly Val Tyr Ala Ala Leu Ala
 200 205 210

ggt ctg gtc atg acg gga cgc ttg tcg tcc gcg cag ccg cag gca ggc 787
 Gly Leu Val Met Thr Gly Arg Leu Ser Ser Ala Gln Pro Gln Ala Gly
 215 220 225

gtg gga tac gaa ctc gat gcg att gcc gcc gtg gtc att ggt ggt gcg 835
 Val Gly Tyr Glu Leu Asp Ala Ile Ala Ala Val Val Ile Gly Gly Ala
 230 235 240 245

tca ctt gct ggc gga acc gga aaa gca acg ggc act ttg att ggt gcc 883

BGI-131CP: 1-1000

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<212> PRT
<213> Corynebacterium glutamicum

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Leu Phe Ile Ala Thr Pro His Phe Leu Thr Ile Pro Asn Leu Ile Asn
          20          25          30
Ile Gly Ile Gln Ser Ala Thr Val Ala Ile Leu Ala Phe Gly Met Thr
          35          40          45
Phe Val Ile Val Thr Ala Gly Ile Asp Leu Ser Val Gly Ser Val Ala
          50          55          60
Ala Leu Gly Ala Met Thr Ser Ala Tyr Phe Phe Ala Glu Val Gly Leu
          65          70          75          80
Pro Gly Trp Ile Thr Leu Leu Ile Gly Leu Phe Ile Gly Leu Leu Ala
          85          90          95
Gly Ala Ile Ser Gly Ile Ser Ile Ala Tyr Gly Lys Leu Pro Ala Phe
          100          105          110
Ile Ala Thr Leu Ala Met Met Ser Ile Ala Arg Gly Ile Thr Leu Val
          115          120          125
Ile Ser Gln Gly Ser Pro Ile Pro Ser Ala Pro Ala Val Asn Ala Leu
          130          135          140
Gly Arg Thr Tyr Phe Gly Ile Pro Met Pro Ile Leu Met Met Ala Leu
          145          150          155          160
Ala Gly Ile Val Cys Trp Phe Ile Leu Ser Arg Thr Val Leu Gly Arg
          165          170          175
Ser Met Tyr Ala Ile Gly Gly Asn Met Glu Ala Ala Arg Leu Ser Gly
          180          185          190
Leu Pro Val Lys Lys Ile Leu Val Met Val Tyr Ala Leu Ala Gly Val

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[illegible]

Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	35.2	12.5	18	65	0.15	3.2	0.98
Gender	0.45	0.50	0	1	-0.05	3.0	0.99
Education	12.5	2.5	8	16	0.20	3.5	0.97
Income	45000	15000	20000	80000	0.30	3.8	0.96
Health	0.75	0.25	0	1	-0.10	3.1	0.99
Stress	0.60	0.20	0	1	-0.05	3.0	0.99
Depression	0.55	0.25	0	1	-0.05	3.0	0.99
Life Satisfaction	0.70	0.20	0	1	-0.05	3.0	0.99
Resilience	0.65	0.25	0	1	-0.05	3.0	0.99
Optimism	0.60	0.25	0	1	-0.05	3.0	0.99
Gratitude	0.55	0.25	0	1	-0.05	3.0	0.99
Forgiveness	0.50	0.25	0	1	-0.05	3.0	0.99
Compassion	0.45	0.25	0	1	-0.05	3.0	0.99
Kindness	0.40	0.25	0	1	-0.05	3.0	0.99
Generosity	0.35	0.25	0	1	-0.05	3.0	0.99
Patience	0.30	0.25	0	1	-0.05	3.0	0.99
Humility	0.25	0.25	0	1	-0.05	3.0	0.99
Modesty	0.20	0.25	0	1	-0.05	3.0	0.99
Shyness	0.15	0.25	0	1	-0.05	3.0	0.99
Introversion	0.10	0.25	0	1	-0.05	3.0	0.99
Neuroticism	0.05	0.25	0	1	-0.05	3.0	0.99
Extraversion	0.00	0.25	0	1	-0.05	3.0	0.99
Agreeableness	0.00	0.25	0	1	-0.05	3.0	0.99
Conscientiousness	0.00	0.25	0	1	-0.05	3.0	0.99
Openness	0.00	0.25	0	1	-0.05	3.0	0.99
Emotional Stability	0.00	0.25	0	1	-0.05	3.0	0.99
Psychological Well-being	0.00	0.25	0	1	-0.05	3.0	0.99
Life Satisfaction	0.00	0.25	0	1	-0.05	3.0	0.99
Meaning in Life	0.00	0.25	0	1	-0.05	3.0	0.99
Positive Psychology	0.00	0.25	0	1	-0.05	3.0	0.99
Flow	0.00	0.25	0	1	-0.05	3.0	0.99
Resilience	0.00	0.25	0	1	-0.05	3.0	0.99
Optimism	0.00	0.25	0	1	-0.05	3.0	0.99
Gratitude	0.00	0.25	0	1	-0.05	3.0	0.99
Forgiveness	0.00	0.25	0	1	-0.05	3.0	0.99
Compassion	0.00	0.25	0	1	-0.05	3.0	0.99
Kindness	0.00	0.25	0	1	-0.05	3.0	0.99
Generosity	0.00	0.25	0	1	-0.05	3.0	0.99
Patience	0.00	0.25	0	1	-0.05	3.0	0.99
Humility	0.00	0.25	0	1	-0.05	3.0	0.99
Modesty	0.00	0.25	0	1	-0.05	3.0	0.99
Shyness	0.00	0.25	0	1	-0.05	3.0	0.99
Introversion	0.00	0.25	0	1	-0.05	3.0	0.99
Neuroticism	0.00	0.25	0	1	-0.05	3.0	0.99
Extraversion	0.00	0.25	0	1	-0.05	3.0	0.99
Agreeableness	0.00	0.25	0	1	-0.05	3.0	0.99
Conscientiousness	0.00	0.25	0	1	-0.05	3.0	0.99
Openness	0.00	0.25	0	1	-0.05	3.0	0.99
Emotional Stability	0.00	0.25	0	1	-0.05	3.0	0.99
Psychological Well-being	0.00	0.25	0	1	-0.05	3.0	0.99
Life Satisfaction	0.00	0.25	0	1	-0.05	3.0	0.99

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<223> RXA00270
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gag	ttc	gga	ttg	ttg	tac	gga	g	tt	g	tc	gca	ttg	ggc	g	tc	tat	ttg	acg			163
Glu	Phe	Gly	Leu	Leu	Tyr	Gly	Val	Val	Val	Ala	Leu	Gly	Val	Tyr	Leu	Thr					
ttc	cgt	gtg	ctc	aac	ttt	ccc	gac	ctc	acc	g	tt	gac	ggc	agc	ctg	acc					211
Phe	Arg	Val	Leu	Asn	Phe	Pro	Asp	Leu	Thr	Val	Asp	Gly	Ser	Leu	Thr						
act	ggc	gcg	gca	aca	gct	gcg	aca	gct	ctt	atg	tct	ggc	tgg	cct	ccc					259	
Thr	Gly	Ala	Ala	Thr	Ala	Ala	Thr	Ala	Leu	Met	Ser	Gly	Trp	Pro	Pro						
ctt	atg	gct	act	gcc	gct	ggt	ttc	g	tt	act	ggc	ttt	atc	gct	ggc	atg					307
Leu	Met	Ala	Thr	Ala	Ala	Gly	Phe	Val	Thr	Gly	Phe	Ile	Ala	Gly	Met						
atc	acc	ggt	ttg	ctg	cac	acc	aag	ggc	aag	atc	gat	ggt	ttg	ctc	gca					355	
Ile	Thr	Gly	Leu	Leu	His	Thr	Lys	Gly	Lys	Ile	Asp	Gly	Leu	Leu	Ala						

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ggg att ttg acc atg att gcg ttg tgg tcg gtt aac ttg cgc atc atg 403
Gly Ile Leu Thr Met Ile Ala Leu Trp Ser Val Asn Leu Arg Ile Met
          90                      95                      100

ggg ggc gcg aac gtg cca ttg ttg cgc acc gat aac ctc ttc acc ccg 451
Gly Gly Ala Asn Val Pro Leu Leu Arg Thr Asp Asn Leu Phe Thr Pro
          105                      110                      115

ctt cgc gac gcc ggc ctc ctc ggc aca tgg gca ggc ccg gcg atc ctc 499
Leu Arg Asp Ala Gly Leu Leu Gly Thr Trp Ala Gly Pro Ala Ile Leu
          120                      125                      130

gcc gtt gca gtg gga att ttg gga ctc atc gtc atc tgg ttc ctc aac 547
Ala Val Ala Val Gly Ile Leu Gly Leu Ile Val Ile Trp Phe Leu Asn
          135                      140                      145

act gat atc gga ctg tcg ctg cga tcc acc ggc gac aac ggg ccg atg 595
Thr Asp Ile Gly Leu Ser Leu Arg Ser Thr Gly Asp Asn Gly Pro Met
          150                      155                      160

gtg cag tcc ttt ggt gtt tca acg gat ttc acc aaa atc ctc acc atc 643
Val Gln Ser Phe Gly Val Ser Thr Asp Phe Thr Lys Ile Leu Thr Ile
          170                      175                      180

tcc ctg tcc aat ggt ttt gtt ggt ctt gcc ggt gca ctc atc gct cag 691
Ser Leu Ser Asn Gly Phe Val Gly Leu Ala Gly Ala Leu Ile Ala Gln
          185                      190                      195

tac cag ggc ttc gca gat att tcg atg ggt att ggc ctc atc gtg atc 739
Tyr Gln Gly Phe Ala Asp Ile Ser Met Gly Ile Gly Leu Ile Val Ile
          200                      205                      210

ggg ctc gca tcg gtt att ttg ggc cag gcc atc ttc ggt cag cgt cgc 787
Gly Leu Ala Ser Val Ile Leu Gly Gln Ala Ile Phe Gly Gln Arg Arg
          215                      220                      225

gtg tgg ttg gct gtg ttg gct gtc atc gtc ggt gcc atc gcg tac cgc 835
Val Trp Leu Ala Val Leu Ala Val Ile Val Gly Ala Ile Ala Tyr Arg
          230                      235                      240

ctg atc att ttc gca gca ctg cgc gtt ggc ctt gac ccc aac gat atg 883
Leu Ile Ile Phe Ala Ala Leu Arg Val Gly Leu Asp Pro Asn Asp Met
          250                      255                      260

aag gca att tct gcg atc ttg gtg gtt gtc gcc atg ctg ctg ccg agg 931
Lys Ala Ile Ser Ala Ile Leu Val Val Val Ala Met Leu Leu Pro Arg
          265                      270                      275

tgg cgt gcg aag ttc tcc aag gca ccg aag cct aag caa cca gta gca 979
Trp Arg Ala Lys Phe Ser Lys Ala Pro Lys Pro Lys Gln Pro Val Ala
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gtg gag gct taagacatgt tatccatcaa cgg 1011
Val Glu Ala
          295

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<210> 16

<211> 296

<212> PRT

<213> Corynebacterium glutamicum

<400> 16

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Gly	Val	Tyr	Leu	Thr	Phe	Arg	Val	Leu	Asn	Phe	Pro	Asp	Leu	Thr	Val	20	25	30	
Asp	Gly	Ser	Leu	Thr	Thr	Gly	Ala	Ala	Thr	Ala	Ala	Thr	Ala	Leu	Met	35	40	45	
Ser	Gly	Trp	Pro	Pro	Leu	Met	Ala	Thr	Ala	Ala	Gly	Phe	Val	Thr	Gly	50	55	60	
Phe	Ile	Ala	Gly	Met	Ile	Thr	Gly	Leu	Leu	His	Thr	Lys	Gly	Lys	Ile	65	70	75	80
Asp	Gly	Leu	Leu	Ala	Gly	Ile	Leu	Thr	Met	Ile	Ala	Leu	Trp	Ser	Val	85	90	95	
Asn	Leu	Arg	Ile	Met	Gly	Gly	Ala	Asn	Val	Pro	Leu	Leu	Arg	Thr	Asp	100	105	110	
Asn	Leu	Phe	Thr	Pro	Leu	Arg	Asp	Ala	Gly	Leu	Leu	Gly	Thr	Trp	Ala	115	120	125	
Gly	Pro	Ala	Ile	Leu	Ala	Val	Ala	Val	Gly	Ile	Leu	Gly	Leu	Ile	Val	130	135	140	
Ile	Trp	Phe	Leu	Asn	Thr	Asp	Ile	Gly	Leu	Ser	Leu	Arg	Ser	Thr	Gly	145	150	155	160
Asp	Asn	Gly	Pro	Met	Val	Gln	Ser	Phe	Gly	Val	Ser	Thr	Asp	Phe	Thr	165	170	175	
Lys	Ile	Leu	Thr	Ile	Ser	Leu	Ser	Asn	Gly	Phe	Val	Gly	Leu	Ala	Gly	180	185	190	
Ala	Leu	Ile	Ala	Gln	Tyr	Gln	Gly	Phe	Ala	Asp	Ile	Ser	Met	Gly	Ile	195	200	205	
Gly	Leu	Ile	Val	Ile	Gly	Leu	Ala	Ser	Val	Ile	Leu	Gly	Gln	Ala	Ile	210	215	220	
Phe	Gly	Gln	Arg	Arg	Val	Trp	Leu	Ala	Val	Leu	Ala	Val	Ile	Val	Gly	225	230	235	240
Ala	Ile	Ala	Tyr	Arg	Leu	Ile	Ile	Phe	Ala	Ala	Leu	Arg	Val	Gly	Leu	245	250	255	
Asp	Pro	Asn	Asp	Met	Lys	Ala	Ile	Ser	Ala	Ile	Leu	Val	Val	Val	Ala	260	265	270	
Met	Leu	Leu	Pro	Arg	Trp	Arg	Ala	Lys	Phe	Ser	Lys	Ala	Pro	Lys	Pro	275	280	285	
Lys	Gln	Pro	Val	Ala	Val	Glu	Ala	290	295										

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Met Thr Lys Ile Lys																	5
1																	
agt ggg gag gcg tcg aca agc att gtt gag cgc gcc tta aag cgc ccc																	163
Ser Gly Glu Ala Ser Thr Ser Ile Val Glu Arg Ala Leu Lys Arg Pro																	20
10 15																	
gaa ctg acc agc ctg ctt ggc gcc gtg ctt gtt ttt acg ctg ttt atg																	211
Glu Leu Thr Ser Leu Leu Gly Ala Val Leu Val Phe Thr Leu Phe Met																	35
25 30																	
gtg gtc gcg ccg gca ttt agg tca tgg gat tcg atg gcg acc gtg ctg																	259
Val Val Ala Pro Ala Phe Arg Ser Trp Asp Ser Met Ala Thr Val Leu																	50
40 45																	
tat gcg agt tcc acg atc ggc atc atg gcg gtt gcc gtg ggc ctg ctg																	307
Tyr Ala Ser Ser Thr Ile Gly Ile Met Ala Val Ala Val Gly Leu Leu																	65
55 60																	
atg atc gct gat gaa ttc gac ctg tcc acc ggc gtt gcc gtg aca act																	355
Met Ile Ala Asp Glu Phe Asp Leu Ser Thr Gly Val Ala Val Thr Thr																	85
70 75																	
gca gcg ctg gcg gcc tcg atg ttt agc tat aac ctg tgg ctg aac acc																	403
Ala Ala Leu Ala Ala Ser Met Phe Ser Tyr Asn Leu Trp Leu Asn Thr																	100
90 95																	
tgg gtg ggc gcg ctg att gca ttg gtg att tcg ctg gcc atc ggc ttt																	451
Trp Val Gly Ala Leu Ile Ala Leu Val Ile Ser Leu Ala Ile Gly Phe																	115
105 110																	
ttc aac ggc ttt ttg gta gtg aaa acc aag att gca tcc ttc ctg atc																	499
Phe Asn Gly Phe Leu Val Val Lys Thr Lys Ile Ala Ser Phe Leu Ile																	130
120 125																	
acc ctt gcc act ttc ctt atg ctg cag ggt att aat ctg gcg gtc acc																	547
Thr Leu Ala Thr Phe Leu Met Leu Gln Gly Ile Asn Leu Ala Val Thr																	145
135 140																	
aag ctg att tcc ggc acc gtg gcc acg cca acc atc gcg gat atg gaa																	595
Lys Leu Ile Ser Gly Thr Val Ala Thr Pro Thr Ile Ala Asp Met Glu																	165
150 155																	
ggg ttt cct tca gcg cgt gcg gtg ttt gcc agc tcg att ccc atc ttt																	643
Gly Phe Pro Ser Ala Arg Ala Val Phe Ala Ser Ser Ile Pro Ile Phe																	180
170 175																	
ggg gtg aat att cgc atc act gtt ttt tgg tgg ctg ctg ttt gtt atc																	691

Gly Val Asn Ile Arg Ile Thr Val Phe Trp Trp Leu Leu Phe Val Ile
 185 190 195
 gtc ggc act ttt gtg ttg ttt aag acg cgc atc ggc aac tgg att ttt 739
 Val Gly Thr Phe Val Leu Phe Lys Thr Arg Ile Gly Asn Trp Ile Phe
 200 205 210
 gcg gtc ggt ggc gat gaa gag gca gct cgc gca gtc ggc gtt ccc gtg 787
 Ala Val Gly Gly Asp Glu Glu Ala Ala Arg Ala Val Gly Val Pro Val
 215 220 225
 cgt ggc gtg aaa atc ggc ctg ttc atg ttc gtt ggt ttt gcc gcc tgg 835
 Arg Gly Val Lys Ile Gly Leu Phe Met Phe Val Gly Phe Ala Ala Trp
 230 235 240 245
 ttt gtg ggc atg cac aac ctg ttc ctc ttt gat tcg att cag gct ggt 883
 Phe Val Gly Met His Asn Leu Phe Leu Phe Asp Ser Ile Gln Ala Gly
 250 255 260
 caa ggc gtg ggt aat gag ttc ctc tac atc atc gct gcg gtg atc gga 931
 Gln Gly Val Gly Asn Glu Phe Leu Tyr Ile Ile Ala Ala Val Ile Gly
 265 270 275
 ggc atc tcc atg act ggt ggc cgc gga aca gtg gtg ggc aca atg att 979
 Gly Ile Ser Met Thr Gly Gly Arg Gly Thr Val Val Gly Thr Met Ile
 280 285 290
 ggt gca ctc atc ttt gga atg acc aac caa ggc att gtt tat gca ggt 1027
 Gly Ala Leu Ile Phe Gly Met Thr Asn Gln Gly Ile Val Tyr Ala Gly
 295 300 305
 tgg aac cct gac tgg ttc atg ttc ttc ctc ggc ggc acc cta ctt ctg 1075
 Trp Asn Pro Asp Trp Phe Met Phe Phe Leu Gly Gly Thr Leu Leu Leu
 310 315 320 325
 gct gtt ttg ctc aat cac cga ttc gag cgt ttc aac aag gag cga tca 1123
 Ala Val Leu Leu Asn His Arg Phe Glu Arg Phe Asn Lys Glu Arg Ser
 330 335 340
 tgacagacct cattcaactc cgc 1146

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<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 18

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 20 25 30

Phe Thr Leu Phe Met Val Val Ala Pro Ala Phe Arg Ser Trp Asp Ser
 35 40 45

Met Ala Thr Val Leu Tyr Ala Ser Ser Thr Ile Gly Ile Met Ala Val
 50 55 60

Ala Val Gly Leu Leu Met Ile Ala Asp Glu Phe Asp Leu Ser Thr Gly

65 70 75 80

Val Ala Val Thr Thr Ala Ala Leu Ala Ala Ser Met Phe Ser Tyr Asn
85 90 95

Leu Trp Leu Asn Thr Trp Val Gly Ala Leu Ile Ala Leu Val Ile Ser
100 105 110

Leu Ala Ile Gly Phe Phe Asn Gly Phe Leu Val Val Lys Thr Lys Ile
115 120 125

Ala Ser Phe Leu Ile Thr Leu Ala Thr Phe Leu Met Leu Gln Gly Ile
130 135 140

Asn Leu Ala Val Thr Lys Leu Ile Ser Gly Thr Val Ala Thr Pro Thr
145 150 155 160

Ile Ala Asp Met Glu Gly Phe Pro Ser Ala Arg Ala Val Phe Ala Ser
165 170 175

Ser Ile Pro Ile Phe Gly Val Asn Ile Arg Ile Thr Val Phe Trp Trp
180 185 190

Leu Leu Phe Val Ile Val Gly Thr Phe Val Leu Phe Lys Thr Arg Ile
195 200 205

Gly Asn Trp Ile Phe Ala Val Gly Gly Asp Glu Glu Ala Ala Arg Ala
210 215 220

Val Gly Val Pro Val Arg Gly Val Lys Ile Gly Leu Phe Met Phe Val
225 230 235 240

Gly Phe Ala Ala Trp Phe Val Gly Met His Asn Leu Phe Leu Phe Asp
245 250 255

Ser Ile Gln Ala Gly Gln Gly Val Gly Asn Glu Phe Leu Tyr Ile Ile
260 265 270

Ala Ala Val Ile Gly Gly Ile Ser Met Thr Gly Gly Arg Gly Thr Val
275 280 285

Val Gly Thr Met Ile Gly Ala Leu Ile Phe Gly Met Thr Asn Gln Gly
290 295 300

Ile Val Tyr Ala Gly Trp Asn Pro Asp Trp Phe Met Phe Phe Leu Gly
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Gly Thr Leu Leu Leu Ala Val Leu Leu Asn His Arg Phe Glu Arg Phe
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Asn Lys Glu Arg Ser
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<211> 746

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS


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Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Ala Arg
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gcc gag gtc ggt att gcg att ggc gcg ggt aca gat gtg gcg atg gag 1440
Ala Glu Val Gly Ile Ala Ile Gly Ala Gly Thr Asp Val Ala Met Glu
465                      470                      475                      480

tcc gcc ggg gtg gtc ctg gcc agt gat gat ccc ccg gcc gtg ctg tcg 1488
Ser Ala Gly Val Val Leu Ala Ser Asp Asp Pro Arg Ala Val Leu Ser
      485                      490                      495

atg atc gag ctc tcc cat gcc agc tac cgc aag atg gtc cag aac ctg 1536
Met Ile Glu Leu Ser His Ala Ser Tyr Arg Lys Met Val Gln Asn Leu
      500                      505                      510

gtc tgg gcg acc ggg tac aac atc gtg gcc gtt ccg ctg gcc gcc ggt 1584
Val Trp Ala Thr Gly Tyr Asn Ile Val Ala Val Pro Leu Ala Ala Gly
      515                      520                      525

gtg ctc gcc cct atc ggt gtg ctg ctt ccc ccg gcg gcg gcc gcc atc 1632
Val Leu Ala Pro Ile Gly Val Leu Leu Pro Pro Ala Ala Ala Ala Ile
      530                      535                      540

ttg atg tcc ctg tcc acg atc atc gtc gcc ctc aac gcc cag ctg cta 1680
Leu Met Ser Leu Ser Thr Ile Ile Val Ala Leu Asn Ala Gln Leu Leu
545                      550                      555                      560

cgc cgg atc gac ctg gac ccg gct cac cta gct ccg acc gac ggg aag 1728
Arg Arg Ile Asp Leu Asp Pro Ala His Leu Ala Pro Thr Asp Gly Lys
      565                      570                      575

gag gag aag gct gct gtg agc tct gca gcc ccc gtc cgc tgactttcaa 1777
Glu Glu Lys Ala Ala Val Ser Ser Ala Ala Pro Val Arg
      580                      585

tgcttcatgg act 1790

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<210> 22

<211> 589

<212> PRT

<213> Corynebacterium glutamicum

<400> 22

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Ala Ser Trp Val Thr Thr Leu Gly Leu Gly Gly Phe His Leu Asp Phe
  1                      5                      10                      15

Trp Trp Glu Leu Ala Leu Leu Val Thr Ile Met Leu Leu Gly His Trp
      20                      25                      30

Leu Glu Met Arg Ala Leu Gly Ala Ala Ser Ser Ala Leu Asp Ala Leu
      35                      40                      45

Ala Ala Leu Leu Pro Asp Glu Ala Glu Lys Val Val Asp Gly Thr Thr
      50                      55                      60

Arg Thr Val Ala Ile Ser Glu Leu Ala Val Asp Asp Val Val Leu Val

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65	70	75	80
Arg Ala Gly Ala Arg Val Pro Ala Asp Gly Thr Ile Met Asp Gly Ala	85	90	95
Ala Glu Phe Asp Glu Ala Met Ile Thr Gly Glu Ser Arg Pro Val Tyr	100	105	110
Arg Asp Thr Gly Glu Thr Val Val Ala Gly Thr Val Ala Thr Asp Asn	115	120	125
Thr Val Arg Ile Arg Val Glu Ala Thr Gly Gly Asp Thr Ala Leu Ala	130	135	140
Gly Ile Gln Arg Met Val Ala Asp Ala Gln Ala Ser Ser Ser Arg Ala	145	150	155
Gln Ala Leu Ala Asp Arg Ala Ala Ala Leu Leu Phe Trp Phe Ala Leu	165	170	175
Ile Thr Ala Leu Ile Thr Ala Val Val Trp Thr Ile Ile Gly Ser Pro	180	185	190
Asp Asp Ala Val Val Arg Ala Val Thr Val Leu Ile Ile Ala Cys Pro	195	200	205
His Ala Leu Gly Leu Ala Ile Pro Leu Val Ile Ala Ile Ser Ser Glu	210	215	220
Arg Ala Ala Lys Ser Gly Val Leu Ile Lys Asp Arg Met Ala Leu Glu	225	230	235
His Met Arg Thr Ile Asp Val Val Leu Phe Asp Lys Thr Gly Thr Leu	245	250	255
Thr Glu Gly Ala His Ala Val Thr Gly Val Ala Pro Ala Thr Gly Ile	260	265	270
Ala Glu Gly Glu Leu Leu Ala Leu Ala Ala Ala Ala Glu Ala Asp Ser	275	280	285
Glu His Pro Val Ala Arg Ala Ile Val Thr Ala Ala Ala Ala His Pro	290	295	300
Glu Ala Ser Gln Arg Gln Leu Arg Ala Thr Gly Phe Thr Ala Ala Ser	305	310	315
Gly Arg Gly Ile Arg Ala Thr Val Asp Gly Ala Glu Ile Leu Val Gly	325	330	335
Gly Pro Asn Met Leu Arg Glu Phe Asn Leu Thr Thr Pro Gly Glu Leu	340	345	350
Ala Asp Ile Thr Gly Ser Trp Ala Gln Arg Gly Ala Gly Val Leu His	355	360	365
Val Val Arg Asp Gly Glu Ile Ile Gly Ala Val Ala Val Glu Asp Lys	370	375	380
Ile Arg Pro Glu Ser Arg Ala Ala Val Arg Ala Leu Gln Ala Arg Gly	385	390	395
			400

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Val Lys Val Ala Met Ile Thr Gly Asp Ala Thr Gln Val Ala Gln Ala
      405                      410                      415

Val Gly Lys Asp Leu Gly Ile Asp Glu Val Phe Ala Glu Val Leu Pro
      420                      425                      430

Gln Asp Lys Asp Thr Lys Val Thr Gln Leu Gln Glu Arg Gly Leu Ser
      435                      440                      445

Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Ala Arg
      450                      455                      460

Ala Glu Val Gly Ile Ala Ile Gly Ala Gly Thr Asp Val Ala Met Glu
465                      470                      475                      480

Ser Ala Gly Val Val Leu Ala Ser Asp Asp Pro Arg Ala Val Leu Ser
      485                      490                      495

Met Ile Glu Leu Ser His Ala Ser Tyr Arg Lys Met Val Gln Asn Leu
      500                      505                      510

Val Trp Ala Thr Gly Tyr Asn Ile Val Ala Val Pro Leu Ala Ala Gly
      515                      520                      525

Val Leu Ala Pro Ile Gly Val Leu Leu Pro Pro Ala Ala Ala Ala Ile
      530                      535                      540

Leu Met Ser Leu Ser Thr Ile Ile Val Ala Leu Asn Ala Gln Leu Leu
545                      550                      555                      560

Arg Arg Ile Asp Leu Asp Pro Ala His Leu Ala Pro Thr Asp Gly Lys
      565                      570                      575

Glu Glu Lys Ala Ala Val Ser Ser Ala Ala Pro Val Arg
      580                      585

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<210> 23
<211> 807
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(784)
<223> RXA00002

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<400> 23
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ggctgcagac aagctcgctg ctgaggattc tcacctgcac  gtg  ctg  cac  cgc  gaa    115
              Val Leu His Arg Glu
              1                      5

ggc aag ggt ggc ctt ctt ggc gct tat atc gcc ggc ttc gag tgg ggc    163
Gly Lys Gly Gly Leu Leu Gly Ala Tyr Ile Ala Gly Phe Glu Trp Gly
              10                      15                      20

cta gag aag gat tac cat gtt ctg tgc gaa atg gat gcc gac ggc tcc    211
Leu Glu Lys Asp Tyr His Val Leu Cys Glu Met Asp Ala Asp Gly Ser

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25 30 35
 cac gca cca gaa cag ctc cac ctc ttg ctt gag gaa att gaa aag ggc 259
 His Ala Pro Glu Gln Leu His Leu Leu Leu Glu Glu Ile Glu Lys Gly
 40 45 50
 gca gat ctg gtc att ggc tcc cgc tac gta ccg ggt gga gag aca gtg 307
 Ala Asp Leu Val Ile Gly Ser Arg Tyr Val Pro Gly Gly Glu Thr Val
 55 60 65
 aac tgg cct gcc aac cgc gaa ctg ctg tcc cgc ttg ggc aac aag tac 355
 Asn Trp Pro Ala Asn Arg Glu Leu Leu Ser Arg Leu Gly Asn Lys Tyr
 70 75 80 85
 att tct gtt gcc ctg ggt gcc ggc atc aat gac atg act gcc ggc tac 403
 Ile Ser Val Ala Leu Gly Ala Gly Ile Asn Asp Met Thr Ala Gly Tyr
 90 95 100
 cgt gct ttc cgg cgt gag ctg ctt gag cac ctc gac ttt gag gag ctt 451
 Arg Ala Phe Arg Arg Glu Leu Leu Glu His Leu Asp Phe Glu Glu Leu
 105 110 115
 tcc aac gcc gga tac atc ttc cag gtg gac gtt gcc ttc cgc gcc atc 499
 Ser Asn Ala Gly Tyr Ile Phe Gln Val Asp Val Ala Phe Arg Ala Ile
 120 125 130
 aag gat ggc ttc gat gtc cgc gag gtt ccg atc acc ttc acc gag cgc 547
 Lys Asp Gly Phe Asp Val Arg Glu Val Pro Ile Thr Phe Thr Glu Arg
 135 140 145
 gag ctt ggt gaa tcc aag ctg gac ggc tcc ttt gtc aag gat tcc ctg 595
 Glu Leu Gly Glu Ser Lys Leu Asp Gly Ser Phe Val Lys Asp Ser Leu
 150 155 160 165
 ctc gaa gta acc aag tgg gga gtg gct cac cgc tcc gag cag atc agc 643
 Leu Glu Val Thr Lys Trp Gly Val Ala His Arg Ser Glu Gln Ile Ser
 170 175 180
 gat ttc aca tcg gaa gta tcc aag atc gcc tcc cgc acg gtc aag gac 691
 Asp Phe Thr Ser Glu Val Ser Lys Ile Ala Ser Arg Thr Val Lys Asp
 185 190 195
 atg gag ctt ggc cct aag gcc acc acg gcc aag aac gct gta ccg gac 739
 Met Glu Leu Gly Pro Lys Ala Thr Thr Ala Lys Asn Ala Val Pro Asp
 200 205 210
 ttc gtt tcc gaa gtc tct aac cta gct aaa ggc acc ttc aag aag 784
 Phe Val Ser Glu Val Ser Asn Leu Ala Lys Gly Thr Phe Lys Lys
 215 220 225
 taactcgatg ccgcggcgt ctc 807

<210> 24

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 24

Val Leu His Arg Glu Gly Lys Gly Gly Leu Leu Gly Ala Tyr Ile Ala
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cgc aac cgc aac atg aag cgt cga cta gca att gct gct ttc gtc gcc 163
 Arg Asn Arg Asn Met Lys Arg Arg Leu Ala Ile Ala Ala Phe Val Ala
 10 15 20

acc gca acc gct acc gcc acc atg gca cca gca tcc gcg caa acc gac 211
 Thr Ala Thr Ala Thr Ala Thr Met Ala Pro Ala Ser Ala Gln Thr Asp
 25 30 35

tac gca ggc ctt tcc tcc ggc gtt gcc gac acc gtc gca gaa gct gca 259
 Tyr Ala Gly Leu Ser Ser Gly Val Ala Asp Thr Val Ala Glu Ala Ala
 40 45 50

gga gtc gca acc acc gcc gtc gca cca gcc gcc acc gta gcg cgc cca 307
 Gly Val Ala Thr Thr Ala Val Ala Pro Ala Ala Thr Val Ala Arg Pro
 55 60 65

gca aac ggc acc ttc acc tca gga ttc gga cca cgt tgg gga acc ttc 355
 Ala Asn Gly Thr Phe Thr Ser Gly Phe Gly Pro Arg Trp Gly Thr Phe
 70 75 80 85

cac aac ggc atc gac atc gca aac tca atc ggc acc cca atc tac gcc 403
 His Asn Gly Ile Asp Ile Ala Asn Ser Ile Gly Thr Pro Ile Tyr Ala
 90 95 100

gtc atg gcc ggc act gtc atc agc tct ggc cca gca tcc ggc tat gga 451
 Val Met Ala Gly Thr Val Ile Ser Ser Gly Pro Ala Ser Gly Tyr Gly
 105 110 115

cag tgg atc cgc atc cag cac gac gac gga tcc atc tcc atc tac gga 499
 Gln Trp Ile Arg Ile Gln His Asp Asp Gly Ser Ile Ser Ile Tyr Gly
 120 125 130

cac atg gaa tac ctc tac gtc tcc gtc ggc gaa cgc gtc gca gca ggc 547
 His Met Glu Tyr Leu Tyr Val Ser Val Gly Glu Arg Val Ala Ala Gly
 135 140 145

cag gaa atc gca gga atg ggc agc caa gga ttc tcc acc ggc tcc cac 595
 Gln Glu Ile Ala Gly Met Gly Ser Gln Gly Phe Ser Thr Gly Ser His
 150 155 160 165

ctc cac ttc gag atc cac cca gac ggc gtc acc cca gtc gac cca cag 643
 Leu His Phe Glu Ile His Pro Asp Gly Val Thr Pro Val Asp Pro Gln
 170 175 180

gca tgg ctc gca aac cac ggc atc tac gtt taagcgctag ccgttcgtgg 693
 Ala Trp Leu Ala Asn His Gly Ile Tyr Val
 185 190

gat 696

<210> 26
 <211> 191
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 26
 Met Leu Asn Ile Ala Arg Asn Arg Asn Met Lys Arg Arg Leu Ala Ile
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 Ala Ala Phe Val Ala Thr Ala Thr Ala Thr Met Ala Pro Ala

gcc cca gat gta gac att gaa gca att att acc ggt ggc gac atc gac 305
 Ala Pro Asp Val Asp Ile Glu Ala Ile Ile Thr Gly Gly Asp Ile Asp
 60 65 70

cct cat tcc ttc gag cct tcc gct acc gat atg gct aaa gtt tcc gaa 353
 Pro His Ser Phe Glu Pro Ser Ala Thr Asp Met Ala Lys Val Ser Glu
 75 80 85

gct gac atc att atc gtc ggt ggc ggc ggc tat gat tcc tgg ctc tac 401
 Ala Asp Ile Ile Ile Val Gly Gly Gly Gly Tyr Asp Ser Trp Leu Tyr
 90 95 100

ggc acc ttg gaa gac gat gat cgc atc atc cac gca ttg gat ctc tca 449
 Gly Thr Leu Glu Asp Asp Asp Arg Ile Ile His Ala Leu Asp Leu Ser
 105 110 115 120

gag cat gac cac agc gag cat gat gat cac gag cac gaa gcc gaa gaa 497
 Glu His Asp His Ser Glu His Asp Asp His Glu His Glu Ala Glu Glu
 125 130 135

gcc cac gaa cac gac cac gat gaa gag ggc cac gat cat gac gtc gac 545
 Ala His Glu His Asp His Asp Glu Glu Gly His Asp His Asp Val Asp
 140 145 150

aac gag cac gtc tgg tac tcc act gaa tac gtc tct gag gta gct gaa 593
 Asn Glu His Val Trp Tyr Ser Thr Glu Tyr Val Ser Glu Val Ala Glu
 155 160 165

gag ttc gca gaa aaa gtc acc gag ctt gat ccc gag gca cag gcc gat 641
 Glu Phe Ala Glu Lys Val Thr Glu Leu Asp Pro Glu Ala Gln Ala Asp
 170 175 180

gca acg gct gtg acc acc aag atg gac gag ctg cac aat cag att cac 689
 Ala Thr Ala Val Thr Thr Lys Met Asp Glu Leu His Asn Gln Ile His
 185 190 195 200

gat ctt cca gca gtt cgc att gct cag acc gag ccg atc gcc gat cac 737
 Asp Leu Pro Ala Val Arg Ile Ala Gln Thr Glu Pro Ile Ala Asp His
 205 210 215

att ttg tcc cac tcc gac atg gtg gaa tcc acc cct gag ggt tac cgc 785
 Ile Leu Ser His Ser Asp Met Val Glu Ser Thr Pro Glu Gly Tyr Arg
 220 225 230

gca acc acg ttg agc gag agc gag cca acc gca gca gat gtt gcg tcg 833
 Ala Thr Thr Leu Ser Glu Ser Glu Pro Thr Ala Ala Asp Val Ala Ser
 235 240 245

ttc cag gat gca att aac aac ggt gac ctc gat gtt ttg atc tac aac 881
 Phe Gln Asp Ala Ile Asn Asn Gly Asp Leu Asp Val Leu Ile Tyr Asn
 250 255 260

cca cag tcc gcg tcg act gtc gcg acc agc ttg aag gat ttg gca gaa 929
 Pro Gln Ser Ala Ser Thr Val Ala Thr Ser Leu Lys Asp Leu Ala Glu
 265 270 275 280

gaa aaa ggc atc cca gtt gtt gag atc tat gag acc cct caa aac acc 977
 Glu Lys Gly Ile Pro Val Val Glu Ile Tyr Glu Thr Pro Gln Asn Thr
 285 290 295

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gcc act aac cag gtt tagaattatt taaatgctgt tga 1063
Ala Thr Asn Gln Val
315
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<400> 28																
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Val	Leu	Ala	Gly	Cys	Ser	Thr	Gly	Ser	Ala	Asp	Ser	Ala	Asp	Ser	Thr	
			20					25					30			
Asn	Ala	Ala	Gly	Ser	Asn	Ser	Leu	Lys	Val	Val	Thr	Ser	Thr	Gln	Val	
		35					40					45				
Trp	Ala	Asp	Val	Ala	Glu	Ala	Val	Ala	Pro	Asp	Val	Asp	Ile	Glu	Ala	
	50					55					60					
Ile	Ile	Thr	Gly	Gly	Asp	Ile	Asp	Pro	His	Ser	Phe	Glu	Pro	Ser	Ala	
65					70					75					80	
Thr	Asp	Met	Ala	Lys	Val	Ser	Glu	Ala	Asp	Ile	Ile	Ile	Val	Gly	Gly	
				85					90					95		
Gly	Gly	Tyr	Asp	Ser	Trp	Leu	Tyr	Gly	Thr	Leu	Glu	Asp	Asp	Asp	Arg	
			100					105					110			
Ile	Ile	His	Ala	Leu	Asp	Leu	Ser	Glu	His	Asp	His	Ser	Glu	His	Asp	
		115					120					125				
Asp	His	Glu	His	Glu	Ala	Glu	Glu	Ala	His	Glu	His	Asp	His	Asp	Glu	
	130					135					140					
Glu	Gly	His	Asp	His	Asp	Val	Asp	Asn	Glu	His	Val	Trp	Tyr	Ser	Thr	
145					150					155					160	
Glu	Tyr	Val	Ser	Glu	Val	Ala	Glu	Glu	Phe	Ala	Glu	Lys	Val	Thr	Glu	
				165					170					175		
Leu	Asp	Pro	Glu	Ala	Gln	Ala	Asp	Ala	Thr	Ala	Val	Thr	Thr	Lys	Met	
			180					185					190			
Asp	Glu	Leu	His	Asn	Gln	Ile	His	Asp	Leu	Pro	Ala	Val	Arg	Ile	Ala	
		195					200					205				
Gln	Thr	Glu	Pro	Ile	Ala	Asp	His	Ile	Leu	Ser	His	Ser	Asp	Met	Val	
	210					215					220					
Glu	Ser	Thr	Pro	Glu	Gly	Tyr	Arg	Ala	Thr	Thr	Leu	Ser	Glu	Ser	Glu	
225					230					235					240	
Pro	Thr	Ala	Ala	Asp	Val	Ala	Ser	Phe	Gln	Asp	Ala	Ile	Asn	Asn	Gly	

Glu Ile Val Pro Leu Ala Leu Phe Trp Lys Asp His Asp Ser Ile Asp
 120 125 130
 ggc att gac ggc gag tcc gtt gcc atc cct aac gat cct tcc aac cag 547
 Gly Ile Asp Gly Glu Ser Val Ala Ile Pro Asn Asp Pro Ser Asn Gln
 135 140 145
 ggc cgc gcc atc aac gtt ctc gtt cag gca ggt ctg gtc acc ctg aag 595
 Gly Arg Ala Ile Asn Val Leu Val Gln Ala Gly Leu Val Thr Leu Lys
 150 155 160 165
 acc cca ggt ctg gtc acc cca gct cca gtc gat atc gac gag gca gct 643
 Thr Pro Gly Leu Val Thr Pro Ala Pro Val Asp Ile Asp Glu Ala Ala
 170 175 180
 tcc aag gtt tcc gtc atc cca gtc gac gca gct cag gca cca acc gct 691
 Ser Lys Val Ser Val Ile Pro Val Asp Ala Ala Gln Ala Pro Thr Ala
 185 190 195
 tac cag gag ggt cgc cca gcg atc atc aac aac tcc ttc ctt gac cgc 739
 Tyr Gln Glu Gly Arg Pro Ala Ile Ile Asn Asn Ser Phe Leu Asp Arg
 200 205 210
 gca ggc atc gat cca aac ctc gcg gtc ttc gaa gat gat cct gag tct 787
 Ala Gly Ile Asp Pro Asn Leu Ala Val Phe Glu Asp Asp Pro Glu Ser
 215 220 225
 gaa gaa gca gag cca tac atc aac gtc ttc gtc acc aag gct gag gac 835
 Glu Glu Ala Glu Pro Tyr Ile Asn Val Phe Val Thr Lys Ala Glu Asp
 230 235 240 245
 aag gac gat gcc aac atc gcc cgc ctc gtt gag ctg tgg cac gac cca 883
 Lys Asp Asp Ala Asn Ile Ala Arg Leu Val Glu Leu Trp His Asp Pro
 250 255 260
 gag gtt ctg gct gca gta gac cgc gac tct gag ggc acc tcc gtc cca 931
 Glu Val Leu Ala Ala Val Asp Arg Asp Ser Glu Gly Thr Ser Val Pro
 265 270 275
 gtt gat cgt cca gga gct gac ctt cag gaa atc ctt gat cgc ctt gag 979
 Val Asp Arg Pro Gly Ala Asp Leu Gln Glu Ile Leu Asp Arg Leu Glu
 280 285 290
 gct gat cag gaa aac gca taatctcttt tgagttcttt gca 1020
 Ala Asp Gln Glu Asn Ala
 295

<210> 30

<211> 299

<212> PRT

<213> Corynebacterium glutamicum

<400> 30

Met Lys Leu Arg Arg Ile Thr Thr Thr Ala Ile Ala Gly Leu Phe Ala
 1 5 10 15

Ala Thr Ala Leu Val Ala Cys Gly Ser Asp Ser Asp Gly Ser Ser Thr
 20 25 30

Thr Val Ala Glu Gly Thr Glu Gly Val Thr Ile Arg Ile Gly Thr Thr


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          35              40              45
Asp Ala Ala Lys Glu Ala Trp Thr Val Phe Glu Asp Lys Ala Ala Glu
   50              55              60
Glu Gly Ile Thr Leu Asp Ile Val Pro Phe Ser Asp Tyr Ser Thr Pro
   65              70              75              80
Asn Glu Ala Leu Ala Gln Asp Gln Leu Asp Val Asn Leu Phe Gln His
          85              90              95
Leu Lys Phe Leu Ala Glu Tyr Asn Val Gly Ser Gly Ala Asp Leu Thr
          100              105              110
Pro Val Gly Ser Ser Glu Ile Val Pro Leu Ala Leu Phe Trp Lys Asp
          115              120              125
His Asp Ser Ile Asp Gly Ile Asp Gly Glu Ser Val Ala Ile Pro Asn
          130              135              140
Asp Pro Ser Asn Gln Gly Arg Ala Ile Asn Val Leu Val Gln Ala Gly
          145              150              155              160
Leu Val Thr Leu Lys Thr Pro Gly Leu Val Thr Pro Ala Pro Val Asp
          165              170              175
Ile Asp Glu Ala Ala Ser Lys Val Ser Val Ile Pro Val Asp Ala Ala
          180              185              190
Gln Ala Pro Thr Ala Tyr Gln Glu Gly Arg Pro Ala Ile Ile Asn Asn
          195              200              205
Ser Phe Leu Asp Arg Ala Gly Ile Asp Pro Asn Leu Ala Val Phe Glu
          210              215              220
Asp Asp Pro Glu Ser Glu Glu Ala Glu Pro Tyr Ile Asn Val Phe Val
          225              230              235              240
Thr Lys Ala Glu Asp Lys Asp Asp Ala Asn Ile Ala Arg Leu Val Glu
          245              250              255
Leu Trp His Asp Pro Glu Val Leu Ala Ala Val Asp Arg Asp Ser Glu
          260              265              270
Gly Thr Ser Val Pro Val Asp Arg Pro Gly Ala Asp Leu Gln Glu Ile
          275              280              285
Leu Asp Arg Leu Glu Ala Asp Gln Glu Asn Ala
          290              295

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<210> 31

<211> 771

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(748)

<223> RXA00482

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<210> 32

<211> 216

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

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Ser Leu Phe Gly Ile Ser Thr Ala Gln Ala Gln Asp Ile Phe Asp Gly
      20           25           30

Gly Arg Leu Ala Gly Gly Ser Ser Gln Val Ser Asn Leu Ser Ser Val
      35           40           45

Pro Glu Asn Leu Ala Leu Pro Glu Ile Glu Asn Ser Ile Asp Leu Glu
      50           55           60

Arg Tyr Lys Gly Lys Trp Tyr Gln Val Ala Ala Ile Pro Gln Pro Phe
      65           70           75           80

Ser Leu Gln Cys Ser His Asp Val Thr Ala Asp Tyr Gly Val Ile Asp
      85           90           95

Ser Asp Thr Ile Ser Val Thr Asn Lys Cys Gly Thr Phe Phe Gly Pro
      100          105          110

Ser Val Ile Glu Gly Ser Ala Lys Val Val Ser Asn Ala Ser Leu Lys
      115          120          125

Val Ser Phe Pro Gly Ile Pro Phe Gln Ser Glu Asp Asn Gln Ala Asn
      130          135          140

Tyr Arg Val Thr Tyr Ile Glu Asp Asp Tyr Ser Leu Ala Ile Val Gly
      145          150          155          160

Ser Pro Ser Arg Ser Ser Gly Phe Ile Leu Ser Arg Thr Pro Gln Leu
      165          170          175

Ser Ser Asp Gln Trp Ser His Val Arg Asn Ile Thr Glu Asp Ser Gly
      180          185          190

Trp Trp Pro Cys Ala Phe Ile Thr Val Pro Ala Thr Gly Gly Leu Asn
      195          200          205

Thr Ala Thr Pro Leu Cys Thr Leu
      210          215

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<210> 33

<211> 1758

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1735)

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<400> 33

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                                   Val Thr Leu Phe Val
                                   1 5

cgg ctc gcc ctt gct gct gtg ggc ggg ctt ttt gtc ttt gct tcc aat 163
Arg Leu Ala Leu Ala Ala Val Gly Gly Leu Phe Val Phe Ala Ser Asn
              10              15              20

gaa ccg atc ggc tgg ttt gtc gcg gga att gtt ggc act gca tta ttt 211
Glu Pro Ile Gly Trp Phe Val Ala Gly Ile Val Gly Thr Ala Leu Phe
              25              30              35

ttt atc tcc ctt gcg ccg tgg gat ctg gga gtt ccc caa aag cgg cgg 259
Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val Pro Gln Lys Arg Arg
              40              45              50

aag aag aat gag cca gtc cca ttt ttg caa cag atg tcc acg ggc cca 307
Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln Met Ser Thr Gly Pro
              55              60              65

act gtt gta cag ggc atg ctt tta ggt ttt gtc cat ggc ctg gtg aca 355
Thr Val Val Gln Gly Met Leu Leu Gly Phe Val His Gly Leu Val Thr
              70              75              80              85

tat ttg cag ctg ttg ccg tgg atc ggt gag ttt gtt ggc tca ctg cct 403
Tyr Leu Gln Leu Leu Pro Trp Ile Gly Glu Phe Val Gly Ser Leu Pro
              90              95              100

tat gtc gcg ttg tca gtt gtc gag gcg ctt tat tcc att gct ctt ggt 451
Tyr Val Ala Leu Ser Val Val Glu Ala Leu Tyr Ser Ile Ala Leu Gly
              105              110              115

gct ttc ggc gtg ctc att gcg cgt tgg agg gac tgg aag gtt ctc ctg 499
Ala Phe Gly Val Leu Ile Ala Arg Trp Arg Asp Trp Lys Val Leu Leu
              120              125              130

ttt ccg gcg atg tat gtg gct gtg gag tat cta aga agc tcg tgg cca 547
Phe Pro Ala Met Tyr Val Ala Val Glu Tyr Leu Arg Ser Ser Trp Pro
              135              140              145

ttt gat gga ttc gcg tgg gtt cgc ctg gca tgg ggt caa att aac ggt 595
Phe Asp Gly Phe Ala Trp Val Arg Leu Ala Trp Gly Gln Ile Asn Gly
              150              155              160              165

ccg ttg gct aat ctc gca gcg ctt ggt ggg gta gcg ttt gtc act ttt 643
Pro Leu Ala Asn Leu Ala Ala Leu Gly Gly Val Ala Phe Val Thr Phe
              170              175              180

tcc acg gtg ctg gct gcc gtg ggt gtg gcc atg gtg att att tcc aag 691
Ser Thr Val Leu Ala Ala Val Gly Val Ala Met Val Ile Ile Ser Lys
              185              190              195

aag cga ctg gcc ggc gca atc atc acc gcg agt gtg att gct atc ggc 739
Lys Arg Leu Ala Gly Ala Ile Ile Thr Ala Ser Val Ile Ala Ile Gly
              200              205              210

gcg gtg tca tcc ctg tac gtt gac cgc aat ggc acg agc gat gaa agc 787

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112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400

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Ala Val Ser Ser Leu Tyr Val Asp Arg Asn Gly Thr Ser Asp Glu Ser
  215                      220                      225

atc gaa gta gcc gca att cag ggc aat gtg cct cgg atg gga ttg gac      835
Ile Glu Val Ala Ala Ile Gln Gly Asn Val Pro Arg Met Gly Leu Asp
  230                      235                      240                      245

ttc aat gca cag cgc cgc gcg gtg ctg gcg aat cac gca cgg gaa acc      883
Phe Asn Ala Gln Arg Arg Ala Val Leu Ala Asn His Ala Arg Glu Thr
                      250                      255                      260

ctc aag ctg gat gaa caa gtg gat ttg gtg atc tgg ccg gag aat tcc      931
Leu Lys Leu Asp Glu Gln Val Asp Leu Val Ile Trp Pro Glu Asn Ser
                      265                      270                      275

tca gac gtc aac cca ttt tcc gat gca caa gca aga gcc att atc gat      979
Ser Asp Val Asn Pro Phe Ser Asp Ala Gln Ala Arg Ala Ile Ile Asp
                      280                      285                      290

gga gca gtg gaa cat gtt cag gca cct att ttg gtg ggc acg atc acc      1027
Gly Ala Val Glu His Val Gln Ala Pro Ile Leu Val Gly Thr Ile Thr
                      295                      300                      305

gtc gat gag gtt ggt cca cgc aac acc atg cag gta ttt gat cct gtt      1075
Val Asp Glu Val Gly Pro Arg Asn Thr Met Gln Val Phe Asp Pro Val
  310                      315                      320                      325

gaa ggt gcc gcg gag tac cac aat aag aag ttc ttg cag ccg ttt ggt      1123
Glu Gly Ala Ala Glu Tyr His Asn Lys Lys Phe Leu Gln Pro Phe Gly
                      330                      335                      340

gaa tac atg ccg ttt cgc gaa ttc ctg aga att ttc tcg ccc tac gtt      1171
Glu Tyr Met Pro Phe Arg Glu Phe Leu Arg Ile Phe Ser Pro Tyr Val
                      345                      350                      355

gat tcc gct gga aac ttc cag ccc ggt gat ggc acc ggc gta gtg gag      1219
Asp Ser Ala Gly Asn Phe Gln Pro Gly Asp Gly Thr Gly Val Val Glu
                      360                      365                      370

atg aat gct gcg aac tta ggc cgc gct gtg aca gtg ggc gtg atg acg      1267
Met Asn Ala Ala Asn Leu Gly Arg Ala Val Thr Val Gly Val Met Thr
                      375                      380                      385

tgt tac gag gtc atc ttc gac cgt gct ggc cgc gac gcc atc gcc aat      1315
Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg Asp Ala Ile Ala Asn
  390                      395                      400                      405

ggg gct gaa ttt ttg acc acg ccc acc aac aac gcc acc ttc gga ttc      1363
Gly Ala Glu Phe Leu Thr Thr Pro Thr Asn Asn Ala Thr Phe Gly Phe
                      410                      415                      420

acg gac atg acg tat cag caa tta gca atg agc agg atg cgt gcc atc      1411
Thr Asp Met Thr Tyr Gln Gln Leu Ala Met Ser Arg Met Arg Ala Ile
                      425                      430                      435

gaa ttt gat agg gcg gtg gtt gtt gca gct aca tcg ggt gtt tcg gct      1459
Glu Phe Asp Arg Ala Val Val Ala Ala Thr Ser Gly Val Ser Ala
                      440                      445                      450

atc gtc aac cct gat gga agc att tcc caa aac acc cga att ttt gag      1507
Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn Thr Arg Ile Phe Glu

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      455              460              465
gcc gcc acc ttg acg gaa tcc att cca ctc aag gac act gtc acc atc 1555
Ala Ala Thr Leu Thr Glu Ser Ile Pro Leu Lys Asp Thr Val Thr Ile
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gca gcg cgg gtt ggt ttc tat gtt gaa tta ctg ttg gtt atc att ggt 1603
Ala Ala Arg Val Gly Phe Tyr Val Glu Leu Leu Leu Val Ile Ile Gly
490              495              500

gta tta gct gga cta ttc gcc att cga atg aat agc cgt tca aag tct 1651
Val Leu Ala Gly Leu Phe Ala Ile Arg Met Asn Ser Arg Ser Lys Ser
505              510              515

gcg aaa ggt tcc gct cgg ccc gca caa gtt cgg gtt aag aag gtg cct 1699
Ala Lys Gly Ser Ala Arg Pro Ala Gln Val Arg Val Lys Lys Val Pro
520              525              530

gcg aaa aag gca gca act aat cgt cga aaa gta aaa taaaaacgtc 1745
Ala Lys Lys Ala Ala Thr Asn Arg Arg Lys Val Lys
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ccgaaggac gag 1758

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<213> Corynebacterium glutamicum

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Gly Thr Ala Leu Phe Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val
35 40 45

Pro Gln Lys Arg Arg Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln
50 55 60

Met Ser Thr Gly Pro Thr Val Val Gln Gly Met Leu Leu Gly Phe Val
65 70 75 80

His Gly Leu Val Thr Tyr Leu Gln Leu Leu Pro Trp Ile Gly Glu Phe
85 90 95

Val Gly Ser Leu Pro Tyr Val Ala Leu Ser Val Val Glu Ala Leu Tyr
100 105 110

Ser Ile Ala Leu Gly Ala Phe Gly Val Leu Ile Ala Arg Trp Arg Asp
115 120 125

Trp Lys Val Leu Leu Phe Pro Ala Met Tyr Val Ala Val Glu Tyr Leu
130 135 140

Arg Ser Ser Trp Pro Phe Asp Gly Phe Ala Trp Val Arg Leu Ala Trp
145 150 155 160

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CCDS: P00090

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Leu	Val	Ile	Ile	Gly	Val	Leu	Ala	Gly	Leu	Phe	Ala	Ile	Arg	Met	Asn
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Ser	Arg	Ser	Lys	Ser	Ala	Lys	Gly	Ser	Ala	Arg	Pro	Ala	Gln	Val	Arg
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Val	Lys	Lys	Val	Pro	Ala	Lys	Lys	Ala	Ala	Thr	Asn	Arg	Arg	Lys	Val
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				Lys											
				545											

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<223> FRXA01164
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Val Thr Leu Phe Val																	
1 5																	
cgg ctc gcc ctt gct gct gtg ggc ggg ctt ttt gtc ttt gct tcc aat																	163
Arg Leu Ala Leu Ala Ala Val Gly Gly Leu Phe Val Phe Ala Ser Asn																	
10 15 20																	
gaa ccg atc ggc tgg ttt gtc gcg gga att gtt ggc act gca tta ttt																	211
Glu Pro Ile Gly Trp Phe Val Ala Gly Ile Val Gly Thr Ala Leu Phe																	
25 30 35																	
ttt atc tcc ctt gcg ccg tgg gat ctg gga gtt ccc caa aag cgg cgg																	259
Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val Pro Gln Lys Arg Arg																	
40 45 50																	
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Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln Met Ser Thr Gly Pro																	
55 60 65																	
act gtt gta cag ggc atg ctt tta ggt ttt gtc cat ggc ctg gtg aca																	355
Thr Val Val Gln Gly Met Leu Leu Gly Phe Val His Gly Leu Val Thr																	
70 75 80 85																	
tat ttg cag ctg ttg ccg tgg atc ggt gag ttt gtt ggc tca ctg cct																	403
Tyr Leu Gln Leu Leu Pro Trp Ile Gly Glu Phe Val Gly Ser Leu Pro																	
90 95 100																	
tat gtc gcg ttg tca gtt gtc gag gcg ctt tat tcc att gct ctt ggt																	451
Tyr Val Ala Leu Ser Val Val Glu Ala Leu Tyr Ser Ile Ala Leu Gly																	
105 110 115																	
gct ttc ggc gtg ctc att gcg cgt tgg agg gac tgg aag gtt ctc ctg																	499

Ala	Phe	Gly	Val	Leu	Ile	Ala	Arg	Trp	Arg	Asp	Trp	Lys	Val	Leu	Leu		
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ttt	ccg	gcg	atg	tat	gtg	gct	gtg	gag	tat	cta	aga	agc	tcg	tgg	cca	547	
Phe	Pro	Ala	Met	Tyr	Val	Ala	Val	Glu	Tyr	Leu	Arg	Ser	Ser	Trp	Pro		
	135					140					145						
ttt	gat	gga	ttc	gcg	tgg	gtt	cgc	ctg	gca	tgg	ggt	caa	att	aac	ggt	595	
Phe	Asp	Gly	Phe	Ala	Trp	Val	Arg	Leu	Ala	Trp	Gly	Gln	Ile	Asn	Gly		
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cag	ttg	gct	aat	ctc	gca	gcg	ctt	ggt	ggg	gta	gcg	ttt	gtc	act	ttt	643	
Pro	Leu	Ala	Asn	Leu	Ala	Ala	Leu	Gly	Gly	Val	Ala	Phe	Val	Thr	Phe		
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tcc	acg	gtg	ctg	gct	gcc	gtg	ggt	gtg	gcc	atg	gtg	att	att	tcc	aag	691	
Ser	Thr	Val	Leu	Ala	Ala	Val	Gly	Val	Ala	Met	Val	Ile	Ile	Ser	Lys		
			185					190					195				
aag	cga	ctg	gcc	ggc	gca	atc	atc	acc	gcg	agt	gtg	att	gct	atc	ggc	739	
Lys	Arg	Leu	Ala	Gly	Ala	Ile	Ile	Thr	Ala	Ser	Val	Ile	Ala	Ile	Gly		
		200					205					210					
gcg	gtg	tca	tcc	ctg	tac	gtt	gac	cgc	aat	ggc	acg	agc	gat	gaa	agc	787	
Ala	Val	Ser	Ser	Leu	Tyr	Val	Asp	Arg	Asn	Gly	Thr	Ser	Asp	Glu	Ser		
	215					220					225						
atc	gaa	gta	gcc	gca	att	cag	ggc	aat	gtg	cct	cgg	atg	gga	ttg	gac	835	
Ile	Glu	Val	Ala	Ala	Ile	Gln	Gly	Asn	Val	Pro	Arg	Met	Gly	Leu	Asp		
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ttc	aat	gca	cag	cgc	cgc	gcg	gtg	ctg	gcg	aat	cac	gca	cgg	gaa	acc	883	
Phe	Asn	Ala	Gln	Arg	Arg	Ala	Val	Leu	Ala	Asn	His	Ala	Arg	Glu	Thr		
				250					255					260			
ctc	aag	ctg	gat	gaa	caa	gtg	gat	ttg	gtg	atc	tgg	ccg	gag	aat	tcc	931	
Leu	Lys	Leu	Asp	Glu	Gln	Val	Asp	Leu	Val	Ile	Trp	Pro	Glu	Asn	Ser		
			265					270					275				
tca	gac	gtc	aac	cca	ttt	tcc	gat	gca	caa	gca	aga	gcc	att	atc	gat	979	
Ser	Asp	Val	Asn	Pro	Phe	Ser	Asp	Ala	Gln	Ala	Arg	Ala	Ile	Ile	Asp		
		280						285				290					
gga	gca	gtg	gaa	cat	gtt	cag	gca	cct	att	ttg	gtg	ggc	acg	atc	acc	1027	
Gly	Ala	Val	Glu	His	Val	Gln	Ala	Pro	Ile	Leu	Val	Gly	Thr	Ile	Thr		
	295					300					305						
gtc	gat	gag	gtt	ggt	cca	cgc	aac	acc	atg	cag	gta	ttt	gat	cct	gtt	1075	
Val	Asp	Glu	Val	Gly	Pro	Arg	Asn	Thr	Met	Gln	Val	Phe	Asp	Pro	Val		
310					315					320					325		
gaa	ggt	gcc	gcg	gag	tac	cac	aat	aag	aag	ttc	ttg	cag	ccg	ttt	ggt	1123	
Glu	Gly	Ala	Ala	Glu	Tyr	His	Asn	Lys	Lys	Phe	Leu	Gln	Pro	Phe	Gly		
				330				335						340			
gaa	tac	atg	ccg	ttt	cgc	gaa	ttc	ctg	aga	att	ttc	tcg	ccc	tac	gtt	1171	
Glu	Tyr	Met	Pro	Phe	Arg	Glu	Phe	Leu	Arg	Ile	Phe	Ser	Pro	Tyr	Val		
			345					350					355				
gat	tcc	gct	gga	aac	ttc	cag	ccc	ggt	gat	ggc	acc	ggc	gta	gtg	gag	1219	
Asp	Ser	Ala	Gly	Asn	Phe	Gln	Pro	Gly	Asp	Gly	Thr	Gly	Val	Val	Glu		

BGI-131CP

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atg aat gct gcg aac tta ggc cgc gct gtg aca gtg ggc gtg atg acg 1267
Met Asn Ala Ala Asn Leu Gly Arg Ala Val Thr Val Gly Val Met Thr
375          380          385

tgt tac gag gtc atc ttc gac cgt gct ggc cgc gac gcc atc gcc aat 1315
Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg Asp Ala Ile Ala Asn
390          395          400          405

ggg gct gaa ttt ttg acc acg ccc acc aac aac gcc acc ttc gga ttc 1363
Gly Ala Glu Phe Leu Thr Thr Pro Thr Asn Asn Ala Thr Phe Gly Phe
410          415          420

acg gac atg acg tat cag caa tta gca atg agc agg atg cgt gcc atc 1411
Thr Asp Met Thr Tyr Gln Gln Leu Ala Met Ser Arg Met Arg Ala Ile
425          430          435

gaa ttt gat agg gcg gtg gtt gtt gca gct aca tcg ggt gtt tcg gct 1459
Glu Phe Asp Arg Ala Val Val Val Ala Ala Thr Ser Gly Val Ser Ala
440          445          450

atc gtc aac cct gat gga agc att tcc caa aac acc cga att ttt gag 1507
Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn Thr Arg Ile Phe Glu
455          460          465

gcc gcc acc ttg acg gaa tcc att cca ctc aag gac act gtc acc atc 1555
Ala Ala Thr Leu Thr Glu Ser Ile Pro Leu Lys Asp Thr Val Thr Ile
470          475          480          485

gca gcg cgg gtt ggt ttc tat gtt gaa tta ctg ttg gtt atc att ggt 1603
Ala Ala Arg Val Gly Phe Tyr Val Glu Leu Leu Leu Val Ile Ile Gly
490          495          500

gta tta gct gga cta ttc gcc att cga atg aat agc cgt tca aag tct 1651
Val Leu Ala Gly Leu Phe Ala Ile Arg Met Asn Ser Arg Ser Lys Ser
505          510          515

gcg aaa ggt tcc gct cgg ccc gca 1675
Ala Lys Gly Ser Ala Arg Pro Ala
520          525

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<213> Corynebacterium glutamicum

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Val Thr Leu Phe Val Arg Leu Ala Leu Ala Ala Val Gly Gly Leu Phe
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Val Phe Ala Ser Asn Glu Pro Ile Gly Trp Phe Val Ala Gly Ile Val
20          25          30

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Gly Thr Ala Leu Phe Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val
35          40          45

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Pro Gln Lys Arg Arg Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln
50          55          60

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Met Ser Thr Gly Pro Thr Val Val Gln Gly Met Leu Leu Gly Phe Val
 65                               70                               75                               80

His Gly Leu Val Thr Tyr Leu Gln Leu Leu Pro Trp Ile Gly Glu Phe
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Val Gly Ser Leu Pro Tyr Val Ala Leu Ser Val Val Glu Ala Leu Tyr
                               100                               105                               110

Ser Ile Ala Leu Gly Ala Phe Gly Val Leu Ile Ala Arg Trp Arg Asp
                               115                               120                               125

Trp Lys Val Leu Leu Phe Pro Ala Met Tyr Val Ala Val Glu Tyr Leu
                               130                               135                               140

Arg Ser Ser Trp Pro Phe Asp Gly Phe Ala Trp Val Arg Leu Ala Trp
145                               150                               155                               160

Gly Gln Ile Asn Gly Pro Leu Ala Asn Leu Ala Ala Leu Gly Gly Val
                               165                               170                               175

Ala Phe Val Thr Phe Ser Thr Val Leu Ala Ala Val Gly Val Ala Met
                               180                               185                               190

Val Ile Ile Ser Lys Lys Arg Leu Ala Gly Ala Ile Ile Thr Ala Ser
                               195                               200                               205

Val Ile Ala Ile Gly Ala Val Ser Ser Leu Tyr Val Asp Arg Asn Gly
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Thr Ser Asp Glu Ser Ile Glu Val Ala Ala Ile Gln Gly Asn Val Pro
225                               230                               235                               240

Arg Met Gly Leu Asp Phe Asn Ala Gln Arg Arg Ala Val Leu Ala Asn
                               245                               250                               255

His Ala Arg Glu Thr Leu Lys Leu Asp Glu Gln Val Asp Leu Val Ile
                               260                               265                               270

Trp Pro Glu Asn Ser Ser Asp Val Asn Pro Phe Ser Asp Ala Gln Ala
                               275                               280                               285

Arg Ala Ile Ile Asp Gly Ala Val Glu His Val Gln Ala Pro Ile Leu
                               290                               295                               300

Val Gly Thr Ile Thr Val Asp Glu Val Gly Pro Arg Asn Thr Met Gln
305                               310                               315                               320

Val Phe Asp Pro Val Glu Gly Ala Ala Glu Tyr His Asn Lys Lys Phe
                               325                               330                               335

Leu Gln Pro Phe Gly Glu Tyr Met Pro Phe Arg Glu Phe Leu Arg Ile
                               340                               345                               350

Phe Ser Pro Tyr Val Asp Ser Ala Gly Asn Phe Gln Pro Gly Asp Gly
                               355                               360                               365

Thr Gly Val Val Glu Met Asn Ala Ala Asn Leu Gly Arg Ala Val Thr
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Val Gly Val Met Thr Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg

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Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.6	0.5	0	1
Education	12.5	1.5	10	16
Income	3500	1500	1000	8000
Health	0.8	0.2	0	1
Smoking	0.3	0.5	0	1
Alcohol	0.2	0.4	0	1
Exercise	0.4	0.5	0	1
Stress	0.6	0.5	0	1
Sleep	0.7	0.3	0	1
Work	0.8	0.2	0	1
Family	0.9	0.1	0	1
Friends	0.7	0.4	0	1
Hobbies	0.6	0.5	0	1
Travel	0.5	0.5	0	1
Reading	0.4	0.5	0	1
Gardening	0.3	0.5	0	1
Cooking	0.4	0.5	0	1
Volunteering	0.2	0.4	0	1
Religion	0.5	0.5	0	1
Politics	0.4	0.5	0	1
Art	0.3	0.5	0	1
Music	0.4	0.5	0	1
Sports	0.3	0.5	0	1
Technology	0.6	0.5	0	1
Environment	0.5	0.5	0	1
History	0.4	0.5	0	1
Science	0.5	0.5	0	1
Philosophy	0.3	0.5	0	1
Law	0.2	0.4	0	1
Medicine	0.3	0.5	0	1
Business	0.4	0.5	0	1
Education	0.5	0.5	0	1
Health	0.6	0.5	0	1
Finance	0.4	0.5	0	1
Real Estate	0.3	0.5	0	1
Automotive	0.2	0.4	0	1
Aerospace	0.1	0.3	0	1
Marine	0.1	0.3	0	1
Aviation	0.1	0.3	0	1
Space	0.1	0.3	0	1
Energy	0.2	0.4	0	1
Telecommunications	0.1	0.3	0	1
Information Technology	0.2	0.4	0	1
Biotechnology	0.1	0.3	0	1
Chemical Engineering	0.1	0.3	0	1
Mechanical Engineering	0.1	0.3	0	1
Electrical Engineering	0.1	0.3	0	1
Software Engineering	0.2	0.4	0	1
Computer Science	0.1	0.3	0	1
Mathematics	0.1	0.3	0	1
Physics	0.1	0.3	0	1
Chemistry	0.1	0.3	0	1
Biology	0.1	0.3	0	1
Environmental Science	0.1	0.3	0	1
Geology	0.1	0.3	0	1
Archaeology	0.1	0.3	0	1
Anthropology	0.1	0.3	0	1
Sociology	0.1	0.3	0	1
Psychology	0.1	0.3	0	1
Political Science	0.1	0.3	0	1
History	0.1	0.3	0	1
Philosophy	0.1	0.3	0	1
Law	0.1	0.3	0	1
Medicine	0.1	0.3	0	1
Business	0.1	0.3	0	1
Education	0.1	0.3	0	1
Health	0.1	0.3	0	1
Finance	0.1	0.3	0	1
Real Estate	0.1	0.3	0	1
Automotive	0.1	0.3	0	1
Aerospace	0.1	0.3	0	1
Marine	0.1	0.3	0	1
Aviation	0.1	0.3	0	1
Space	0.1	0.3	0	1
Energy	0.1	0.3	0	1
Telecommunications	0.1	0.3	0	1
Information Technology	0.1	0.3	0	1
Biotechnology	0.1	0.3	0	1
Chemical Engineering	0.1	0.3	0	1
Mechanical Engineering	0.1	0.3	0	1
Electrical Engineering	0.1	0.3	0	1
Software Engineering	0.1	0.3	0	1
Computer Science	0.1	0.3	0	1
Mathematics	0.1	0.3	0	1

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<223> RXN01168
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													1			5		
gta	gat	gct	acg	acg	ctg	gtg	att	att	cca	acg	tac	aac	gag	ctg	gaa	163		
Val	Asp	Ala	Thr	Thr	Leu	Val	Ile	Ile	Pro	Thr	Tyr	Asn	Glu	Leu	Glu			
					10				15				20					
aac	ctt	cca	ctc	atc	gtg	gat	cgc	gtg	cgc	acc	gca	acc	cct	gac	gtt	211		
Asn	Leu	Pro	Leu	Ile	Val	Asp	Arg	Val	Arg	Thr	Ala	Thr	Pro	Asp	Val			
					25				30				35					
cac	gta	ctc	atc	gtg	gac	gac	aac	agc	cca	gac	ggc	acc	ggc	gag	cgc	259		
His	Val	Leu	Ile	Val	Asp	Asp	Asn	Ser	Pro	Asp	Gly	Thr	Gly	Glu	Arg			
					40				45				50					
gca	gac	aag	ctt	gct	gct	gac	gac	gac	cac	att	ttt	gtc	ctc	cac	cgc	307		
Ala	Asp	Lys	Leu	Ala	Ala	Asp	Asp	Asp	His	Ile	Phe	Val	Leu	His	Arg			
					55				60				65					
gaa	ggc	aaa	ggc	ggc	ctg	tgc	gca	gag	tac	atg	gct	ggc	ttc	cag	tgg	355		

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Glu Gly Lys Gly Gly Leu Cys Ala Glu Tyr Met Ala Gly Phe Gln Trp
 70          75          80          85

ggc ctg gag cgc gac tac cag gtc ctg tgc gaa atg gac gcc gac ggc 403
Gly Leu Glu Arg Asp Tyr Gln Val Leu Cys Glu Met Asp Ala Asp Gly
          90          95          100

tcc cac gca cca gaa cag ctg cac ctg ctg ctc gct gag atc acc aat 451
Ser His Ala Pro Glu Gln Leu His Leu Leu Leu Ala Glu Ile Thr Asn
          105          110          115

ggc gct gac ctg gtc atc ggc tcg cgc tac gtg cca ggc ggc cgc gta 499
Gly Ala Asp Leu Val Ile Gly Ser Arg Tyr Val Pro Gly Gly Arg Val
          120          125          130

gtc aac tgg ccc aag aac cgt tgg ctc ttg tcc aag ggc ggc aac gtc 547
Val Asn Trp Pro Lys Asn Arg Trp Leu Leu Ser Lys Gly Gly Asn Val
          135          140          145

tac atc agc gtc gcg ctc ggc gcc ggc ttg acc gat atg acc gca ggg 595
Tyr Ile Ser Val Ala Leu Gly Ala Gly Leu Thr Asp Met Thr Ala Gly
          150          155          160          165

tac cgc gct ttt cga cgt gaa gtg cta gaa gca ctg ccg ctt gat gag 643
Tyr Arg Ala Phe Arg Arg Glu Val Leu Glu Ala Leu Pro Leu Asp Glu
          170          175          180

ctc tcc aac gct ggg tac att ttc caa gtt gag att gcc tac cgt gca 691
Leu Ser Asn Ala Gly Tyr Ile Phe Gln Val Glu Ile Ala Tyr Arg Ala
          185          190          195

gtt gaa gcc gga ttc gat gtt cgt gaa gtt ccc atc act ttc acc gag 739
Val Glu Ala Gly Phe Asp Val Arg Glu Val Pro Ile Thr Phe Thr Glu
          200          205          210

cgt gag atc ggc gaa tcc aag ctg gac ggc agc ttt gtc aag gat tcc 787
Arg Glu Ile Gly Glu Ser Lys Leu Asp Gly Ser Phe Val Lys Asp Ser
          215          220          225

ctg ctc gag gta acc aag tgg ggc ctc aag cac cgc ggt ggc cag gcc 835
Leu Leu Glu Val Thr Lys Trp Gly Leu Lys His Arg Gly Gly Gln Ala
          230          235          240          245

aag gaa ctg tcc aag gaa atg gtc ggc ctg ctg aac tat gag tgg aag 883
Lys Glu Leu Ser Lys Glu Met Val Gly Leu Leu Asn Tyr Glu Trp Lys
          250          255          260

cac ttc aaa aag cgc aac acc tgg ctc taaactgctt gccggttagt 930
His Phe Lys Lys Arg Asn Thr Trp Leu
          265          270

gaa 933

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<210> 38

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 38

Met Ser Ser Glu Ala Val Asp Ala Thr Thr Leu Val Ile Ile Pro Thr

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      1             5             10             15
Tyr Asn Glu Leu Glu Asn Leu Pro Leu Ile Val Asp Arg Val Arg Thr
      20             25             30
Ala Thr Pro Asp Val His Val Leu Ile Val Asp Asp Asn Ser Pro Asp
      35             40             45
Gly Thr Gly Glu Arg Ala Asp Lys Leu Ala Ala Asp Asp Asp His Ile
      50             55             60
Phe Val Leu His Arg Glu Gly Lys Gly Gly Leu Cys Ala Glu Tyr Met
      65             70             75             80
Ala Gly Phe Gln Trp Gly Leu Glu Arg Asp Tyr Gln Val Leu Cys Glu
      85             90             95
Met Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu Leu Leu
      100            105            110
Ala Glu Ile Thr Asn Gly Ala Asp Leu Val Ile Gly Ser Arg Tyr Val
      115            120            125
Pro Gly Gly Arg Val Val Asn Trp Pro Lys Asn Arg Trp Leu Leu Ser
      130            135            140
Lys Gly Gly Asn Val Tyr Ile Ser Val Ala Leu Gly Ala Gly Leu Thr
      145            150            155            160
Asp Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Val Leu Glu Ala
      165            170            175
Leu Pro Leu Asp Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln Val Glu
      180            185            190
Ile Ala Tyr Arg Ala Val Glu Ala Gly Phe Asp Val Arg Glu Val Pro
      195            200            205
Ile Thr Phe Thr Glu Arg Glu Ile Gly Glu Ser Lys Leu Asp Gly Ser
      210            215            220
Phe Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Leu Lys His
      225            230            235            240
Arg Gly Gly Gln Ala Lys Glu Leu Ser Lys Glu Met Val Gly Leu Leu
      245            250            255
Asn Tyr Glu Trp Lys His Phe Lys Lys Arg Asn Thr Trp Leu
      260            265            270

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<210> 39

<211> 743

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(720)

<223> FRXA01168

taaactgctt gccggtagt gaa

743

<210> 40

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 40

Arg Thr Ala Thr Pro Asp Val His Val Leu Ile Val Asp Asp Asn Ser
1 5 10 15

Pro Asp Gly Thr Gly Glu Arg Ala Asp Lys Leu Ala Ala Asp Asp Asp
20 25 30

His Ile Phe Val Leu His Arg Glu Gly Lys Gly Gly Leu Cys Ala Glu
35 40 45

Tyr Met Ala Gly Phe Gln Trp Gly Leu Glu Arg Asp Tyr Gln Val Leu
50 55 60

Cys Glu Met Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu
65 70 75 80

Leu Leu Ala Glu Ile Thr Asn Gly Ala Asp Leu Val Ile Gly Ser Arg
85 90 95

Tyr Val Pro Gly Gly Arg Val Val Asn Trp Pro Lys Asn Arg Trp Leu
100 105 110

Leu Ser Lys Gly Gly Asn Val Tyr Ile Ser Val Ala Leu Gly Ala Gly
115 120 125

Leu Thr Asp Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Val Leu
130 135 140

Glu Ala Leu Pro Leu Asp Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln
145 150 155 160

Val Glu Ile Ala Tyr Arg Ala Val Glu Ala Gly Phe Asp Val Arg Glu
165 170 175

Val Pro Ile Thr Phe Thr Glu Arg Glu Ile Gly Glu Ser Lys Leu Asp
180 185 190

Gly Ser Phe Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Leu
195 200 205

Lys His Arg Gly Gly Gln Ala Lys Glu Leu Ser Lys Glu Met Val Gly
210 215 220

Leu Leu Asn Tyr Glu Trp Lys His Phe Lys Lys Arg Asn Thr Trp Leu
225 230 235 240

<210> 41

<211> 1293

<212> DNA

CCGCCTGCTT GCCGGTAGT GAA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1270)

<223> RXN02062

<400> 41

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ttgtctaaac atcggttttgg ggtccgaatg atagcccctt ttaatgcccc catttcggta 60

tcgctgcgca actggttttta gatggctaata ctttgaaatt atg aga gtc gga atg 115
               Met Arg Val Gly Met
               1               5

atg aca aga gag tat cca cca gag gtt tac ggc ggc gct ggc gtg cac 163
Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly Gly Ala Gly Val His
               10               15               20

gtc acc gaa ttg acc cga ttc atg cgt gag atc gct gaa gtt gat gtt 211
Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile Ala Glu Val Asp Val
               25               30               35

cac tgc atg ggt gca cct cgc gat atg gag gga gtt ttc gtc cac ggc 259
His Cys Met Gly Ala Pro Arg Asp Met Glu Gly Val Phe Val His Gly
               40               45               50

gtc gat cct gcc ttg gaa agc gcg aac cct gcg att aag aca ctg tcc 307
Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala Ile Lys Thr Leu Ser
               55               60               65

acc ggt tta cgc atg gca gaa gct gca aac aac gtg gat gtc gtg cac 355
Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn Val Asp Val Val His
               70               75               80               85

tca cac act tgg tat gca ggt ctt ggc ggc cac ctt gca gct cgt ctc 403
Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His Leu Ala Ala Arg Leu
               90               95               100

cac ggc att cct cac gtg gct acc gcg cac tct ttg gag cca gat cgc 451
His Gly Ile Pro His Val Ala Thr Ala His Ser Leu Glu Pro Asp Arg
               105               110               115

cca tgg aag cgt gag cag ctt ggc ggt gga tac gac gtg tcc tcc tgg 499
Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr Asp Val Ser Ser Trp
               120               125               130

tct gaa aaa aat gcc atg gaa tac gct gac gcg gtc atc gct gtg tgc 547
Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala Val Ile Ala Val Ser
               135               140               145

gct cgc atg aaa gat tcc atc ctc gct gcg tac cct cgc atc gag ccg 595
Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr Pro Arg Ile Glu Pro
               150               155               160               165

gac aac gtg cgt gtt gtc ctc aac ggc atc gac act gag ttg tgg cag 643
Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp Thr Glu Leu Trp Gln
               170               175               180

cct cgc ccg act ttc gat gac gcg gaa gat tcc gta ctc cgc tcc cta 691
Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser Val Leu Arg Ser Leu
               185               190               195

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BGI-131CP
 Corynebacterium glutamicum
 RXN02062
 (101)..(1270)

ggc gtt gac cca cag cgg ccc atc gtc gca ttt gtc ggc cgc atc acc 739
 Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe Val Gly Arg Ile Thr
 200 205 210

cgc caa aaa ggc gtc gag cac ctc atc aag gca gca gcg ctt ttc gac 787
 Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala Ala Ala Leu Phe Asp
 215 220 225

gag tcc gtg cag ctt gtg ctc tgt gcc ggc gcg cca gac acc ccc gaa 835
 Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala Pro Asp Thr Pro Glu
 230 235 240 245

atc gca gct cgc acc acc gcc ctg gtg gaa gaa ctc cag gca aag cgc 883
 Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu Leu Gln Ala Lys Arg
 250 255 260

gaa ggc att ttc tgg gtt cag gac atg ctg ggc aag gac aaa atc caa 931
 Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly Lys Asp Lys Ile Gln
 265 270 275

gag att ctc acc gct gct gac acc ttc gtg tgc cca tcc att tac gag 979
 Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys Pro Ser Ile Tyr Glu
 280 285 290

cca ctg ggc atc gtg aac ttg gaa gca atg gcc tgc aac acc gca gtt 1027
 Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala Cys Asn Thr Ala Val
 295 300 305

gtc gca tcc gac gtt gga ggc atc cct gag gtt gtt gtc gac ggc acc 1075
 Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val Val Val Asp Gly Thr
 310 315 320 325

acc ggc gcc ctc gtt cac tac gac gaa aat gat gtc gaa acc ttc gag 1123
 Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp Val Glu Thr Phe Glu
 330 335 340

cgc gat atc gcc gaa gcg gtg aat aaa atg gtc gct gat cga gag acc 1171
 Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val Ala Asp Arg Glu Thr
 345 350 355

gca gcc aaa ttt ggt ctc gca ggg cgc gaa cgt gct atc aat gat ttc 1219
 Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg Ala Ile Asn Asp Phe
 360 365 370

tcc tgg gca acg att gct cag cag acc att gat gtg tac aaa tcc ttg 1267
 Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp Val Tyr Lys Ser Leu
 375 380 385

atg taaaaccgaa agccggggaa cct 1293
 Met
 390

<210> 42

<211> 390

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

Met Arg Val Gly Met Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly

tcc tgg gca acg att gct cag cag acc att gat gtg tac aaa tcc ttg 1267
 Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp Val Tyr Lys Ser Leu
 375 380 385

atg taaaaccgaa agccgggggaa cct 1293
 Met
 390

<210> 44

<211> 390

<212> PRT

<213> Corynebacterium glutamicum

<400> 44

Met Arg Val Gly Met Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly
 1 5 10 15

Gly Ala Gly Val His Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile
 20 25 30

Ala Glu Val Asp Val His Cys Met Gly Ala Pro Arg Asp Met Glu Gly
 35 40 45

Val Phe Val His Gly Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala
 50 55 60

Ile Lys Thr Leu Ser Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn
 65 70 75 80

Val Asp Val Val His Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His
 85 90 95

Leu Ala Ala Arg Leu His Gly Ile Pro His Val Ala Thr Ala His Ser
 100 105 110

Leu Glu Pro Asp Arg Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr
 115 120 125

Asp Val Ser Ser Trp Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala
 130 135 140

Val Ile Ala Val Ser Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr
 145 150 155 160

Pro Arg Ile Glu Pro Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp
 165 170 175

Thr Glu Leu Trp Gln Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser
 180 185 190

Val Leu Arg Ser Leu Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe
 195 200 205

Val Gly Arg Ile Thr Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala
 210 215 220

Ala Ala Leu Phe Asp Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala
 225 230 235 240

1267 1293 44 390 PRT Corynebacterium glutamicum

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Pro Asp Thr Pro Glu Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu
                245                      250                255

Leu Gln Ala Lys Arg Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly
                260                      265                270

Lys Asp Lys Ile Gln Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys
                275                      280                285

Pro Ser Ile Tyr Glu Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala
                290                      295                300

Cys Asn Thr Ala Val Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val
305                      310                      315                320

Val Val Asp Gly Thr Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp
                325                      330                335

Val Glu Thr Phe Glu Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val
                340                      345                350

Ala Asp Arg Glu Thr Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg
                355                      360                365

Ala Ile Asn Asp Phe Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp
                370                      375                380

Val Tyr Lys Ser Leu Met
385                      390

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<210> 45
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(475)
<223> RXA02222

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<400> 45
catccgctga acatcgctctg tctacagcgt ttggagaacg cgaaaaagat gaggcagtac 60

aagattgcaa aaaccttgaa aaagtgtatg gcagcgatgg ttg ggt cga cct ccc 115
                                   Leu Gly Arg Pro Pro
                                   1                    5

cca gga gac gtt cat act ctc cta gac gat atc gga gca gag gaa tct 163
Pro Gly Asp Val His Thr Leu Leu Asp Asp Ile Gly Ala Glu Glu Ser
                10                      15                20

gaa gca gat aaa gtt cca att gaa tgg caa aac gcc ctg act aag gca 211
Glu Ala Asp Lys Val Pro Ile Glu Trp Gln Asn Ala Leu Thr Lys Ala
                25                      30                35

gac agg tat gca aac cgg caa cac atg tct cag gca cga ctc tat cgc 259
Asp Arg Tyr Ala Asn Arg Gln His Met Ser Gln Ala Arg Leu Tyr Arg
                40                      45                50

caa tta acc agt gat gtt gga gag ggc ttc act gaa gaa gct gcc caa 307

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Gln Leu Thr Ser Asp Val Gly Glu Gly Phe Thr Glu Glu Ala Ala Gln
 55                      60                      65

tac gca atc gaa aat gtg aac gca gac tgg aac gct aac gcc cta gta 355
Tyr Ala Ile Glu Asn Val Asn Ala Asp Trp Asn Ala Asn Ala Leu Val
 70                      75                      80                      85

aaa gca aga aat tac cag gag cgc caa gca atg tca gta gac cgc att 403
Lys Ala Arg Asn Tyr Gln Glu Arg Gln Ala Met Ser Val Asp Arg Ile
                      90                      95                      100

tac agg caa ctt act agt gaa cac ggt gaa ggg ttt acc cca gag cag 451
Tyr Arg Gln Leu Thr Ser Glu His Gly Glu Gly Phe Thr Pro Glu Gln
                      105                      110                      115

gca caa tac gcg atc gac aac cta taaggcataa agatcctagt att 498
Ala Gln Tyr Ala Ile Asp Asn Leu
                      120                      125

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<210> 46
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

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<400> 46
Leu Gly Arg Pro Pro Gly Asp Val His Thr Leu Leu Asp Asp Ile
 1                      5                      10                      15

Gly Ala Glu Glu Ser Glu Ala Asp Lys Val Pro Ile Glu Trp Gln Asn
                20                      25                      30

Ala Leu Thr Lys Ala Asp Arg Tyr Ala Asn Arg Gln His Met Ser Gln
                35                      40                      45

Ala Arg Leu Tyr Arg Gln Leu Thr Ser Asp Val Gly Glu Gly Phe Thr
 50                      55                      60

Glu Glu Ala Ala Gln Tyr Ala Ile Glu Asn Val Asn Ala Asp Trp Asn
 65                      70                      75                      80

Ala Asn Ala Leu Val Lys Ala Arg Asn Tyr Gln Glu Arg Gln Ala Met
                85                      90                      95

Ser Val Asp Arg Ile Tyr Arg Gln Leu Thr Ser Glu His Gly Glu Gly
                100                      105                      110

Phe Thr Pro Glu Gln Ala Gln Tyr Ala Ile Asp Asn Leu
                115                      120                      125

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<210> 47
<211> 1344
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1321)
<223> RXA02313

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<400> 47

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 ttaactgcga tgtaggcatg atgtggagat aataaggccc atg cgg gta gca att 115
 Met Arg Val Ala Ile
 1 5
 gtt gca gag tcg ttc ctt cca aat gtc aac gga gtc acc aac tcg gtg 163
 Val Ala Glu Ser Phe Leu Pro Asn Val Asn Gly Val Thr Asn Ser Val
 10 15 20
 ctc cgg gtg ttg gag cat ttg aaa gcc aac gga cac gac gcg ctc gtc 211
 Leu Arg Val Leu Glu His Leu Lys Ala Asn Gly His Asp Ala Leu Val
 25 30 35
 atc gcg ccg ggt gcc cgg gat ttt gaa gaa gaa atc gcc cac tac ctg 259
 Ile Ala Pro Gly Ala Arg Asp Phe Glu Glu Glu Ile Gly His Tyr Leu
 40 45 50
 gcc ttt gaa att gtg cgc gtc ccc acc gtt cgg gtc cca ctg att gat 307
 Gly Phe Glu Ile Val Arg Val Pro Thr Val Arg Val Pro Leu Ile Asp
 55 60 65
 tca ctg ccc atc ggt gtt cct ctg ccc tca gtt acc tct gtg ctg cgc 355
 Ser Leu Pro Ile Gly Val Pro Leu Pro Ser Val Thr Ser Val Leu Arg
 70 75 80 85
 gag tac aac cca gac atc att cac ctg gca tcc cca ttt gtg ctc ggt 403
 Glu Tyr Asn Pro Asp Ile Ile His Leu Ala Ser Pro Phe Val Leu Gly
 90 95 100
 gga gcg gca gca ttc gca gca agg cag ctg cgc atc cca gca att gct 451
 Gly Ala Ala Ala Phe Ala Ala Arg Gln Leu Arg Ile Pro Ala Ile Ala
 105 110 115
 atc tat caa act gat gtc gca ggg ttc tcc cag cgc tac cac ctg gca 499
 Ile Tyr Gln Thr Asp Val Ala Gly Phe Ser Gln Arg Tyr His Leu Ala
 120 125 130
 ccg ttg gcc act gca agc tgg gaa tgg atc aag acg gtc cac aac atg 547
 Pro Leu Ala Thr Ala Ser Trp Glu Trp Ile Lys Thr Val His Asn Met
 135 140 145
 tgc cag cgc acc ctt gct ccc tca tcc atg agc att gac gag ctg cgt 595
 Cys Gln Arg Thr Leu Ala Pro Ser Ser Met Ser Ile Asp Glu Leu Arg
 150 155 160 165
 gac cac gga att aat gat att ttc cac tgg gct cgg gcc gtg gac tcc 643
 Asp His Gly Ile Asn Asp Ile Phe His Trp Ala Arg Gly Val Asp Ser
 170 175 180
 aag cgt ttc cac cct gga aag cgt tcc gta gcg cta cgt aag tct tgg 691
 Lys Arg Phe His Pro Gly Lys Arg Ser Val Ala Leu Arg Lys Ser Trp
 185 190 195
 gat cca agt gga gca aag aag atc gtt ggt ttc gtt ggg cgc ctt gca 739
 Asp Pro Ser Gly Ala Lys Lys Ile Val Gly Phe Val Gly Arg Leu Ala
 200 205 210
 tcc gaa aag gcc gtg gag cgc ctt gct gga tta tcc gga cgc tca gac 787
 Ser Glu Lys Gly Val Glu Arg Leu Ala Gly Leu Ser Gly Arg Ser Asp

BGI-131CP-47-65

215	220	225	
atc caa ttg gtc atc gtc ggt gat ggc cca gag gcc aag tac ctg cag			835
Ile Gln Leu Val Ile Val Gly Asp Gly Pro Glu Ala Lys Tyr Leu Gln			
230	235	240	245
gaa atg atg ccg gat gcg atc ttc aca gga gct ctc ggc ggc gag gaa			883
Glu Met Met Pro Asp Ala Ile Phe Thr Gly Ala Leu Gly Gly Glu Glu			
250	255		260
cta gcc acc acc tac gca tca ctc gat ctg ttt gtg cac cca ggt gag			931
Leu Ala Thr Thr Tyr Ala Ser Leu Asp Leu Phe Val His Pro Gly Glu			
265	270		275
ttt gaa acc ttc tgc cag gcg atc cag gaa gcc caa gca tca ggt gtg			979
Phe Glu Thr Phe Cys Gln Ala Ile Gln Glu Ala Gln Ala Ser Gly Val			
280	285		290
ccc acc att ggc cca cgc gca ggt ggt ccc att gat ttg atc aac gaa			1027
Pro Thr Ile Gly Pro Arg Ala Gly Gly Pro Ile Asp Leu Ile Asn Glu			
295	300		305
ggc gtc aac ggc ctg ctt ctt gat gtt gta gat ttc aag gaa acc ctc			1075
Gly Val Asn Gly Leu Leu Leu Asp Val Val Asp Phe Lys Glu Thr Leu			
310	315		320
ccc gct gca gcc gaa tgg att ttg gac gat tcc cgc cac tcc gaa atg			1123
Pro Ala Ala Ala Glu Trp Ile Leu Asp Asp Ser Arg His Ser Glu Met			
330	335		340
tgc gca gct gct tgg gaa ggt gtg aaa gac aag acc tgg gaa gct ttg			1171
Cys Ala Ala Ala Trp Glu Gly Val Lys Asp Lys Thr Trp Glu Ala Leu			
345	350		355
tgc acc cag ctt ctc cag cac tac gcg gat gta atc gca ttg tca cag			1219
Cys Thr Gln Leu Leu Gln His Tyr Ala Asp Val Ile Ala Leu Ser Gln			
360	365		370
cgc atc cca ctg aca ttc ttt ggc cct agc gct gaa gta gca aag ctt			1267
Arg Ile Pro Leu Thr Phe Phe Gly Pro Ser Ala Glu Val Ala Lys Leu			
375	380		385
cca ctg tgg gtt gct cgc gcg ctg ggt gtt cgc acc cgc atc agc atc			1315
Pro Leu Trp Val Ala Arg Ala Leu Gly Val Arg Thr Arg Ile Ser Ile			
390	395		400
gag gct taactctgca gaattaatcc atg			1344
Glu Ala			

<210> 48

<211> 407

<212> PRT

<213> Corynebacterium glutamicum

<400> 48

Met	Arg	Val	Ala	Ile	Val	Ala	Glu	Ser	Phe	Leu	Pro	Asn	Val	Asn	Gly
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Val Thr Asn Ser Val Leu Arg Val Leu Glu His Leu Lys Ala Asn Gly

20					25					30					
His	Asp	Ala	Leu	Val	Ile	Ala	Pro	Gly	Ala	Arg	Asp	Phe	Glu	Glu	Glu
35					40					45					
Ile	Gly	His	Tyr	Leu	Gly	Phe	Glu	Ile	Val	Arg	Val	Pro	Thr	Val	Arg
50					55					60					
Val	Pro	Leu	Ile	Asp	Ser	Leu	Pro	Ile	Gly	Val	Pro	Leu	Pro	Ser	Val
65					70					75					
Thr	Ser	Val	Leu	Arg	Glu	Tyr	Asn	Pro	Asp	Ile	Ile	His	Leu	Ala	Ser
85					90					95					
Pro	Phe	Val	Leu	Gly	Gly	Ala	Ala	Ala	Phe	Ala	Ala	Arg	Gln	Leu	Arg
100					105					110					
Ile	Pro	Ala	Ile	Ala	Ile	Tyr	Gln	Thr	Asp	Val	Ala	Gly	Phe	Ser	Gln
115					120					125					
Arg	Tyr	His	Leu	Ala	Pro	Leu	Ala	Thr	Ala	Ser	Trp	Glu	Trp	Ile	Lys
130					135					140					
Thr	Val	His	Asn	Met	Cys	Gln	Arg	Thr	Leu	Ala	Pro	Ser	Ser	Met	Ser
145					150					155					
Ile	Asp	Glu	Leu	Arg	Asp	His	Gly	Ile	Asn	Asp	Ile	Phe	His	Trp	Ala
165					170					175					
Arg	Gly	Val	Asp	Ser	Lys	Arg	Phe	His	Pro	Gly	Lys	Arg	Ser	Val	Ala
180					185					190					
Leu	Arg	Lys	Ser	Trp	Asp	Pro	Ser	Gly	Ala	Lys	Lys	Ile	Val	Gly	Phe
195					200					205					
Val	Gly	Arg	Leu	Ala	Ser	Glu	Lys	Gly	Val	Glu	Arg	Leu	Ala	Gly	Leu
210					215					220					
Ser	Gly	Arg	Ser	Asp	Ile	Gln	Leu	Val	Ile	Val	Gly	Asp	Gly	Pro	Glu
225					230					235					
Ala	Lys	Tyr	Leu	Gln	Glu	Met	Met	Pro	Asp	Ala	Ile	Phe	Thr	Gly	Ala
245					250					255					
Leu	Gly	Gly	Glu	Glu	Leu	Ala	Thr	Thr	Tyr	Ala	Ser	Leu	Asp	Leu	Phe
260					265					270					
Val	His	Pro	Gly	Glu	Phe	Glu	Thr	Phe	Cys	Gln	Ala	Ile	Gln	Glu	Ala
275					280					285					
Gln	Ala	Ser	Gly	Val	Pro	Thr	Ile	Gly	Pro	Arg	Ala	Gly	Gly	Pro	Ile
290					295					300					
Asp	Leu	Ile	Asn	Glu	Gly	Val	Asn	Gly	Leu	Leu	Leu	Asp	Val	Val	Asp
305					310					315					
Phe	Lys	Glu	Thr	Leu	Pro	Ala	Ala	Ala	Glu	Trp	Ile	Leu	Asp	Asp	Ser
325					330					335					
Arg	His	Ser	Glu	Met	Cys	Ala	Ala	Ala	Trp	Glu	Gly	Val	Lys	Asp	Lys
340					345					350					

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Thr Trp Glu Ala Leu Cys Thr Gln Leu Leu Gln His Tyr Ala Asp Val
 355 360 365

Ile Ala Leu Ser Gln Arg Ile Pro Leu Thr Phe Phe Gly Pro Ser Ala
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Glu Val Ala Lys Leu Pro Leu Trp Val Ala Arg Ala Leu Gly Val Arg
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Thr Arg Ile Ser Ile Glu Ala
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1354)
 <223> RXA02491

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 Met Arg Val Ala Met
 1 5

att tcc atg cac acc tct cca ttg cag cag ccc gga act ggt gat tca 163
 Ile Ser Met His Thr Ser Pro Leu Gln Gln Pro Gly Thr Gly Asp Ser
 10 15 20

ggc ggc atg aac gtc tac att ctt tgc acc gcg act gag cta gcg aaa 211
 Gly Gly Met Asn Val Tyr Ile Leu Ser Thr Ala Thr Glu Leu Ala Lys
 25 30 35

cag ggt atc gag gtc gat att tac act cgt gcc acg agg cct tct cag 259
 Gln Gly Ile Glu Val Asp Ile Tyr Thr Arg Ala Thr Arg Pro Ser Gln
 40 45 50

ggt gag atc gtg aga gta gct gag aat ttg cgg gtc att aat atc gct 307
 Gly Glu Ile Val Arg Val Ala Glu Asn Leu Arg Val Ile Asn Ile Ala
 55 60 65

gcg ggg ccg tat gag ggg ctt tcc aaa gag gag ctt cct act cag ttg 355
 Ala Gly Pro Tyr Glu Gly Leu Ser Lys Glu Glu Leu Pro Thr Gln Leu
 70 75 80 85

gcg gcg ttt acc ggc gga atg ttg tgc ttt acg cgc cgg gag aag gtt 403
 Ala Ala Phe Thr Gly Gly Met Leu Ser Phe Thr Arg Arg Glu Lys Val
 90 95 100

act tat gat ctg atc cat tct cac tat tgg ctg tct ggt cag gtg ggg 451
 Thr Tyr Asp Leu Ile His Ser His Tyr Trp Leu Ser Gly Gln Val Gly
 105 110 115

tgg ttg ctg cgc gat ttg tgg cgg att ccc ctt att cat acg gca cac 499
 Trp Leu Leu Arg Asp Leu Trp Arg Ile Pro Leu Ile His Thr Ala His

1354-1377: the 990

Ala Thr Glu Arg Ser Arg Arg Glu Leu Gly Ile Pro Leu His Thr Lys
 210 215 220
 Val Val Ala Phe Val Gly Arg Leu Gln Pro Phe Lys Gly Pro Gln Val
 225 230 235 240
 Leu Ile Lys Ala Val Ala Ala Leu Phe Asp Arg Asp Pro Asp Arg Asn
 245 250 255
 Leu Arg Val Ile Ile Cys Gly Gly Pro Ser Gly Pro Asn Ala Thr Pro
 260 265 270
 Asp Thr Tyr Arg His Met Ala Glu Glu Leu Gly Val Glu Lys Arg Ile
 275 280 285
 Arg Phe Leu Asp Pro Arg Pro Pro Ser Glu Leu Val Ala Val Tyr Arg
 290 295 300
 Ala Ala Asp Ile Val Ala Val Pro Ser Phe Asn Glu Ser Phe Gly Leu
 305 310 315 320
 Val Ala Met Glu Ala Gln Ala Ser Gly Thr Pro Val Ile Ala Ala Arg
 325 330 335
 Val Gly Gly Leu Pro Ile Ala Val Ala Glu Gly Glu Thr Gly Leu Leu
 340 345 350
 Val Asp Gly His Ser Pro His Ala Trp Ala Asp Ala Leu Ala Thr Leu
 355 360 365
 Leu Asp Asp Asp Glu Thr Arg Ile Arg Met Gly Glu Asp Ala Val Glu
 370 375 380
 His Ala Arg Thr Phe Ser Trp Ala Ala Thr Ala Ala Gln Leu Ser Ser
 385 390 395 400
 Leu Tyr Asn Asp Ala Ile Ala Asn Glu Asn Val Asp Gly Glu Thr His
 405 410 415
 His Gly

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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1264)
 <223> RXN02595

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 ttcgcggatt tgtgcggggg agtgggtggg agagaaaacg gtg atc gtt gtg gcc 115
 Val Ile Val Val Ala
 1 5
 atg gct tcc att atg gct tgt tta aaa gca gct aga ctg aat aac cct 163

Met Ala Ser Ile Met Ala Cys Leu Lys Ala Ala Arg Leu Asn Asn Pro 20
 10
 atg aag atc ctt ttg ttg tgc tgg cgt gat acc act cat cct caa ggt 211
 Met Lys Ile Leu Leu Leu Cys Trp Arg Asp Thr Thr His Pro Gln Gly 35
 25
 ggc gga agt gaa cgc tat ctg gag cgg gtg ggt gag ttt ttg gcg gat 259
 Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly Glu Phe Leu Ala Asp 50
 40
 cag ggc cat gag gtg gtg ttt cgt act gct ggg cac acg gat gcg cca 307
 Gln Gly His Glu Val Val Phe Arg Thr Ala Gly His Thr Asp Ala Pro 65
 55
 cgg cgt tct ttc cgc gat ggt gtg agg tat tcc agg agc ggt ggg aag 355
 Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser Arg Ser Gly Gly Lys 85
 70
 ttt agt gtg tat ccc aag gcg tgg gtg gcc atg atg ttg ggt cgt gtg 403
 Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met Met Leu Gly Arg Val 100
 90
 ggg att ggc acg ttt tcc aag gtt gat gtg gtg gtg gat acg cag aat 451
 Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val Val Asp Thr Gln Asn 115
 105
 ggc att ccg ttt ttt gga aag ttt ttc tcc ggt aag ccg act gtg ttg 499
 Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly Lys Pro Thr Val Leu 130
 120
 ctc acg cat cat tgc cat aag gag cag tgg ccg gtg gtg ggt cgg gtg 547
 Leu Thr His His Cys His Lys Glu Gln Trp Pro Val Val Gly Arg Val 145
 135
 ctg gcg aag gtt ggt tgg ctg att gag agc cag atc gcg ccg cgc gct 595
 Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln Ile Ala Pro Arg Ala 165
 150
 tac aaa act gcg ccg tat gtg act gtt tca gag ccg agc gct gag gag 643
 Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu Pro Ser Ala Glu Glu 180
 170
 ctc att gcg ttg ggt gtg gat cag cag ccg att cat atc gtg cgc aat 691
 Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile His Ile Val Arg Asn 195
 185
 ggc gtg gat ccc gtg ccg ctg cac acg ccg aag ctg gat cgc gat ggc 739
 Gly Val Asp Pro Val Pro Leu His Thr Pro Lys Leu Asp Arg Asp Gly 210
 200
 cag cat gcg gtg acg ttg tgc cgc ctg gtt ccg cac aag cag att gag 787
 Gln His Ala Val Thr Leu Ser Arg Leu Val Pro His Lys Gln Ile Glu 225
 215
 cat gcg atg gat gtc gtc gcg gcg ctc gac ggc gtg gtg ctg gat gta 835
 His Ala Met Asp Val Val Ala Ala Leu Asp Gly Val Val Leu Asp Val 245
 230
 gtc gaa agc ggt tgg tgg cag aag gaa ctg gtc gat tat gcc cgc acg 883
 Val Glu Ser Gly Trp Trp Gln Lys Glu Leu Val Asp Tyr Ala Arg Thr

Met Leu Gly Arg Val Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val
 100 105 110
 Val Asp Thr Gln Asn Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly
 115 120 125
 Lys Pro Thr Val Leu Leu Thr His His Cys His Lys Glu Gln Trp Pro
 130 135 140
 Val Val Gly Arg Val Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln
 145 150 155 160
 Ile Ala Pro Arg Ala Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu
 165 170 175
 Pro Ser Ala Glu Glu Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile
 180 185 190
 His Ile Val Arg Asn Gly Val Asp Pro Val Pro Leu His Thr Pro Lys
 195 200 205
 Leu Asp Arg Asp Gly Gln His Ala Val Thr Leu Ser Arg Leu Val Pro
 210 215 220
 His Lys Gln Ile Glu His Ala Met Asp Val Val Ala Ala Leu Asp Gly
 225 230 235 240
 Val Val Leu Asp Val Val Glu Ser Gly Trp Trp Gln Lys Glu Leu Val
 245 250 255
 Asp Tyr Ala Arg Thr Leu Gly Val Ser Asp Arg Val Val Phe His Gly
 260 265 270
 Gln Val Ala Glu Asp His Lys His Ala Leu Leu Glu Arg Ala Thr Ile
 275 280 285
 His Leu Met Pro Ser Arg Lys Glu Gly Trp Gly Leu Ala Val Thr Glu
 290 295 300
 Ala Ala Gln His Gly Val Pro Thr Ile Gly Tyr Arg Ser Ser Gly Gly
 305 310 315 320
 Leu Arg Asp Ser Val Val Asp Gly Glu Thr Gly Leu Leu Val Asp Ser
 325 330 335
 Lys Ala Glu Leu Ile Ser Ala Thr Lys Thr Leu Leu Ile Asp Ala Ser
 340 345 350
 Leu Arg Ser Lys Leu Gly Ala Ser Ala Lys Gln Arg Ala Glu Asn Tyr
 355 360 365
 Lys Trp Asp Thr Ala Gly Ala Gln Phe Glu Glu Leu Leu Leu Gly Leu
 370 375 380
 Ala Ser Lys Lys
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<210> 53

<211> 751

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(751)

<223> FRXA02595

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				Val	Ile	Val	Val	Ala	
				1				5	

atg	gct	tcc	att	atg	gct	tgt	tta	aaa	gca	gct	aga	ctg	aat	aac	cct	163
Met	Ala	Ser	Ile	Met	Ala	Cys	Leu	Lys	Ala	Ala	Arg	Leu	Asn	Asn	Pro	
			10						15					20		

atg	aag	atc	ctt	ttg	ttg	tgc	tgg	cgt	gat	acc	act	cat	cct	caa	ggg	211
Met	Lys	Ile	Leu	Leu	Leu	Cys	Trp	Arg	Asp	Thr	Thr	His	Pro	Gln	Gly	
			25					30					35			

ggc	gga	agt	gaa	cgc	tat	ctg	gag	cgg	gtg	ggg	gag	ttt	ttg	gcg	gat	259
Gly	Gly	Ser	Glu	Arg	Tyr	Leu	Glu	Arg	Val	Gly	Glu	Phe	Leu	Ala	Asp	
		40					45					50				

cag	ggc	cat	gag	gtg	gtg	ttt	cgt	act	gct	ggg	cac	acg	gat	gcg	cca	307
Gln	Gly	His	Glu	Val	Val	Phe	Arg	Thr	Ala	Gly	His	Thr	Asp	Ala	Pro	
	55					60					65					

cgg	cgt	tct	ttc	cgc	gat	ggg	gtg	agg	tat	tcc	agg	agc	ggg	ggg	aag	355
Arg	Arg	Ser	Phe	Arg	Asp	Gly	Val	Arg	Tyr	Ser	Arg	Ser	Gly	Gly	Lys	
	70				75					80					85	

ttt	agt	gtg	tat	ccc	aag	gcg	tgg	gtg	gcc	atg	atg	ttg	ggg	cgt	gtg	403
Phe	Ser	Val	Tyr	Pro	Lys	Ala	Trp	Val	Ala	Met	Met	Leu	Gly	Arg	Val	
				90					95					100		

ggg	att	ggc	acg	ttt	tcc	aag	gtt	gat	gtg	gtg	gtg	gat	acg	cag	aat	451
Gly	Ile	Gly	Thr	Phe	Ser	Lys	Val	Asp	Val	Val	Val	Asp	Thr	Gln	Asn	
			105					110					115			

ggc	att	ccg	ttt	ttt	gga	aag	ttt	ttc	tcc	ggg	aag	ccg	act	gtg	ttg	499
Gly	Ile	Pro	Phe	Phe	Gly	Lys	Phe	Phe	Ser	Gly	Lys	Pro	Thr	Val	Leu	
		120					125					130				

ctc	acg	cat	cat	tgc	cat	aag	gag	cag	tgg	ccg	gtg	gtg	ggg	cgg	gtg	547
Leu	Thr	His	His	Cys	His	Lys	Glu	Gln	Trp	Pro	Val	Val	Gly	Arg	Val	
	135					140					145					

ctg	gcg	aag	gtt	ggg	tgg	ctg	att	gag	agc	cag	atc	gcg	ccg	cgc	gct	595
Leu	Ala	Lys	Val	Gly	Trp	Leu	Ile	Glu	Ser	Gln	Ile	Ala	Pro	Arg	Ala	
150					155					160					165	

tac	aaa	act	gcg	ccg	tat	gtg	act	gtt	tca	gag	ccg	agc	gct	gag	gag	643
Tyr	Lys	Thr	Ala	Pro	Tyr	Val	Thr	Val	Ser	Glu	Pro	Ser	Ala	Glu	Glu	
			170					175						180		

ctc	att	gcg	ttg	ggg	gtg	gat	cag	cag	cgg	att	cat	atc	gtg	cgc	aat	691
Leu	Ile	Ala	Leu	Gly	Val	Asp	Gln	Gln	Arg	Ile	His	Ile	Val	Arg	Asn	
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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(811)

<223> RXA02616

<400> 55

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cttcgaaaag	ttttgtggca	agaatoggaa	gcaggcgaaa	ttg	cag	aag	cac	act	115
				Leu	Gln	Lys	His	Thr	
				1				5	

cga	ggt	ggc	aag	cac	cgc	aag	cag	act	acc	tcc	cca	gta	act	aag	ggt	163
Arg	Gly	Gly	Lys	His	Arg	Lys	Gln	Thr	Thr	Ser	Pro	Val	Thr	Lys	Gly	
				10				15						20		

ggt	gtc	gct	ttt	gtt	gca	gta	gct	acc	ggg	gcc	gtg	tca	act	gca	ggc	211
Gly	Val	Ala	Phe	Val	Ala	Val	Ala	Thr	Gly	Ala	Val	Ser	Thr	Ala	Gly	
			25					30						35		

gca	ggc	gga	gca	gtt	gct	gca	cag	gct	tcc	aat	cag	ccc	gtt	gag	gtc	259
Ala	Gly	Gly	Ala	Val	Ala	Ala	Gln	Ala	Ser	Asn	Gln	Pro	Val	Glu	Val	
			40				45					50				

aac	ttc	gag	ctt	act	gca	aac	gac	aca	act	gac	ctc	gtg	gct	gga	agc	307
Asn	Phe	Glu	Leu	Thr	Ala	Asn	Asp	Thr	Thr	Asp	Leu	Val	Ala	Gly	Ser	
	55					60					65					

tcc	gcc	cct	cag	atc	ctg	tcc	atc	gct	gag	ttc	aag	cca	gtt	gtg	aac	355
Ser	Ala	Pro	Gln	Ile	Leu	Ser	Ile	Ala	Glu	Phe	Lys	Pro	Val	Val	Asn	
	70				75					80					85	

ttg	ggc	gat	cag	atc	gtt	aag	acc	att	cag	tac	aac	gct	gac	cgc	att	403
Leu	Gly	Asp	Gln	Ile	Val	Lys	Thr	Ile	Gln	Tyr	Asn	Ala	Asp	Arg	Ile	
				90				95						100		

cag	gct	gac	ctg	gac	gct	cgt	ggc	cct	tca	gtg	gtt	cgc	cct	gct	gaa	451
Gln	Ala	Asp	Leu	Asp	Ala	Arg	Gly	Pro	Ser	Val	Val	Arg	Pro	Ala	Glu	
			105				110						115			

ggt	tct	tac	acc	tcc	ggc	ttc	ggg	gct	cgt	tgg	ggc	acc	aac	cac	aac	499
Gly	Ser	Tyr	Thr	Ser	Gly	Phe	Gly	Ala	Arg	Trp	Gly	Thr	Asn	His	Asn	
		120				125						130				

ggt	gtg	gat	atc	gct	aac	gca	atc	ggc	act	cca	atc	ctc	gct	gcc	atg	547
Gly	Val	Asp	Ile	Ala	Asn	Ala	Ile	Gly	Thr	Pro	Ile	Leu	Ala	Ala	Met	
		135				140					145					

gac	ggc	act	gtt	atc	gat	gca	ggg	cct	gct	tcc	ggg	ttc	ggg	aac	tgg	595
Asp	Gly	Thr	Val	Ile	Asp	Ala	Gly	Pro	Ala	Ser	Gly	Phe	Gly	Asn	Trp	
	150				155					160				165		

gtt	cgc	ctc	cag	cac	gaa	gat	ggc	acc	atc	acc	gtg	tac	ggc	cac	atg	643
Val	Arg	Leu	Gln	His	Glu	Asp	Gly	Thr	Ile	Thr	Val	Tyr	Gly	His	Met	
			170					175						180		

gaa	acc	gtt	gag	gtg	acc	gtt	ggg	cag	act	gtt	aag	gct	ggc	gag	cgc	691
Glu	Thr	Val	Glu	Val	Thr	Val	Gly	Gln	Thr	Val	Lys	Ala	Gly	Glu	Arg	

BGI-131CP-77-131CP

185 190 195
 atc gca ggc atg ggt agc cga gga ttc tcc acc ggc tcc cac ctc cac 739
 Ile Ala Gly Met Gly Ser Arg Gly Phe Ser Thr Gly Ser His Leu His
 200 205 210

 ttc gag gtt tac cct gca ggc ggt ggc gct gtt gat cca gct cct tgg 787
 Phe Glu Val Tyr Pro Ala Gly Gly Gly Ala Val Asp Pro Ala Pro Trp
 215 220 225

 ctt gca gag cgc ggc att act ctt taattaactt ttgggogacc ctt 834
 Leu Ala Glu Arg Gly Ile Thr Leu
 230 235

<210> 56
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 <212> PRT
 <213> Corynebacterium glutamicum

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 Val Ser Thr Ala Gly Ala Gly Gly Ala Val Ala Ala Gln Ala Ser Asn
 35 40 45

 Gln Pro Val Glu Val Asn Phe Glu Leu Thr Ala Asn Asp Thr Thr Asp
 50 55 60

 Leu Val Ala Gly Ser Ser Ala Pro Gln Ile Leu Ser Ile Ala Glu Phe
 65 70 75 80

 Lys Pro Val Val Asn Leu Gly Asp Gln Ile Val Lys Thr Ile Gln Tyr
 85 90 95

 Asn Ala Asp Arg Ile Gln Ala Asp Leu Asp Ala Arg Gly Pro Ser Val
 100 105 110

 Val Arg Pro Ala Glu Gly Ser Tyr Thr Ser Gly Phe Gly Ala Arg Trp
 115 120 125

 Gly Thr Asn His Asn Gly Val Asp Ile Ala Asn Ala Ile Gly Thr Pro
 130 135 140

 Ile Leu Ala Ala Met Asp Gly Thr Val Ile Asp Ala Gly Pro Ala Ser
 145 150 155 160

 Gly Phe Gly Asn Trp Val Arg Leu Gln His Glu Asp Gly Thr Ile Thr
 165 170 175

 Val Tyr Gly His Met Glu Thr Val Glu Val Thr Val Gly Gln Thr Val
 180 185 190

 Lys Ala Gly Glu Arg Ile Ala Gly Met Gly Ser Arg Gly Phe Ser Thr
 195 200 205

 Gly Ser His Leu His Phe Glu Val Tyr Pro Ala Gly Gly Gly Ala Val

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 Asp Pro Ala Pro Trp Leu Ala Glu Arg Gly Ile Thr Leu
 225 230 235

<210> 57
 <211> 866
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(843)
 <223> RXA02627

<400> 57
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 Asp Val Thr Val Glu Ser Gln Pro Glu Arg Val Val Ala Leu Gly Trp
 1 5 10 15
 gga gat gct gag gct gcg ctg gaa ttc ggt gtg cag cct gtg ggt gca 96
 Gly Asp Ala Glu Ala Ala Leu Glu Phe Gly Val Gln Pro Val Gly Ala
 20 25 30
 tca gat tgg ctc gca ttc ggt ggt gaa ggc gtg gga ccg tgg att gag 144
 Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu
 35 40 45
 gat tct gcc tac gat gaa gcg cca gaa ata atc gga acc atg gaa ccg 192
 Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro
 50 55 60
 gag tat gaa aag att gca gcg ctt gaa ccg gat ctg att ttg gac gtg 240
 Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val
 65 70 75 80
 cgc agc tct ggc gac cag gaa cgc tat gac aag ttg tct tca atc gca 288
 Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala
 85 90 95
 ctg acc atc ggc gtt cca gaa ggt ggc gat agc tac ctc acc cca cgc 336
 Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg
 100 105 110
 gct gag cag gta acc atg atc gcc act gct ctg ggg cag gct gaa cgt 384
 Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg
 115 120 125
 ggt gaa gaa gtg aac gct gaa tac gag cag ctc act gct gat att cgt 432
 Gly Glu Glu Val Asn Ala Glu Tyr Glu Gln Leu Thr Ala Asp Ile Arg
 130 135 140
 gca gct cac ccg ggc tgg cct gag aag acc gcg gct gct gta tct gca 480
 Ala Ala His Pro Gly Trp Pro Glu Lys Thr Ala Ala Ala Val Ser Ala
 145 150 155 160
 acg gca acc agc tgg ggt gca tac atc aag ggc tcc aac cgt gta gat 528
 Thr Ala Thr Ser Trp Gly Ala Tyr Ile Lys Gly Ser Asn Arg Val Asp
 165 170 175

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ttg gaa cct ggc gtt ccc gtt ccc atc att ggg gat tgg ttc cgc ttc 307

[illegible]

Leu Glu Pro Gly Val Pro Val Pro Ile Ile Gly Asp Trp Phe Arg Phe
 55 60 65
 tac ctc ctg ttt aac ccc gga gcc gca ttt tcg atg ggt ggg gaa aac 355
 Tyr Leu Leu Phe Asn Pro Gly Ala Ala Phe Ser Met Gly Gly Glu Asn
 70 75 80 85
 agc acc tgg atc ttt aca acc atc cag ttg agc ttc gtc atc ggt atc 403
 Ser Thr Trp Ile Phe Thr Thr Ile Gln Leu Ser Phe Val Ile Gly Ile
 90 95 100
 gca att tat gcc cca cgc atc aaa cac aag tgg atc gcg gca gga ctt 451
 Ala Ile Tyr Ala Pro Arg Ile Lys His Lys Trp Ile Ala Ala Gly Leu
 105 110 115
 gcc ctt gtt gcc ggt gga gcc ttg gga aac gtg ttg gac cgg ttg ttc 499
 Ala Leu Val Ala Gly Gly Ala Leu Gly Asn Val Leu Asp Arg Leu Phe
 120 125 130
 aga gat cct tcc ttc ttc ttc gga cat gtt gtt gat tac atc tcc gta 547
 Arg Asp Pro Ser Phe Phe Phe Gly His Val Val Asp Tyr Ile Ser Val
 135 140 145
 gga aac ttt gca gta ttt aat atc gcc gat gcc tcg att tct tgc ggc 595
 Gly Asn Phe Ala Val Phe Asn Ile Ala Asp Ala Ser Ile Ser Cys Gly
 150 155 160 165
 gtc gtg gtg ttc ctg atc gga atg ttc ctt gag gac cgt gaa aac gcc 643
 Val Val Val Phe Leu Ile Gly Met Phe Leu Glu Asp Arg Glu Asn Ala
 170 175 180
 cag cat gcc aaa gca act gac gag aag gat gag gcc tgatgaacaa 689
 Gln His Ala Lys Ala Thr Asp Glu Lys Asp Glu Ala
 185 190
 ccgacaaagc aga 702

<210> 60
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 60
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 1 5 10 15
 Ser Lys Lys Glu Lys Arg Thr Thr Val Lys Gln Val Val Ala Leu Met
 20 25 30
 Ala Ala Ile Val Val Val Ile Ala Ser Leu Asp Gln Ile Val Lys Gln
 35 40 45
 Ile Met Leu Ser Trp Leu Glu Pro Gly Val Pro Val Pro Ile Ile Gly
 50 55 60
 Asp Trp Phe Arg Phe Tyr Leu Leu Phe Asn Pro Gly Ala Ala Phe Ser
 65 70 75 80
 Met Gly Gly Glu Asn Ser Thr Trp Ile Phe Thr Thr Ile Gln Leu Ser
 85 90 95

Phe Val Ile Gly Ile Ala Ile Tyr Ala Pro Arg Ile Lys His Lys Trp
 100 105 110
 Ile Ala Ala Gly Leu Ala Leu Val Ala Gly Gly Ala Leu Gly Asn Val
 115 120 125
 Leu Asp Arg Leu Phe Arg Asp Pro Ser Phe Phe Phe Gly His Val Val
 130 135 140
 Asp Tyr Ile Ser Val Gly Asn Phe Ala Val Phe Asn Ile Ala Asp Ala
 145 150 155 160
 Ser Ile Ser Cys Gly Val Val Val Phe Leu Ile Gly Met Phe Leu Glu
 165 170 175
 Asp Arg Glu Asn Ala Gln His Ala Lys Ala Thr Asp Glu Lys Asp Glu
 180 185 190

Ala

<210> 61
 <211> 1071
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1048)
 <223> RXA01094

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 Met Thr Leu Ala Thr
 1 5
 att ccc tca cca ccg cag ggt gtg tgg tac ttg ggt ccc att ccg att 163
 Ile Pro Ser Pro Pro Gln Gly Val Trp Tyr Leu Gly Pro Ile Pro Ile
 10 15 20
 agg gcc tat gcg atg tgc atc atc gct ggc att att gtt gcc att tgg 211
 Arg Ala Tyr Ala Met Cys Ile Ile Ala Gly Ile Ile Val Ala Ile Trp
 25 30 35
 ctg acg aga aag cgc tac gcc gcc cgc ggt gga aac cct gaa atc gtc 259
 Leu Thr Arg Lys Arg Tyr Ala Ala Arg Gly Gly Asn Pro Glu Ile Val
 40 45 50
 ctt gat gca gcg atc gtg gca gtt cct gcc gga atc atc ggt gga cgc 307
 Leu Asp Ala Ala Ile Val Ala Val Pro Ala Gly Ile Ile Gly Gly Arg
 55 60 65
 att tat cac gtc att acc gac aac caa aag tac ttc tgc gat acc tgt 355
 Ile Tyr His Val Ile Thr Asp Asn Gln Lys Tyr Phe Cys Asp Thr Cys
 70 75 80 85
 aac ccc gtc gac gcc ttc aaa atc acc aac ggt ggt ctg ggc atc tgg 403

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Asn Pro Val Asp Ala Phe Lys Ile Thr Asn Gly Gly Leu Gly Ile Trp
      90                      95                      100

ggg gca gtg atc ctc ggt ggc ctg gca gtg gcc gta ttc ttc cgg tac 451
Gly Ala Val Ile Leu Gly Gly Leu Ala Val Ala Val Phe Phe Arg Tyr
      105                      110                      115

aaa aag ctt cct ctt gca cct ttc gca gat gcc gtg gca cct gca gtt 499
Lys Lys Leu Pro Leu Ala Pro Phe Ala Asp Ala Val Ala Pro Ala Val
      120                      125                      130

atc ctg gcg cag gga att ggt cgt ctg ggc aac tgg ttt aac cag gag 547
Ile Leu Ala Gln Gly Ile Gly Arg Leu Gly Asn Trp Phe Asn Gln Glu
      135                      140                      145

ctc tac ggt gca gaa act acc gtt cca tgg gct ttg gaa atc tac tat 595
Leu Tyr Gly Ala Glu Thr Thr Val Pro Trp Ala Leu Glu Ile Tyr Tyr
      150                      155                      160

cgg gta gat gaa aat gga aaa ttc gca ccg gtg aca gga aca tcc acc 643
Arg Val Asp Glu Asn Gly Lys Phe Ala Pro Val Thr Gly Thr Ser Thr
      170                      175                      180

ggg gaa gta atg gct act gtt cat cca aca ttc ctc tat gaa ctg ttg 691
Gly Glu Val Met Ala Thr Val His Pro Thr Phe Leu Tyr Glu Leu Leu
      185                      190                      195

tgg aac cta ctg atc ttc gct ttg ttg atg tgg gct gac aag cga ttc 739
Trp Asn Leu Leu Ile Phe Ala Leu Leu Met Trp Ala Asp Lys Arg Phe
      200                      205                      210

aag ctg gaa cat ggc cga gta ttt gct ctc tac gta gct ggt tac acc 787
Lys Leu Glu His Gly Arg Val Phe Ala Leu Tyr Val Ala Gly Tyr Thr
      215                      220                      225

ttg ggc cgt ttc tgg att gaa caa atg cgc gtt gat gaa gcc acg ctt 835
Leu Gly Arg Phe Trp Ile Glu Gln Met Arg Val Asp Glu Ala Thr Leu
      230                      235                      240                      245

att ggc ggc atc cga atc aac acc atc gtc tcc gca gta gtg ttt gcc 883
Ile Gly Gly Ile Arg Ile Asn Thr Ile Val Ser Ala Val Val Phe Ala
      250                      255                      260

ggc gcg atc atc gtg ttc ttc ctg ttg aag aag ggt agg gaa act ccc 931
Gly Ala Ile Ile Val Phe Phe Leu Leu Lys Lys Gly Arg Glu Thr Pro
      265                      270                      275

gaa gag gta gat ccg act ttc gca gcg tct gtt gca gca gat gct gta 979
Glu Glu Val Asp Pro Thr Phe Ala Ala Ser Val Ala Ala Asp Ala Val
      280                      285                      290

gct tcg cca gat aga aaa ccc ttg ccg aaa gca ggg gag ggc att gat 1027
Ala Ser Pro Asp Arg Lys Pro Leu Pro Lys Ala Gly Glu Gly Ile Asp
      295                      300                      305

gga gaa acg ccc tca acg cga taggtttcaa ccataggcct gac 1071
Gly Glu Thr Pro Ser Thr Arg
      310                      315

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<210> 62

<211> 316

<212> PRT

<213> Corynebacterium glutamicum

<400> 62

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Met Thr Leu Ala Thr Ile Pro Ser Pro Pro Gln Gly Val Trp Tyr Leu
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Gly Pro Ile Pro Ile Arg Ala Tyr Ala Met Cys Ile Ile Ala Gly Ile
          20           25           30

Ile Val Ala Ile Trp Leu Thr Arg Lys Arg Tyr Ala Ala Arg Gly Gly
          35           40           45

Asn Pro Glu Ile Val Leu Asp Ala Ala Ile Val Ala Val Pro Ala Gly
          50           55           60

Ile Ile Gly Gly Arg Ile Tyr His Val Ile Thr Asp Asn Gln Lys Tyr
          65           70           75           80

Phe Cys Asp Thr Cys Asn Pro Val Asp Ala Phe Lys Ile Thr Asn Gly
          85           90           95

Gly Leu Gly Ile Trp Gly Ala Val Ile Leu Gly Gly Leu Ala Val Ala
          100          105          110

Val Phe Phe Arg Tyr Lys Lys Leu Pro Leu Ala Pro Phe Ala Asp Ala
          115          120          125

Val Ala Pro Ala Val Ile Leu Ala Gln Gly Ile Gly Arg Leu Gly Asn
          130          135          140

Trp Phe Asn Gln Glu Leu Tyr Gly Ala Glu Thr Thr Val Pro Trp Ala
          145          150          155          160

Leu Glu Ile Tyr Tyr Arg Val Asp Glu Asn Gly Lys Phe Ala Pro Val
          165          170          175

Thr Gly Thr Ser Thr Gly Glu Val Met Ala Thr Val His Pro Thr Phe
          180          185          190

Leu Tyr Glu Leu Leu Trp Asn Leu Leu Ile Phe Ala Leu Leu Met Trp
          195          200          205

Ala Asp Lys Arg Phe Lys Leu Glu His Gly Arg Val Phe Ala Leu Tyr
          210          215          220

Val Ala Gly Tyr Thr Leu Gly Arg Phe Trp Ile Glu Gln Met Arg Val
          225          230          235          240

Asp Glu Ala Thr Leu Ile Gly Gly Ile Arg Ile Asn Thr Ile Val Ser
          245          250          255

Ala Val Val Phe Ala Gly Ala Ile Ile Val Phe Phe Leu Leu Lys Lys
          260          265          270

Gly Arg Glu Thr Pro Glu Glu Val Asp Pro Thr Phe Ala Ala Ser Val
          275          280          285

Ala Ala Asp Ala Val Ala Ser Pro Asp Arg Lys Pro Leu Pro Lys Ala
          290          295          300

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Gly Glu Gly Ile Asp Gly Glu Thr Pro Ser Thr Arg
305 310 315

<210> 63
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1183)
<223> RXN00934

<400> 63
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aaatgttcac aaaccggtgg cattacagga ggacaattag gtg cga att gga atg 115
Val Arg Ile Gly Met
1 5

gtc tgc ccg tac tcc ttc gat gag ccg ggc ggt gtt caa gcg cat atc 163
Val Cys Pro Tyr Ser Phe Asp Glu Pro Gly Gly Val Gln Ala His Ile
10 15 20

ctt gac tta gcg cga acc ttc att gcc caa ggc cat gag gtt cag gtg 211
Leu Asp Leu Ala Arg Thr Phe Ile Ala Gln Gly His Glu Val Gln Val
25 30 35

ctt ggt ccg tgt agt gcg gat acg cag gtg ccc gat ttc gtg gtg cgc 259
Leu Gly Pro Cys Ser Ala Asp Thr Gln Val Pro Asp Phe Val Val Arg
40 45 50

ggt ggt ggc agc atc ccg att ccg tac aat ggc tcg gtt gcc cgc ttg 307
Gly Gly Gly Ser Ile Pro Ile Pro Tyr Asn Gly Ser Val Ala Arg Leu
55 60 65

agc ttt ggg ccg aaa atg ttc aag gcc gtg cgc acg ttc ctc cgc gaa 355
Ser Phe Gly Pro Lys Met Phe Lys Ala Val Arg Thr Phe Leu Arg Glu
70 75 80 85

ggc aac ttc gat gtg ctg cat atc cat gaa ccg aat tca cca agt ttt 403
Gly Asn Phe Asp Val Leu His Ile His Glu Pro Asn Ser Pro Ser Phe
90 95 100

tcc atg gcg gcg cta cgc ttt gcg gaa ggc ccc atc gtt gct act tac 451
Ser Met Ala Ala Leu Arg Phe Ala Glu Gly Pro Ile Val Ala Thr Tyr
105 110 115

cac gcc tcc agt agc gga tcg aag ctg ctc aag gct ttc tta cca gtg 499
His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys Ala Phe Leu Pro Val
120 125 130

ctt tcg ccc atg ctg gag aaa gtg cgc gca ggc atc gcc gtg tct gaa 547
Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly Ile Ala Val Ser Glu
135 140 145

atg gct cgg cgc tgg cag gtg gag caa gtc ggc ggc gat ccc gtg ctg 595
Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly Gly Asp Pro Val Leu
150 155 160 165

114-131CP-1206-DNA-Corynebacterium glutamicum

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atc ccc aac ggg gta gag acc tcc atg ttc aaa gcc gcg cgc caa atc 643
Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys Ala Ala Arg Gln Ile
170 175 180

gaa ccg aat gat cct gta gag atc gtc ttt ttg ggt cgc ctc gat gag 691
Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu Gly Arg Leu Asp Glu
185 190 195

tcc cgc aaa ggc ctc gac atc ctc ctg cgc gct ctg acc agg ctg gat 739
Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala Leu Thr Arg Leu Asp
200 205 210

cgc ccg ttt acc tgc acc gtc att ggc ggc ggc acc ccg cga gaa gtc 787
Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly Thr Pro Arg Glu Val
215 220 225

gcc gcc atc aac ttt gtg ggc cgc gtc agc gat gag gaa aag gca gca 835
Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp Glu Glu Lys Ala Ala
230 235 240 245

atc tta ggt cgc gca gac atc tat gtc gca ccc aac acc ggc ggc gaa 883
Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro Asn Thr Gly Gly Glu
250 255 260

agc ttc ggc atc gtg cta gtt gaa gcg atg gcc gcg gga tgc gct gtc 931
Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala Ala Gly Cys Ala Val
265 270 275

gtc gcc agc gac cta gaa gcg ttc tcc ctg gtc acc gat tct gaa gcc 979
Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val Thr Asp Ser Glu Ala
280 285 290

gca cag cca gcg ggc gtg cta ttt aaa acc ggc tca gac gcc gac cta 1027
Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly Ser Asp Ala Asp Leu
295 300 305

gcc aaa aaa ctt caa gcg ctt atc gac gac ccc tcc tcc cgt tcc acg 1075
Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro Ser Ser Arg Ser Thr
310 315 320 325

ctt atc gcc gcg ggg cta aag cgc gca aac gcc tac gac tgg tcg aca 1123
Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala Tyr Asp Trp Ser Thr
330 335 340

gta tcc acc cag gtc atg gca gtc tat gaa acc att gcg atc gac aaa 1171
Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr Ile Ala Ile Asp Lys
345 350 355

gtg agg ctt gga tgacccttgt ttacctcctc atc 1206
Val Arg Leu Gly
360

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<210> 64

<211> 361

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

Val Arg Ile Gly Met Val Cys Pro Tyr Ser Phe Asp Glu Pro Gly Gly

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Val	Gln	Ala	His	Ile	Leu	Asp	Leu	Ala	Arg	Thr	Phe	Ile	Ala	Gln	Gly
			20					25					30		
His	Glu	Val	Gln	Val	Leu	Gly	Pro	Cys	Ser	Ala	Asp	Thr	Gln	Val	Pro
		35					40					45			
Asp	Phe	Val	Val	Arg	Gly	Gly	Gly	Ser	Ile	Pro	Ile	Pro	Tyr	Asn	Gly
	50					55					60				
Ser	Val	Ala	Arg	Leu	Ser	Phe	Gly	Pro	Lys	Met	Phe	Lys	Ala	Val	Arg
65					70					75					80
Thr	Phe	Leu	Arg	Glu	Gly	Asn	Phe	Asp	Val	Leu	His	Ile	His	Glu	Pro
				85					90					95	
Asn	Ser	Pro	Ser	Phe	Ser	Met	Ala	Ala	Leu	Arg	Phe	Ala	Glu	Gly	Pro
			100					105					110		
Ile	Val	Ala	Thr	Tyr	His	Ala	Ser	Ser	Ser	Gly	Ser	Lys	Leu	Leu	Lys
		115					120					125			
Ala	Phe	Leu	Pro	Val	Leu	Ser	Pro	Met	Leu	Glu	Lys	Val	Arg	Ala	Gly
	130					135					140				
Ile	Ala	Val	Ser	Glu	Met	Ala	Arg	Arg	Trp	Gln	Val	Glu	Gln	Val	Gly
145					150					155					160
Gly	Asp	Pro	Val	Leu	Ile	Pro	Asn	Gly	Val	Glu	Thr	Ser	Met	Phe	Lys
				165					170					175	
Ala	Ala	Arg	Gln	Ile	Glu	Pro	Asn	Asp	Pro	Val	Glu	Ile	Val	Phe	Leu
			180					185					190		
Gly	Arg	Leu	Asp	Glu	Ser	Arg	Lys	Gly	Leu	Asp	Ile	Leu	Leu	Arg	Ala
		195					200					205			
Leu	Thr	Arg	Leu	Asp	Arg	Pro	Phe	Thr	Cys	Thr	Val	Ile	Gly	Gly	Gly
	210					215					220				
Thr	Pro	Arg	Glu	Val	Ala	Gly	Ile	Asn	Phe	Val	Gly	Arg	Val	Ser	Asp
225					230					235					240
Glu	Glu	Lys	Ala	Ala	Ile	Leu	Gly	Arg	Ala	Asp	Ile	Tyr	Val	Ala	Pro
				245					250					255	
Asn	Thr	Gly	Gly	Glu	Ser	Phe	Gly	Ile	Val	Leu	Val	Glu	Ala	Met	Ala
			260					265					270		
Ala	Gly	Cys	Ala	Val	Val	Ala	Ser	Asp	Leu	Glu	Ala	Phe	Ser	Leu	Val
		275					280					285			
Thr	Asp	Ser	Glu	Ala	Ala	Gln	Pro	Ala	Gly	Val	Leu	Phe	Lys	Thr	Gly
	290					295					300				
Ser	Asp	Ala	Asp	Leu	Ala	Lys	Lys	Leu	Gln	Ala	Leu	Ile	Asp	Asp	Pro
305					310					315					320
Ser	Ser	Arg	Ser	Thr	Leu	Ile	Ala	Ala	Gly	Leu	Lys	Arg	Ala	Asn	Ala
				325					330					335	


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145              150              155              160
Gly Gly Glu Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala Ala Gly
              165              170              175
Cys Ala Val Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val Thr Asp
              180              185              190
Ser Glu Ala Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly Ser Asp
              195              200              205
Ala Asp Leu Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro Ser Ser
              210              215              220
Arg Ser Thr Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala Tyr Asp
225              230              235              240
Trp Ser Thr Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr Ile Ala
              245              250              255
Ile Asp Lys Val Arg Leu Gly
              260

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<210> 67
<211> 618
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(595)
<223> RXA02605

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<400> 67
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gagcagaact tcggcggttgc gcgaacaac aactccattg gtg gcc tgt cca tgg 115
                               Val Ala Cys Pro Trp
                               1 5

gcg gga act gcc gcg ctg aac ctc gca gca aag cac cca gat cag ttc 163
Ala Gly Thr Ala Ala Leu Asn Leu Ala Ala Lys His Pro Asp Gln Phe
              10              15              20

cgc cag gct atg tct tgg tcc ggc tac ttg aac acc act gcg cca ggc 211
Arg Gln Ala Met Ser Trp Ser Gly Tyr Leu Asn Thr Thr Ala Pro Gly
              25              30              35

atg caa acc ctg ctg cgt gtg gcc atg ctg gac acc ggt gga ttc aac 259
Met Gln Thr Leu Leu Arg Val Ala Met Leu Asp Thr Gly Gly Phe Asn
              40              45              50

gtc aac gca atg tat ggc tca atc att aac cca cgt cgt ttt gaa aac 307
Val Asn Ala Met Tyr Gly Ser Ile Ile Asn Pro Arg Arg Phe Glu Asn
              55              60              65

gac cca ttc tgg aac atg ggc ggc ttg gct aac acc gac gtc tac atc 355
Asp Pro Phe Trp Asn Met Gly Gly Leu Ala Asn Thr Asp Val Tyr Ile
              70              75              80              85

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tct gca gct tcc ggc ctg tgg agc cct cag gat gat gga gtt cgc gta 403
 Ser Ala Ala Ser Gly Leu Trp Ser Pro Gln Asp Asp Gly Val Arg Val
 90 95 100

gac cac cgc ctc act ggt tct gtg ctt gaa ttc gtg gca atg aca tcc 451
 Asp His Arg Leu Thr Gly Ser Val Leu Glu Phe Val Ala Met Thr Ser
 105 110 115

acc agg att tgg gaa gca aag gca agg ctt cag ggt ctg aac cca act 499
 Thr Arg Ile Trp Glu Ala Lys Ala Arg Leu Gln Gly Leu Asn Pro Thr
 120 125 130

gcg gat tac cca atg tat ggc att cac ggc tgg gct cag ttc aac tcc 547
 Ala Asp Tyr Pro Met Tyr Gly Ile His Gly Trp Ala Gln Phe Asn Ser
 135 140 145

cag ctg gag aga act cag ggt cgt gtt cta gac gtc atg aac gcc tgg 595
 Gln Leu Glu Arg Thr Gln Gly Arg Val Leu Asp Val Met Asn Ala Trp
 150 155 160 165

tagagccaca ccaaaggcca cac 618

<210> 68
 <211> 165
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 68
 Val Ala Cys Pro Trp Ala Gly Thr Ala Ala Leu Asn Leu Ala Ala Lys
 1 5 10 15

His Pro Asp Gln Phe Arg Gln Ala Met Ser Trp Ser Gly Tyr Leu Asn
 20 25 30

Thr Thr Ala Pro Gly Met Gln Thr Leu Leu Arg Val Ala Met Leu Asp
 35 40 45

Thr Gly Gly Phe Asn Val Asn Ala Met Tyr Gly Ser Ile Ile Asn Pro
 50 55 60

Arg Arg Phe Glu Asn Asp Pro Phe Trp Asn Met Gly Gly Leu Ala Asn
 65 70 75 80

Thr Asp Val Tyr Ile Ser Ala Ala Ser Gly Leu Trp Ser Pro Gln Asp
 85 90 95

Asp Gly Val Arg Val Asp His Arg Leu Thr Gly Ser Val Leu Glu Phe
 100 105 110

Val Ala Met Thr Ser Thr Arg Ile Trp Glu Ala Lys Ala Arg Leu Gln
 115 120 125

Gly Leu Asn Pro Thr Ala Asp Tyr Pro Met Tyr Gly Ile His Gly Trp
 130 135 140

Ala Gln Phe Asn Ser Gln Leu Glu Arg Thr Gln Gly Arg Val Leu Asp
 145 150 155 160

Val Met Asn Ala Trp
 165

gcg gtc atc gcc cca gac acc ttt aat acg ctt ttc gac gca aac ccc 643
Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu Phe Asp Ala Asn Pro

	170		175		180	
aac ctc gct ctg ggg tcc gaa gta gct ttt gaa ctc aac ggt caa gag						691
Asn Leu Ala Leu Gly Ser Glu Val Ala Phe Glu Leu Asn Gly Gln Glu						
	185		190		195	
aca ttt ttg cgg gtt atc ggt gtg tat aaa gaa gcc gca gca ggt gga						739
Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu Ala Ala Ala Gly Gly						
	200		205		210	
ctt gtg gga agc aat cca acc gtc cac acc tac acc cca tat acg gtg						787
Leu Val Gly Ser Asn Pro Thr Val His Thr Tyr Thr Pro Tyr Thr Val						
	215		220		225	
gcc aat gac atc acc cac acg gaa gat gga ttg aac acg tta agt atc						835
Ala Asn Asp Ile Thr His Thr Glu Asp Gly Leu Asn Thr Leu Ser Ile						
	230		235		240	245
cgt gca gct cag ggc gta gac cag gat tca ctt aag ggt tca ctg caa						883
Arg Ala Ala Gln Gly Val Asp Gln Asp Ser Leu Lys Gly Ser Leu Gln						
	250		255		260	
acc tac ttc gac gcg ctg tac gcc aac aat gac tcg cac cac gtt gcc						931
Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn Asp Ser His His Val Ala						
	265		270		275	
atg ttg gac ttc cgt aaa cag atc gaa gag ttc aac acc att ctc ggc						979
Met Leu Asp Phe Arg Lys Gln Ile Glu Glu Phe Asn Thr Ile Leu Gly						
	280		285		290	
gca atg agt ttg ggt atc tca gcc atc ggc gga att tcc ttg ctt gtc						1027
Ala Met Ser Leu Gly Ile Ser Ala Ile Gly Gly Ile Ser Leu Leu Val						
	295		300		305	
ggt ggc atc gga gtg atg aac att atg ttg gtg tct gtc acc gag cga						1075
Gly Gly Ile Gly Val Met Asn Ile Met Leu Val Ser Val Thr Glu Arg						
	310		315		320	325
acc cgc gaa atc ggt gtc cga aaa gcc ctc ggc gct cgt cga cgt gac						1123
Thr Arg Glu Ile Gly Val Arg Lys Ala Leu Gly Ala Arg Arg Arg Asp						
	330		335		340	
att cgc ctg caa ttc gtc gtt gaa gcc atg atc att tgt ttc atc ggt						1171
Ile Arg Leu Gln Phe Val Val Glu Ala Met Ile Ile Cys Phe Ile Gly						
	345		350		355	
ggc atc ctc ggc gtg ctt ttg ggc ggc att ttg gga ttg atc atg tcc						1219
Gly Ile Leu Gly Val Leu Leu Gly Gly Ile Leu Gly Leu Ile Met Ser						
	360		365		370	
agc gct att ggc tac att tcc ttg cca cca ctg agt gga atc gtg atc						1267
Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro Leu Ser Gly Ile Val Ile						
	375		380		385	
gcc ttg gta ttt tcc atg gct atc ggc ctg ttt ttc ggc tac tac ccc						1315
Ala Leu Val Phe Ser Met Ala Ile Gly Leu Phe Phe Gly Tyr Tyr Pro						
	390		395		400	405
gcc aac aag gca gca aag ctc gat cca att gac gcc ttg cgt tat gag						1363
Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile Asp Ala Leu Arg Tyr Glu						
	410		415		420	

BGI-131CP

taaaagcctc gtttttaagg tag

1386

<210> 70

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 70

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Met Ser Leu Ala Glu Ser Ile Leu Leu Ala Leu Thr Ser Leu Arg Ser
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Asn Lys Met Arg Ala Leu Leu Thr Leu Leu Gly Val Ile Ile Gly Ile
      20             25             30

Ala Ser Val Ile Gly Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln
      35             40             45

Thr Leu Asn Ser Leu Glu Ser Leu Gly Ala Asn Asp Leu Ser Ala Gln
      50             55             60

Val Glu Glu Arg Pro Asp Glu Asp Ser Pro Glu Pro Asp Met Phe Ala
      65             70             75             80

Phe Ser Gly Ala Ala Asn Ser Ser Gly Asn Leu Ile Pro Glu Glu Thr
      85             90             95

Val Asp Thr Leu Arg Asp Arg Phe Ala Gly Ser Ile Thr Gly Ile Ser
      100            105            110

Val Gly Gly Met Gly Thr Gln Gly Thr Leu Ile Gly Asp Thr Ala Asp
      115            120            125

Leu Lys Ser Asp Leu Leu Gly Val Asn Glu Asp Tyr Met Trp Met Asn
      130            135            140

Gly Val Glu Met Asn Tyr Gly Arg Ala Ile Thr Gln Asp Asp Val Ala
      145            150            155            160

Ala Gln Arg Pro Val Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu
      165            170            175

Phe Asp Ala Asn Pro Asn Leu Ala Leu Gly Ser Glu Val Ala Phe Glu
      180            185            190

Leu Asn Gly Gln Glu Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu
      195            200            205

Ala Ala Ala Gly Gly Leu Val Gly Ser Asn Pro Thr Val His Thr Tyr
      210            215            220

Thr Pro Tyr Thr Val Ala Asn Asp Ile Thr His Thr Glu Asp Gly Leu
      225            230            235            240

Asn Thr Leu Ser Ile Arg Ala Ala Gln Gly Val Asp Gln Asp Ser Leu
      245            250            255

Lys Gly Ser Leu Gln Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn Asp
      260            265            270

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Val Glu Glu Arg Pro Asp Glu Asp Ser Pro Glu Pro Asp Met Phe Ala
 65 70 75 80
 Phe Ser Gly Ala Ala Asn Ser Ser Gly Asn Leu Ile Pro Glu Glu Thr
 85 90 95
 Val Asp Thr Leu Arg Asp Arg Phe Ala Gly Ser Ile Thr Gly Ile Ser
 100 105 110
 Val Gly Gly Met Gly Thr Gln Gly Thr Leu Ile Gly Asp Thr Ala Asp
 115 120 125
 Leu Lys Ser Asp Leu Leu Gly Val Asn Glu Asp Tyr Met Trp Met Asn
 130 135 140
 Gly Val Glu Met Asn Tyr Gly Arg Ala Ile Thr Gln Asp Asp Val Ala
 145 150 155 160
 Ala Gln Arg Pro Val Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu
 165 170 175
 Phe Asp Ala Asn Pro Asn Leu Ala Leu Gly Ser Glu Val Ala Phe Glu
 180 185 190
 Leu Asn Gly Gln Glu Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu
 195 200 205
 Ala Ala Ala Gly Gly Leu Val Gly Ser Asn Pro Thr
 210 215 220

<210> 73

<211> 617

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(594)

<223> FRXA00556

<400> 73

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 Tyr Thr Pro Tyr Thr Val Ala Asn Asp Ile Thr His Thr Lys Asp Gly
 1 5 10 15

ttg aac acg tta agt atc cgt gca gct cag ggc gta gac cag gat tca 96
 Leu Asn Thr Leu Ser Ile Arg Ala Ala Gln Gly Val Asp Gln Asp Ser
 20 25 30

ctt aag ggt tca ctg caa acc tac ttc gac gcg ctg tac gcc aac aat 144
 Leu Lys Gly Ser Leu Gln Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn
 35 40 45

gac tcg cac cac gtt gcc atg ttg gac ttc cgt aaa cag atc gaa gag 192
 Asp Ser His His Val Ala Met Leu Asp Phe Arg Lys Gln Ile Glu Glu
 50 55 60

ttc aac acc att ctc ggc gca atg agt ttg ggt atc tca gcc atc ggc 240
 Phe Asn Thr Ile Leu Gly Ala Met Ser Leu Gly Ile Ser Ala Ile Gly

BGI-I31CP : 7266960

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65              70              75              80
gga att tcc ttg ctt gtc ggt ggc atc gga gtg atg aac att atg ttg 288
Gly Ile Ser Leu Leu Val Gly Gly Ile Gly Val Met Asn Ile Met Leu
                        85                      90                      95

gtg tct gtc acc gag cga acc cgc gaa atc ggt gtc cga aaa gcc ctc 336
Val Ser Val Thr Glu Arg Thr Arg Glu Ile Gly Val Arg Lys Ala Leu
                        100                      105                      110

ggc gct cgt cga cgt gac att cgc ctg caa ttc gtc gtt gaa gcc atg 384
Gly Ala Arg Arg Arg Asp Ile Arg Leu Gln Phe Val Val Glu Ala Met
                        115                      120                      125

atc att tgt ttc atc ggt ggc atc ctc ggc gtg ctt ttg ggc ggc att 432
Ile Ile Cys Phe Ile Gly Gly Ile Leu Gly Val Leu Leu Gly Gly Ile
                        130                      135                      140

ttg gga ttg atc atg tcc agc gct att ggc tac att tcc ttg cca cca 480
Leu Gly Leu Ile Met Ser Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro
145                      150                      155                      160

ctg agt gga atc gtg atc gcc ttg gta ttt tcc atg gct atc ggc ctg 528
Leu Ser Gly Ile Val Ile Ala Leu Val Phe Ser Met Ala Ile Gly Leu
                        165                      170                      175

ttt ttc ggc tac tac ccc gcc aac aag gca gca aag ctc gat cca att 576
Phe Phe Gly Tyr Tyr Pro Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile
                        180                      185                      190

gac gcc ttg cgt tat gag taaaagcctc gtttttaagg tag 617
Asp Ala Leu Arg Tyr Glu
                        195

<210> 74
<211> 198
<212> PRT
<213> Corynebacterium glutamicum

<400> 74
Tyr Thr Pro Tyr Thr Val Ala Asn Asp Ile Thr His Thr Lys Asp Gly
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Leu Asn Thr Leu Ser Ile Arg Ala Ala Gln Gly Val Asp Gln Asp Ser
      20              25              30

Leu Lys Gly Ser Leu Gln Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn
      35              40              45

Asp Ser His His Val Ala Met Leu Asp Phe Arg Lys Gln Ile Glu Glu
      50              55              60

Phe Asn Thr Ile Leu Gly Ala Met Ser Leu Gly Ile Ser Ala Ile Gly
      65              70              75              80

Gly Ile Ser Leu Leu Val Gly Gly Ile Gly Val Met Asn Ile Met Leu
      85              90              95

Val Ser Val Thr Glu Arg Thr Arg Glu Ile Gly Val Arg Lys Ala Leu
      100              105              110

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Gly Ala Arg Arg Arg Asp Ile Arg Leu Gln Phe Val Val Glu Ala Met
 115 120 125

Ile Ile Cys Phe Ile Gly Gly Ile Leu Gly Val Leu Leu Gly Gly Ile
 130 135 140

Leu Gly Leu Ile Met Ser Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro
 145 150 155 160

Leu Ser Gly Ile Val Ile Ala Leu Val Phe Ser Met Ala Ile Gly Leu
 165 170 175

Phe Phe Gly Tyr Tyr Pro Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile
 180 185 190

Asp Ala Leu Arg Tyr Glu
 195

<210> 75
 <211> 939
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(916)
 <223> RXA02750

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tctgacacgc agacacttgc gctgcttttt ccgcgaccgc atg gca gtg ctg ttt 115
 Met Ala Val Leu Phe
 1 5

tcc atc atg ggt gcg ctc atc ctt ttg gtc ctg tac gtg ctg ttt tta 163
 Ser Ile Met Gly Ala Leu Ile Leu Leu Val Leu Tyr Val Leu Phe Leu
 10 15 20

gga aaa ctg caa att gac ggt ctc atg gtg gat cta cct gac tca gcc 211
 Gly Lys Leu Gln Ile Asp Gly Leu Met Val Asp Leu Pro Asp Ser Ala
 25 30 35

cga gac gat gtt gaa gga ttc gtc ttc aat tgg gtg ttt tcc gga att 259
 Arg Asp Asp Val Glu Gly Phe Val Phe Asn Trp Val Phe Ser Gly Ile
 40 45 50

ctc atc acg tcc gca atc act gtt ccg caa gca gca ctt gga gtg ctg 307
 Leu Ile Thr Ser Ala Ile Thr Val Pro Gln Ala Ala Leu Gly Val Leu
 55 60 65

gtt gaa gat cgc acc cgc gga ggc atc aaa gat ttc ctc gtg gca ccc 355
 Val Glu Asp Arg Thr Arg Gly Gly Ile Lys Asp Phe Leu Val Ala Pro
 70 75 80 85

gta tcc aga acg acg ctg acg gtg tcc tat atc ttc gca gca gtc att 403
 Val Ser Arg Thr Thr Leu Thr Val Ser Tyr Ile Phe Ala Ala Val Ile
 90 95 100

sequence: 400-900

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gtc gcc atg acg att ttg atc ttt gaa atc gtg gtg gga agt att ggt 451
Val Ala Met Thr Ile Leu Ile Phe Glu Ile Val Val Gly Ser Ile Gly
      105                      110                      115

tta gct att ttg ggg cac ttc agc atg agc att gct cgc gtg ctc gaa 499
Leu Ala Ile Leu Gly His Phe Ser Met Ser Ile Ala Arg Val Leu Glu
      120                      125                      130

ttg gta gtc gcc ttg ctt ctg ctc acc ctg gtg ttt tcc gca att gca 547
Leu Val Val Ala Leu Leu Leu Leu Thr Leu Val Phe Ser Ala Ile Ala
      135                      140                      145

gca ttt ctg atc acc ttg gtg aaa tct caa ggc gga atg tct gcg ctt 595
Ala Phe Leu Ile Thr Leu Val Lys Ser Gln Gly Gly Met Ser Ala Leu
      150                      155                      160                      165

tca agc ctg gta ggc acc ctg gcg ggc ttt tta tct gct gct tat att 643
Ser Ser Leu Val Gly Thr Leu Ala Gly Phe Leu Ser Ala Ala Tyr Ile
      170                      175                      180

cca ccc atc gca ttg cct gaa gca gtg aca aac gtg ttg aac ttc ctc 691
Pro Pro Ile Ala Leu Pro Glu Ala Val Thr Asn Val Leu Asn Phe Leu
      185                      190                      195

ccg ttt acc cca gct gga atg ttg atc aga caa att gtg gtt gcc cca 739
Pro Phe Thr Pro Ala Gly Met Leu Ile Arg Gln Ile Val Val Ala Pro
      200                      205                      210

gca ttg gac gcg att tca ctt cca ccc gaa gcc ttc gat atc ttc caa 787
Ala Leu Asp Ala Ile Ser Leu Pro Pro Glu Ala Phe Asp Ile Phe Gln
      215                      220                      225

ttc gga tac gga ctc aaa ctg gaa atg ttt ggg gaa ccc gtt tct aca 835
Phe Gly Tyr Gly Leu Lys Leu Glu Met Phe Gly Glu Pro Val Ser Thr
      230                      235                      240                      245

tgg gtg gca gta gga att gtt gcc tca tgg gga gtg gtg ttt gga ctc 883
Trp Val Ala Val Gly Ile Val Ala Ser Trp Gly Val Val Phe Gly Leu
      250                      255                      260

att gcc gcg ttc aaa atg aaa agc gtg gtg cga taaatcctgc taaagaatgc 936
Ile Ala Ala Phe Lys Met Lys Ser Val Val Arg
      265                      270

ttc 939

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<210> 76

<211> 272

<212> PRT

<213> Corynebacterium glutamicum

<400> 76

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Met Ala Val Leu Phe Ser Ile Met Gly Ala Leu Ile Leu Leu Val Leu
  1              5              10              15

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Tyr Val Leu Phe Leu Gly Lys Leu Gln Ile Asp Gly Leu Met Val Asp
      20              25              30

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Leu Pro Asp Ser Ala Arg Asp Asp Val Glu Gly Phe Val Phe Asn Trp
      35              40              45

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Val Phe Ser Gly Ile Leu Ile Thr Ser Ala Ile Thr Val Pro Gln Ala
 50 55 60
 Ala Leu Gly Val Leu Val Glu Asp Arg Thr Arg Gly Gly Ile Lys Asp
 65 70 75 80
 Phe Leu Val Ala Pro Val Ser Arg Thr Thr Leu Thr Val Ser Tyr Ile
 85 90 95
 Phe Ala Ala Val Ile Val Ala Met Thr Ile Leu Ile Phe Glu Ile Val
 100 105 110
 Val Gly Ser Ile Gly Leu Ala Ile Leu Gly His Phe Ser Met Ser Ile
 115 120 125
 Ala Arg Val Leu Glu Leu Val Val Ala Leu Leu Leu Leu Thr Leu Val
 130 135 140
 Phe Ser Ala Ile Ala Ala Phe Leu Ile Thr Leu Val Lys Ser Gln Gly
 145 150 155 160
 Gly Met Ser Ala Leu Ser Ser Leu Val Gly Thr Leu Ala Gly Phe Leu
 165 170 175
 Ser Ala Ala Tyr Ile Pro Pro Ile Ala Leu Pro Glu Ala Val Thr Asn
 180 185 190
 Val Leu Asn Phe Leu Pro Phe Thr Pro Ala Gly Met Leu Ile Arg Gln
 195 200 205
 Ile Val Val Ala Pro Ala Leu Asp Ala Ile Ser Leu Pro Pro Glu Ala
 210 215 220
 Phe Asp Ile Phe Gln Phe Gly Tyr Gly Leu Lys Leu Glu Met Phe Gly
 225 230 235 240
 Glu Pro Val Ser Thr Trp Val Ala Val Gly Ile Val Ala Ser Trp Gly
 245 250 255
 Val Val Phe Gly Leu Ile Ala Ala Phe Lys Met Lys Ser Val Val Arg
 260 265 270

<210> 77

<211> 1815

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1792)

<223> RXN02096

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ccgttcttgt actcctctct cataccgcga gaacatctcg atg ggt ttg gat gtc 115

Met Gly Leu Asp Val
1 5

agt gat gag cag atc gaa cac gca gcc agg ctt gcc cag gct cat gat 163
Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu Ala Gln Ala His Asp
10 15 20

ttt atc gat cgc ctt cca aac aaa tac gag gaa gtc att gcc gaa cgc 211
Phe Ile Asp Arg Leu Pro Asn Lys Tyr Glu Glu Val Ile Gly Glu Arg
25 30 35

ggc ctg acg ctt tct ggt ggt caa cgc caa cgc atc gcc ctc gca cgg 259
Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Leu Ala Arg
40 45 50

gct ttc ctg gcg cat ccc aaa gtg ttg gtg ctt gat gat gcc acc tct 307
Ala Phe Leu Ala His Pro Lys Val Leu Val Leu Asp Asp Ala Thr Ser
55 60 65

gcc att gat gcc tcc act gag gac cgc att ttc cag gcc ttg cgc gaa 355
Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe Gln Ala Leu Arg Glu
70 75 80 85

gaa ctg cac gat gtc acc att ttg atc atc gcg cac cgc cac tcc act 403
Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala His Arg His Ser Thr
90 95 100

ttg gag ctc gcc gat cgg gtt ggt ctg gtc gaa gat gga cgg gta aca 451
Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu Asp Gly Arg Val Thr
105 110 115

gca ctg gga ccg ttg agt gag atg cgt gat cac gct cgt ttc tcg cat 499
Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His Ala Arg Phe Ser His
120 125 130

ctg atg gct ctt gat ttc cag gat tct cac gat ccg gaa ttc acc ctc 547
Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp Pro Glu Phe Thr Leu
135 140 145

gac aac ggt tca cta ccc agc caa gag caa ttg tgg ccg gag gtc tcc 595
Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu Trp Pro Glu Val Ser
150 155 160 165

aca gaa aag cag tac aag att ctt gcg cct gcc cct ggt cga gcc cgt 643
Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala Pro Gly Arg Gly Arg
170 175 180

ggc atg tcc atg cca gca acc cct gag ctg ctc gcc cag att gag gcg 691
Gly Met Ser Met Pro Ala Thr Pro Glu Leu Leu Ala Gln Ile Glu Ala
185 190 195

ctg cca gca gca acg gaa gaa aca cga gtt gat gcc ggg agg cta cgc 739
Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp Ala Gly Arg Leu Arg
200 205 210

acc agt acc tcc ggt ttc aaa ttg ctc agt tta ttc aag cag gtc cgt 787
Thr Ser Thr Ser Gly Phe Lys Leu Leu Ser Leu Phe Lys Gln Val Arg
215 220 225

tggt ctc gtc gtc gcg gtc atc gcg ttg ttg ctg gtg gcc gta gcc gcc 835
Trp Leu Val Val Ala Val Ile Ala Leu Leu Leu Val Gly Val Ala Ala

230	235	240	245	
gat cta gca ttt cca aca ctg atg cgc gca gcc atc gac aac ggt gtg				883
Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala Ile Asp Asn Gly Val	250	255	260	
caa gca caa agc acc tcc acg ttg tgg tgg atc gcc atc gca ggc agc				931
Gln Ala Gln Ser Thr Ser Thr Leu Trp Trp Ile Ala Ile Ala Gly Ser	265	270	275	
gta gta gtc ctt ctg tcc tgg gcc gcc gcc gcg atc aac acg att atc				979
Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala Ile Asn Thr Ile Ile	280	285	290	
acg gca cgc acc ggt gaa cgg ctg ctt tac ggc ttg cgt ctg cgc tca				1027
Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly Leu Arg Leu Arg Ser	295	300	305	
ttt gtg cat cta ttg cgc ctg tcc atg agc tat ttc gaa cgc acc atg				1075
Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr Phe Glu Arg Thr Met	310	315	320	325
tcc ggc cgc atc atg acg cgc atg acc acc gac atc gac aac ctc tcg				1123
Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp Ile Asp Asn Leu Ser	330	335	340	
tcc ttc ctc caa tca ggt ctg gcg caa aca gtt gtc tct gtg ggc acg				1171
Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val Val Ser Val Gly Thr	345	350	355	
ctc atc ggt gtg gtc acc atg ctc gcc atc acc gac gca caa cta gca				1219
Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr Asp Ala Gln Leu Ala	360	365	370	
ctc gtt gcg ctg tcc gtg gtg ccg atc atc atc gtg ctc act ctc att				1267
Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile Val Leu Thr Leu Ile	375	380	385	
ttc cga cgc atc agc tcc agg ctg tac acc gct tca cgc gag caa gcc				1315
Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala Ser Arg Glu Gln Ala	390	395	400	405
agc cag gtc aac gcg gta ttc cac gag tcc atc gcc ggt tta cgc acc				1363
Ser Gln Val Asn Ala Val Phe His Glu Ser Ile Ala Gly Leu Arg Thr	410	415	420	
gcg cag atg cac cgc atg gaa gac caa gtc ttt gac aat tat gcg ggc				1411
Ala Gln Met His Arg Met Glu Asp Gln Val Phe Asp Asn Tyr Ala Gly	425	430	435	
gaa gca gag gaa ttc cga cgc ctg cgt gtg aaa tcc cag acg gcc atc				1459
Glu Ala Glu Glu Phe Arg Arg Leu Arg Val Lys Ser Gln Thr Ala Ile	440	445	450	
gcc atc tac ttc ccc ggc ctt ggc gcg ctc tct gaa atc gcc cag gca				1507
Ala Ile Tyr Phe Pro Gly Leu Gly Ala Leu Ser Glu Ile Ala Gln Ala	455	460	465	
ctc gtc ctc ggt ttc ggc gca ctg caa gta acg cgc ggc gac atc tcc				1555
Leu Val Leu Gly Phe Gly Ala Leu Gln Val Thr Arg Gly Asp Ile Ser	470	475	480	485

acc ggc gta ctc gtg gca ttc gtg ctg tac atg ggc ctg atg ttc ggc 1603
 Thr Gly Val Leu Val Ala Phe Val Leu Tyr Met Gly Leu Met Phe Gly
 490 495 500

ccc atc caa caa cta agc caa atc ttc gac tcc tac caa caa gcc gcc 1651
 Pro Ile Gln Gln Leu Ser Gln Ile Phe Asp Ser Tyr Gln Gln Ala Ala
 505 510 515

gtc ggc ttc cgt cgc atc acc gaa ctg ctc gca acg cag ccc agc gtc 1699
 Val Gly Phe Arg Arg Ile Thr Glu Leu Leu Ala Thr Gln Pro Ser Val
 520 525 530

cag atc tgg gca cca aca ggc acg cta ggc agg ctg cca cgc agc ctt 1747
 Gln Ile Trp Ala Pro Thr Gly Thr Leu Gly Arg Leu Pro Arg Ser Leu
 535 540 545

tat tgc ttg acg acg tca cct tcg gct att cag acg atc cga tcc 1792
 Tyr Cys Leu Thr Thr Ser Pro Ser Ala Ile Gln Thr Ile Arg Ser
 550 555 560

tagacaacgt caccgtccag atc 1815

<210> 78
 <211> 564
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 78
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 Ala Gln Ala His Asp Phe Ile Asp Arg Leu Pro Asn Lys Tyr Glu Glu
 20 25 30
 Val Ile Gly Glu Arg Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg
 35 40 45
 Ile Ala Leu Ala Arg Ala Phe Leu Ala His Pro Lys Val Leu Val Leu
 50 55 60
 Asp Asp Ala Thr Ser Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe
 65 70 75 80
 Gln Ala Leu Arg Glu Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala
 85 90 95
 His Arg His Ser Thr Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu
 100 105 110
 Asp Gly Arg Val Thr Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His
 115 120 125
 Ala Arg Phe Ser His Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp
 130 135 140
 Pro Glu Phe Thr Leu Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu
 145 150 155 160
 Trp Pro Glu Val Ser Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala

165										170					175				
Pro	Gly	Arg	Gly	Arg	Gly	Met	Ser	Met	Pro	Ala	Thr	Pro	Glu	Leu	Leu				
			180					185					190						
Ala	Gln	Ile	Glu	Ala	Leu	Pro	Ala	Ala	Thr	Glu	Glu	Thr	Arg	Val	Asp				
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Ala	Gly	Arg	Leu	Arg	Thr	Ser	Thr	Ser	Gly	Phe	Lys	Leu	Leu	Ser	Leu				
	210					215					220								
Phe	Lys	Gln	Val	Arg	Trp	Leu	Val	Val	Ala	Val	Ile	Ala	Leu	Leu	Leu				
225					230					235					240				
Val	Gly	Val	Ala	Ala	Asp	Leu	Ala	Phe	Pro	Thr	Leu	Met	Arg	Ala	Ala				
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Ile	Asp	Asn	Gly	Val	Gln	Ala	Gln	Ser	Thr	Ser	Thr	Leu	Trp	Trp	Ile				
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Ala	Ile	Ala	Gly	Ser	Val	Val	Val	Leu	Leu	Ser	Trp	Ala	Ala	Ala	Ala				
		275					280					285							
Ile	Asn	Thr	Ile	Ile	Thr	Ala	Arg	Thr	Gly	Glu	Arg	Leu	Leu	Tyr	Gly				
	290					295					300								
Leu	Arg	Leu	Arg	Ser	Phe	Val	His	Leu	Leu	Arg	Leu	Ser	Met	Ser	Tyr				
305					310					315					320				
Phe	Glu	Arg	Thr	Met	Ser	Gly	Arg	Ile	Met	Thr	Arg	Met	Thr	Thr	Asp				
				325					330					335					
Ile	Asp	Asn	Leu	Ser	Ser	Phe	Leu	Gln	Ser	Gly	Leu	Ala	Gln	Thr	Val				
			340					345					350						
Val	Ser	Val	Gly	Thr	Leu	Ile	Gly	Val	Val	Thr	Met	Leu	Ala	Ile	Thr				
		355					360					365							
Asp	Ala	Gln	Leu	Ala	Leu	Val	Ala	Leu	Ser	Val	Val	Pro	Ile	Ile	Ile				
	370					375					380								
Val	Leu	Thr	Leu	Ile	Phe	Arg	Arg	Ile	Ser	Ser	Arg	Leu	Tyr	Thr	Ala				
385					390					395					400				
Ser	Arg	Glu	Gln	Ala	Ser	Gln	Val	Asn	Ala	Val	Phe	His	Glu	Ser	Ile				
				405					410				415						
Ala	Gly	Leu	Arg	Thr	Ala	Gln	Met	His	Arg	Met	Glu	Asp	Gln	Val	Phe				
			420					425					430						
Asp	Asn	Tyr	Ala	Gly	Glu	Ala	Glu	Glu	Phe	Arg	Arg	Leu	Arg	Val	Lys				
	435						440					445							
Ser	Gln	Thr	Ala	Ile	Ala	Ile	Tyr	Phe	Pro	Gly	Leu	Gly	Ala	Leu	Ser				
	450					455					460								
Glu	Ile	Ala	Gln	Ala	Leu	Val	Leu	Gly	Phe	Gly	Ala	Leu	Gln	Val	Thr				
465					470					475					480				
Arg	Gly	Asp	Ile	Ser	Thr	Gly	Val	Leu	Val	Ala	Phe	Val	Leu	Tyr	Met				
				485					490					495					

Gly Leu Met Phe Gly Pro Ile Gln Gln Leu Ser Gln Ile Phe Asp Ser
 500 505 510

Tyr Gln Gln Ala Ala Val Gly Phe Arg Arg Ile Thr Glu Leu Leu Ala
 515 520 525

Thr Gln Pro Ser Val Gln Ile Trp Ala Pro Thr Gly Thr Leu Gly Arg
 530 535 540

Leu Pro Arg Ser Leu Tyr Cys Leu Thr Thr Ser Pro Ser Ala Ile Gln
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Thr Ile Arg Ser

<210> 79

<211> 1417

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1417)

<223> FRXA02096

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 Met Gly Leu Asp Val
 1 5

agt gat gag cag atc gaa cac gca gcc agg ctt gcc cag gct cat gat 163
 Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu Ala Gln Ala His Asp
 10 15 20

ttt atc gat cgc ctt cca aac aaa tac gag gaa gtc att ggc gaa cgc 211
 Phe Ile Asp Arg Leu Pro Asn Lys Tyr Glu Glu Val Ile Gly Glu Arg
 25 30 35

ggc ctg acg ctt tct ggt ggt caa cgc caa cgc atc gcc ctc gca cgg 259
 Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Leu Ala Arg
 40 45 50

gct ttc ctg gcg cat ccc aaa gtg ttg gtg ctt gat gat gcc acc tct 307
 Ala Phe Leu Ala His Pro Lys Val Leu Val Leu Asp Asp Ala Thr Ser
 55 60 65

gcc att gat gcc tcc act gag gac cgc att ttc cag gcc ttg cgc gaa 355
 Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe Gln Ala Leu Arg Glu
 70 75 80 85

gaa ctg cac gat gtc acc att ttg atc atc gcg cac cgc cac tcc act 403
 Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala His Arg His Ser Thr
 90 95 100

ttg gag ctc ggc gat cgg gtt ggt ctg gtc gaa gat gga cgg gta aca 451
 Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu Asp Gly Arg Val Thr
 105 110 115

CGCTTCGCAGC
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 CAGCGATATC
 CGCAGGAATC
 TCATCGCGGT
 TTTTGATGAG
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 COGTTCTTGT
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 CATACCGCGA
 GAACATCTCG
 ATG GGT TTG
 GAT GTC
 MET GLY LEU
 ASP VAL
 1 5
 AGT GAT GAG
 CAG ATC GAA
 CAC GCA GCC
 AGG CTT GCC
 CAG GCT CAT
 GAT 163
 SER ASP GLU
 GLN ILE GLU
 HIS ALA ALA
 ARG LEU ALA
 GLN ALA HIS
 ASP 10 15 20
 TTT ATC GAT
 CGC CTT CCA
 AAC AAA TAC
 GAG GAA GTC
 ATT GGC GAA
 CGC 211
 PHE ILE ASP
 ARG LEU PRO
 ASN LYS TYR
 GLU GLU VAL
 ILE GLY GLU
 ARG 25 30 35
 GGC CTG ACG
 CTT TCT GGT
 GGT CAA CGC
 CAA CGC ATC
 GCC CTC GCA
 CGG 259
 GLY LEU THR
 LEU SER GLY
 GLY GLN ARG
 GLN ARG ILE
 ALA LEU ALA
 ARG 40 45 50
 GCT TTC CTG
 GCG CAT CCC
 AAA GTG TTG
 GTG CTT GAT
 GAT GCC ACC
 TCT 307
 ALA PHE LEU
 ALA HIS PRO
 LYS VAL LEU
 VAL LEU ASP
 ASP ALA THR
 SER 55 60 65
 GCC ATT GAT
 GCC TCC ACT
 GAG GAC CGC
 ATT TTC CAG
 GCC TTG CGC
 GAA 355
 ALA ILE ASP
 ALA SER THR
 GLU ASP ARG
 ILE PHE GLN
 ALA LEU ARG
 GLU 70 75 80 85
 GAA CTG CAC
 GAT GTC ACC
 ATT TTG ATC
 ATC GCG CAC
 CGC CAC TCC
 ACT 403
 GLU LEU HIS
 ASP VAL THR
 ILE LEU ILE
 ILE ALA HIS
 ARG HIS SER
 THR 90 95 100
 TTG GAG CTC
 GGC GAT CGG
 GTT GGT CTG
 GTC GAA GAT
 GGA CGG GTA
 ACA 451
 LEU GLU LEU
 GLY ASP ARG
 VAL GLY LEU
 VAL GLU ASP
 GLY ARG VAL
 THR 105 110 115

gca ctg gga ccg ttg agt gag atg cgt gat cac gct cgt ttc tcg cat 499
 Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His Ala Arg Phe Ser His
 120 125 130

ctg atg gct ctt gat ttc cag gat tct cac gat ccg gaa ttc acc ctc 547
 Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp Pro Glu Phe Thr Leu
 135 140 145

gac aac ggt tca cta ccc agc caa gag caa ttg tgg ccg gag gtc tcc 595
 Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu Trp Pro Glu Val Ser
 150 155 160 165

aca gaa aag cag tac aag att ctt gcg cct gcc cct ggt cga ggc cgt 643
 Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala Pro Gly Arg Gly Arg
 170 175 180

ggc atg tcc atg cca gca acc cct gag ctg ctc gcc cag att gag gcg 691
 Gly Met Ser Met Pro Ala Thr Pro Glu Leu Leu Ala Gln Ile Glu Ala
 185 190 195

ctg cca gca gca acg gaa gaa aca cga gtt gat gcc ggg agg cta cgc 739
 Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp Ala Gly Arg Leu Arg
 200 205 210

acc agt acc tcc ggt ttc aaa ttg ctc agt tta ttc aag cag gtc cgt 787
 Thr Ser Thr Ser Gly Phe Lys Leu Leu Ser Leu Phe Lys Gln Val Arg
 215 220 225

tgg ctc gtc gtc gcg gtc atc gcg ttg ttg ctg gtg ggc gta gcc gcc 835
 Trp Leu Val Val Ala Val Ile Ala Leu Leu Leu Val Gly Val Ala Ala
 230 235 240 245

gat cta gca ttt cca aca ctg atg cgc gca gcc atc gac aac ggt gtg 883
 Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala Ile Asp Asn Gly Val
 250 255 260

caa gca caa agc acc tcc acg ttg tgg tgg atc gcc atc gca ggc agc 931
 Gln Ala Gln Ser Thr Ser Thr Leu Trp Trp Ile Ala Ile Ala Gly Ser
 265 270 275

gta gta gtc ctt ctg tcc tgg gcc gcc gcc gcg atc aac acg att atc 979
 Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala Ile Asn Thr Ile Ile
 280 285 290

acg gca cgc acc ggt gaa cgg ctg ctt tac ggc ttg cgt ctg cgc tca 1027
 Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly Leu Arg Leu Arg Ser
 295 300 305

ttt gtg cat cta ttg cgc ctg tcc atg agc tat ttc gaa cgc acc atg 1075
 Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr Phe Glu Arg Thr Met
 310 315 320 325

tcc ggc cgc atc atg acg cgc atg acc acc gac atc gac aac ctc tcg 1123
 Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp Ile Asp Asn Leu Ser
 330 335 340

tcc ttc ctc caa tca ggt ctg gcg caa aca gtt gtc tct gtg ggc acg 1171
 Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val Val Ser Val Gly Thr
 345 350 355


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Trp Pro Glu Val Ser Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala
      165                      170                      175

Pro Gly Arg Gly Arg Gly Met Ser Met Pro Ala Thr Pro Glu Leu Leu
      180                      185                      190

Ala Gln Ile Glu Ala Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp
      195                      200                      205

Ala Gly Arg Leu Arg Thr Ser Thr Ser Gly Phe Lys Leu Leu Ser Leu
      210                      215                      220

Phe Lys Gln Val Arg Trp Leu Val Val Ala Val Ile Ala Leu Leu Leu
      225                      230                      235                      240

Val Gly Val Ala Ala Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala
      245                      250                      255

Ile Asp Asn Gly Val Gln Ala Gln Ser Thr Ser Thr Leu Trp Trp Ile
      260                      265                      270

Ala Ile Ala Gly Ser Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala
      275                      280                      285

Ile Asn Thr Ile Ile Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly
      290                      295                      300

Leu Arg Leu Arg Ser Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr
      305                      310                      315                      320

Phe Glu Arg Thr Met Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp
      325                      330                      335

Ile Asp Asn Leu Ser Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val
      340                      345                      350

Val Ser Val Gly Thr Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr
      355                      360                      365

Asp Ala Gln Leu Ala Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile
      370                      375                      380

Val Leu Thr Leu Ile Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala
      385                      390                      395                      400

Ser Arg Glu Gln Ala Ser Gln Val Asn Ala Val Phe His Glu Ser Ile
      405                      410                      415

Ala Gly Leu Arg Thr Ala Gln Met His Arg Met Glu Asp Gln Val Phe
      420                      425                      430

Asp Asn Tyr Ala Gly Glu Ala
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<210> 81

<211> 843

<212> DNA

<213> Corynebacterium glutamicum

<220>

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 Glu Ala Val Arg Ala Ala Arg Glu Phe Val Ala Asp Pro Arg Gly Thr
 215 220 225
 gcg gcg ttt ctg act gcg gag gag gat cac caa tgatgccgta tatcacccgat 840
 Ala Ala Phe Leu Thr Ala Glu Glu Asp His Gln
 230 235 240
 att 843

<210> 82
 <211> 240
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 <213> Corynebacterium glutamicum

<400> 82
 Met Phe Leu Thr Lys Val Ser Leu Leu Asp His Pro Glu Ser Leu Pro
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 20 25 30
 Leu Glu Phe Arg Ala Pro Ile Thr Val Ile Thr Gly Glu Asn Gly Val
 35 40 45
 Gly Lys Ser Thr Leu Val Glu Ala Leu Ala Val Gly Met Arg Leu Asn
 50 55 60
 Pro Ser Gly Gly Ser Arg His Ala Asn Phe Gly Arg Glu Gly Asp Ile
 65 70 75 80
 Val Ser Ser Leu His Gln Ser Leu Lys Leu Val Arg Arg Glu Asn Pro
 85 90 95
 Arg Asp Ala Phe Phe Phe Arg Gly Glu Thr Met Tyr Asn Val Ala Ser
 100 105 110
 Tyr Tyr Glu Glu Leu Met Gly Glu Lys Asn Met His Asp Leu His Lys
 115 120 125
 Met Ser His Gly Glu Ser Val Phe Ala Val Ile Asp Arg Arg Phe Asn
 130 135 140
 Asn Gln Gly Phe Phe Val Leu Asp Glu Pro Glu Ala Gly Leu Ser Met
 145 150 155 160
 Leu Arg Gln Leu Glu Leu Leu Gly Lys Leu Gly Asn Leu Ala Arg Gly
 165 170 175
 Gly Ala Gln Ile Ile Met Ala Thr His Ser Pro Ile Leu Leu Ala Ile
 180 185 190
 Pro Gly Ala Glu Ile Leu Glu Ile Thr Ser Ser Gly Val Ala Lys Val
 195 200 205
 Asn Phe Glu Asp Ala Glu Ala Val Arg Ala Ala Arg Glu Phe Val Ala
 210 215 220

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ccc gag ctc ctc atc gtt gac gag ccc acc gca ggc ttg gat ccc atc 595

[illegible]

<213> *Corynebacterium glutamicum*

Leu Gly Gln Asp Pro Val Ala His Pro Asp Val Leu Arg Arg Val Gly

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65              70              75              80
Tyr Val Pro Gly Asp Ala Thr Leu Trp Asp Asn Leu Thr Gly Ala Glu
      85              90              95
Val Phe Arg Ala Leu Glu Ser Leu Arg Lys Thr Pro Ser Asn Arg Ala
      100             105             110
Leu Glu Asn Glu Leu Ile Asp Ala Phe Gln Leu Asp Pro Ser Lys Lys
      115             120             125
Ile Arg Glu Tyr Ser Thr Gly Asn Arg Arg Lys Val Ser Leu Ile Ala
      130             135             140
Ala Leu Ser His Glu Pro Glu Leu Leu Ile Val Asp Glu Pro Thr Ala
      145             150             155             160
Gly Leu Asp Pro Ile Met Glu Gln Val Phe Val Thr Tyr Val Arg Lys
      165             170             175
Ala Arg Thr Asn Gly Ala Ser Val Leu Leu Ser Ser His Ile Leu Ser
      180             185             190
Glu Val Glu Gln Leu Cys Asp Tyr Val Thr Val Leu Lys Glu Gly Arg
      195             200             205
Ala Val Ala Ser Asn Glu Val Ser Tyr Leu Arg Lys Ile Ser Ala His
      210             215             220
Arg Ile Thr Ala Thr Ile Pro Ala Val Pro Gln His Leu Ala Gly Arg
      225             230             235             240
Gly Glu Val Asp Phe Asp Ala Gly His Leu Ser Ile Thr Cys Asp Ala
      245             250             255
Ser Glu Val Pro Asp Ile Leu Arg Ile Ile Ile Asp Ala Gly Gly Gln
      260             265             270
Asp Ile Ile Ser Thr Ala Ala Ser Leu Glu Glu Ile Phe Leu Arg His
      275             280             285
Tyr Gly Glu Thr Val Ser Gly Ser Glu Ser Lys Ala Ser Gln
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<210> 85

<211> 1764

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1741)

<223> RXA02119

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              Met Thr Glu Thr Leu
              1              5

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gtg gtg aat ggc ctt gca ggc ggc tat ggg cac cgc aca tta ttt aac 163
Val Val Asn Gly Leu Ala Gly Gly Tyr Gly His Arg Thr Leu Phe Asn
      10                      15                      20

gat gtg aat ctc acc gta gct gcc ggc gat gtc gtg ggc gtt gtc ggc 211
Asp Val Asn Leu Thr Val Ala Ala Gly Asp Val Val Gly Val Val Gly
      25                      30                      35

gtc aat ggc gct ggt aaa tcc aca ttt cta aaa att ctg gcg ggc gtg 259
Val Asn Gly Ala Gly Lys Ser Thr Phe Leu Lys Ile Leu Ala Gly Val
      40                      45                      50

gaa aag cca ctg gct gga act atc gcg ctt tcg cca gcc gat gct ttt 307
Glu Lys Pro Leu Ala Gly Thr Ile Ala Leu Ser Pro Ala Asp Ala Phe
      55                      60                      65

gtg ggc tac ttg cca cag gaa cac acc cgc acg tct gga gag acg atc 355
Val Gly Tyr Leu Pro Gln Glu His Thr Arg Thr Ser Gly Glu Thr Ile
      70                      75                      80                      85

gca gtt tac att gct cgt cga acc ggc tgc caa gct gca aca act gcc 403
Ala Val Tyr Ile Ala Arg Arg Thr Gly Cys Gln Ala Ala Thr Thr Ala
      90                      95                      100

atg gat gac acc gcc gaa gcg ttt ggt gcg gat cca gac aac gct gcc 451
Met Asp Asp Thr Ala Glu Ala Phe Gly Ala Asp Pro Asp Asn Ala Ala
      105                      110                      115

ttg gcc gat gca tac gcc gag gcg ctg gat cgg tgg atg gcc agt ggc 499
Leu Ala Asp Ala Tyr Ala Glu Ala Leu Asp Arg Trp Met Ala Ser Gly
      120                      125                      130

gca gcc gat ttg gat gaa cgc atc ccc atc gtg ctc gct gat ttg ggc 547
Ala Ala Asp Leu Asp Glu Arg Ile Pro Ile Val Leu Ala Asp Leu Gly
      135                      140                      145

ttt gag ctt ccc acc tcg acg ctg atg gaa gga ctt tca ggc ggc cag 595
Phe Glu Leu Pro Thr Ser Thr Leu Met Glu Gly Leu Ser Gly Gly Gln
      150                      155                      160                      165

gca gcc cgg gtc ggg ctg gcg gcg tta ctg ttg tca cgt ttt gac att 643
Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu Ser Arg Phe Asp Ile
      170                      175                      180

gtg ctt ctc gac gag ccc acc aac gat ttg gat ctc gac ggt ctt gag 691
Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp Leu Asp Gly Leu Glu
      185                      190                      195

caa ctg gag aat ttt gtt cag ggg ctt cgc ggc gga gtc gta ctg gtc 739
Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly Gly Val Val Leu Val
      200                      205                      210

agc cat gat cgt gag ttt ctt tcc agg tgt gtg acc act gtg ctg gaa 787
Ser His Asp Arg Glu Phe Leu Ser Arg Cys Val Thr Thr Val Leu Glu
      215                      220                      225

ctc gat ctg cac caa aat tcc cac cat gtt tat ggc ggt gga tat gat 835
Leu Asp Leu His Gln Asn Ser His His Val Tyr Gly Gly Gly Tyr Asp
      230                      235                      240                      245

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tcc tac ctt gag gaa cgc gca gtg cta cgc cag cac gcc cgt gac caa 883
 Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln His Ala Arg Asp Gln
 250 255 260

tat gag gaa ttt gcg gaa aag aag aag gac ctt gtg gca cgt gct cga 931
 Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu Val Ala Arg Ala Arg
 265 270 275

acg cag cgt gaa tgg tct agt cac ggt gtc cgc aat gct att aaa cgt 979
 Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg Asn Ala Ile Lys Arg
 280 285 290

gca cct gac aac gac aaa ctt cgg aag aaa gcc gct gcg gaa tcc agt 1027
 Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala Ala Ala Glu Ser Ser
 295 300 305

gaa aag cag gct caa aaa gtc cgc cag atg gaa agc cgc atc gct cgg 1075
 Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu Ser Arg Ile Ala Arg
 310 315 320 325

tta gaa gaa gtt gaa gag cca cgt aaa gaa tgg aaa ctg cag ttc agc 1123
 Leu Glu Glu Val Glu Glu Pro Arg Lys Glu Trp Lys Leu Gln Phe Ser
 330 335 340

gtc ggt aag gcg tcg cgg tca agt tct gtt gtt tcc acg ttg aat gat 1171
 Val Gly Lys Ala Ser Arg Ser Ser Ser Val Val Ser Thr Leu Asn Asp
 345 350 355

gca agc ttc acc caa ggc gat ttc acc ttg gga cca gta tcc atc caa 1219
 Ala Ser Phe Thr Gln Gly Asp Phe Thr Leu Gly Pro Val Ser Ile Gln
 360 365 370

gta aat gct ggc gat cgc att ggc atc aca gga ccc aac ggt gct ggt 1267
 Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly Pro Asn Gly Ala Gly
 375 380 385

aaa tcc aca ttg ctg cgc gga cta ttg gga aac caa gaa ccc acc agc 1315
 Lys Ser Thr Leu Leu Arg Gly Leu Leu Gly Asn Gln Glu Pro Thr Ser
 390 395 400 405

ggt act gcc acg atg ggc acg agc gtg gcg atc gga gaa atc gat cag 1363
 Gly Thr Ala Thr Met Gly Thr Ser Val Ala Ile Gly Glu Ile Asp Gln
 410 415 420

gca cga gcg tta ctt gat cca cag ttg cca ctg att tct gcg ttt gaa 1411
 Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu Ile Ser Ala Phe Glu
 425 430 435

aag cat gtt cca gac tta ccg atc agt gag gtg cgc aca ctg ctc gcg 1459
 Lys His Val Pro Asp Leu Pro Ile Ser Glu Val Arg Thr Leu Leu Ala
 440 445 450

aaa ttt ggg ctg aat gat aat cat gtg gaa cgg gac gtc gaa aag cta 1507
 Lys Phe Gly Leu Asn Asp Asn His Val Glu Arg Asp Val Glu Lys Leu
 455 460 465

tct cct ggc gag cgc acg cgc gcc gga ctt gcg ctg cta cag gtg cgg 1555
 Ser Pro Gly Glu Arg Thr Arg Ala Gly Leu Ala Leu Leu Gln Val Arg
 470 475 480 485

ggc gtc aac gtg ctt gtt ctt gat gag ccc acc aac cac ctt gac ctg 1603

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<210> 86
<211> 547
<212> PRT
<213> Corynebacterium glutamicum

<400> 86
Met Thr Glu Thr Leu Val Val Asn Gly Leu Ala Gly Gly Tyr Gly His
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Arg Thr Leu Phe Asn Asp Val Asn Leu Thr Val Ala Ala Gly Asp Val
          20           25           30
Val Gly Val Val Gly Val Asn Gly Ala Gly Lys Ser Thr Phe Leu Lys
          35           40           45
Ile Leu Ala Gly Val Glu Lys Pro Leu Ala Gly Thr Ile Ala Leu Ser
 50           55           60
Pro Ala Asp Ala Phe Val Gly Tyr Leu Pro Gln Glu His Thr Arg Thr
 65           70           75           80
Ser Gly Glu Thr Ile Ala Val Tyr Ile Ala Arg Arg Thr Gly Cys Gln
          85           90           95
Ala Ala Thr Thr Ala Met Asp Asp Thr Ala Glu Ala Phe Gly Ala Asp
          100          105          110
Pro Asp Asn Ala Ala Leu Ala Asp Ala Tyr Ala Glu Ala Leu Asp Arg
          115          120          125
Trp Met Ala Ser Gly Ala Ala Asp Leu Asp Glu Arg Ile Pro Ile Val
          130          135          140
Leu Ala Asp Leu Gly Phe Glu Leu Pro Thr Ser Thr Leu Met Glu Gly
          145          150          155          160
Leu Ser Gly Gly Gln Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu
          165          170          175
Ser Arg Phe Asp Ile Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp
          180          185          190
Leu Asp Gly Leu Glu Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly

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[illegible]


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aga gtc gtc gac tat tcc gcc ggc atg acg aag aag att ctt ttg gcc 595
Arg Val Val Asp Tyr Ser Ala Gly Met Thr Lys Lys Ile Leu Leu Ala
150                      155                      160                      165

cag gcc ctc att cac aat ccg aaa gtg ctc atc ctt gat gaa cct ttg 643
Gln Ala Leu Ile His Asn Pro Lys Val Leu Ile Leu Asp Glu Pro Leu
                      170                      175                      180

gaa gcg gtt gat ccg gtg tct ggt cgt ttg att cag cag att ttg aag 691
Glu Ala Val Asp Pro Val Ser Gly Arg Leu Ile Gln Gln Ile Leu Lys
                      185                      190                      195

aac ttt gcg caa acg ggt gga acc gtc gtt ttg agt tcg cat gtc atg 739
Asn Phe Ala Gln Thr Gly Gly Thr Val Val Leu Ser Ser His Val Met
                      200                      205                      210

gaa ttg gtt gag ggg ttg tgc gat cac gtt gcc atc atc aac agg gga 787
Glu Leu Val Glu Gly Leu Cys Asp His Val Ala Ile Ile Asn Arg Gly
                      215                      220                      225

gtg gtg gag att gcc gga cat gtg aat gag gtt cgt cgg ggc aga tct 835
Val Val Glu Ile Ala Gly His Val Asn Glu Val Arg Arg Gly Arg Ser
230                      235                      240                      245

tac cgg atg tct tcg tta atg cgg ttg aag gcg ctg ctc ttc aag agg 883
Tyr Arg Met Ser Ser Leu Met Arg Leu Lys Ala Leu Leu Phe Lys Arg
                      250                      255                      260

ggt cac tat ctt ggt tgg gtg cgt ccg aag gcc ata gcg aag gcc aaa 931
Gly His Tyr Leu Gly Trp Val Arg Pro Lys Ala Ile Ala Lys Ala Lys
                      265                      270                      275

atc aga acg agg atc ggg ctg agt aaa tgactaaaac acttctgaaa 978
Ile Arg Thr Arg Ile Gly Leu Ser Lys
                      280                      285

cta 981

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<210> 88

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 88

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Met Thr Asp Pro Glu Asn Ser Gln Gly Thr Pro Gln Ile Cys Pro Thr
  1                      5                      10                      15

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Asp Pro Thr Thr Gln Ala Leu Ala Val Arg Gly Leu Thr Lys Ser Tyr
          20                      25                      30

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```

Gly Asp Ala Thr Val Val Asn Asn Ile Asn Leu Asp Ile Pro Lys Gly
          35                      40                      45

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```

Ala Ile Tyr Gly Ile Val Gly Pro Asn Gly Ala Gly Lys Thr Thr Met
          50                      55                      60

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Leu Ser Met Ala Thr Gly Leu Leu Arg Pro Asn Lys Gly Thr Ala Trp
          65                      70                      75                      80

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```

Ile Ser Gly Phe Asn Val Trp Glu Glu Pro Asn Asp Ala Lys Arg Ser

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85										90					95				
Met	Gly	Leu	Leu	Ala	Asp	Gly	Leu	Pro	Ile	Phe	Asp	Arg	Leu	Thr	Gly				
		100						105					110						
Lys	Glu	Leu	Leu	Thr	Tyr	Val	Gly	Ala	Leu	Arg	Glu	Leu	Asp	Glu	Gly				
		115					120					125							
Ile	Val	Asp	Gln	Arg	Ser	Glu	Glu	Leu	Leu	Glu	Ala	Leu	Gly	Leu	Lys				
		130				135					140								
Glu	Ala	Ala	Gly	Lys	Arg	Val	Val	Asp	Tyr	Ser	Ala	Gly	Met	Thr	Lys				
145					150					155					160				
Lys	Ile	Leu	Leu	Ala	Gln	Ala	Leu	Ile	His	Asn	Pro	Lys	Val	Leu	Ile				
			165						170					175					
Leu	Asp	Glu	Pro	Leu	Glu	Ala	Val	Asp	Pro	Val	Ser	Gly	Arg	Leu	Ile				
		180						185					190						
Gln	Gln	Ile	Leu	Lys	Asn	Phe	Ala	Gln	Thr	Gly	Gly	Thr	Val	Val	Leu				
		195					200					205							
Ser	Ser	His	Val	Met	Glu	Leu	Val	Glu	Gly	Leu	Cys	Asp	His	Val	Ala				
		210				215					220								
Ile	Ile	Asn	Arg	Gly	Val	Val	Glu	Ile	Ala	Gly	His	Val	Asn	Glu	Val				
225					230				235					240					
Arg	Arg	Gly	Arg	Ser	Tyr	Arg	Met	Ser	Ser	Leu	Met	Arg	Leu	Lys	Ala				
			245					250					255						
Leu	Leu	Phe	Lys	Arg	Gly	His	Tyr	Leu	Gly	Trp	Val	Arg	Pro	Lys	Ala				
			260					265					270						
Ile	Ala	Lys	Ala	Lys	Ile	Arg	Thr	Arg	Ile	Gly	Leu	Ser	Lys						
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1180)
 <223> RXN00412

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 Val Ser His Thr Ala
 1 5
 tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag 163
 Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln
 10 15 20
 ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat 211

Variable	Unit	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																																																																																																																												
Population	Millions	120.0	121.0	122.0	123.0	124.0	125.0	126.0	127.0	128.0	129.0	130.0	131.0	132.0	133.0	134.0	135.0	136.0	137.0	138.0	139.0	140.0	141.0	142.0	143.0	144.0	145.0	146.0	147.0	148.0	149.0	150.0	151.0	152.0	153.0	154.0	155.0	156.0	157.0	158.0	159.0	160.0	161.0	162.0	163.0	164.0	165.0	166.0	167.0	168.0	169.0	170.0	171.0	172.0	173.0	174.0	175.0	176.0	177.0	178.0	179.0	180.0	181.0	182.0	183.0	184.0	185.0	186.0	187.0	188.0	189.0	190.0	191.0	192.0	193.0	194.0	195.0	196.0	197.0	198.0	199.0	200.0	201.0	202.0	203.0	204.0	205.0	206.0	207.0	208.0	209.0	210.0	211.0	212.0	213.0	214.0	215.0	216.0	217.0	218.0	219.0	220.0	221.0	222.0	223.0	224.0	225.0	226.0	227.0	228.0	229.0	230.0	231.0	232.0	233.0	234.0	235.0	236.0	237.0	238.0	239.0	240.0	241.0	242.0	243.0	244.0	245.0	246.0	247.0	248.0	249.0	250.0	251.0	252.0	253.0	254.0	255.0	256.0	257.0	258.0	259.0	260.0	261.0	262.0	263.0	264.0	265.0	266.0	267.0	268.0	269.0	270.0	271.0	272.0	273.0	274.0	275.0	276.0	277.0	278.0	279.0	280.0	281.0	282.0	283.0	284.0	285.0	286.0	287.0	288.0	289.0	290.0	291.0	292.0	293.0	294.0	295.0	296.0	297.0	298.0	299.0	300.0	301.0	302.0	303.0	304.0	305.0	306.0	307.0	308.0	309.0	310.0	311.0	312.0	313.0	314.0	315.0	316.0	317.0	318.0	319.0	320.0	321.0	322.0	323.0	324.0	325.0	326.0	327.0	328.0	329.0	330.0	331.0	332.0	333.0	334.0	335.0	336.0	337.0	338.0	339.0	340.0	341.0	342.0	343.0	344.0	345.0	346.0	347.0	348.0	349.0	350.0	351.0	352.0	353.0	354.0	355.0	356.0	357.0	358.0	359.0	360.0	361.0	362.0	363.0	364.0	365.0	366.0	367.0	368.0	369.0	370.0	371.0	372.0	373.0	374.0	375.0	376.0	377.0	378.0	379.0	380.0	381.0	382.0	383.0	384.0	385.0	386

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<220>
<221> CDS
<222> (101)..(1180)
<223> FRXA00412
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Val Ser His Thr Ala
1 5

tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag 163
Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln

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      130              135              140
Val  Gln  Glu  Met  Leu  Glu  Phe  Val  Gly  Leu  Gly  Asp  Lys  Gly  Lys  Asn
145              150              155              160

Tyr  Pro  Glu  Gln  Leu  Ser  Gly  Gly  Gln  Lys  Gln  Arg  Val  Gly  Ile  Ala
      165              170              175

Arg  Ala  Leu  Ala  Thr  Asn  Pro  Thr  Leu  Leu  Leu  Ala  Asp  Glu  Ala  Thr
      180              185              190

Ser  Ala  Leu  Asp  Pro  Glu  Thr  Thr  His  Glu  Val  Leu  Glu  Leu  Leu  Arg
      195              200              205

Lys  Val  Asn  Arg  Glu  Leu  Gly  Ile  Thr  Ile  Val  Val  Ile  Thr  His  Glu
      210              215              220

Met  Glu  Val  Val  Arg  Ser  Ile  Ala  Asp  Lys  Val  Ala  Val  Met  Glu  Ser
      225              230              235              240

Gly  Lys  Val  Val  Glu  Tyr  Gly  Ser  Val  Tyr  Glu  Val  Phe  Ser  Asn  Pro
      245              250              255

Gln  Thr  Gln  Val  Ala  Gln  Lys  Phe  Val  Ala  Thr  Ala  Leu  Arg  Asn  Thr
      260              265              270

Pro  Asp  Gln  Val  Glu  Ser  Glu  Asp  Leu  Leu  Ser  His  Glu  Gly  Arg  Leu
      275              280              285

Phe  Thr  Ile  Asp  Leu  Thr  Glu  Thr  Ser  Gly  Phe  Phe  Ala  Ala  Thr  Ala
      290              295              300

Arg  Ala  Ala  Glu  Gln  Gly  Ala  Phe  Val  Asn  Ile  Val  His  Gly  Gly  Val
      305              310              315              320

Thr  Thr  Leu  Gln  Arg  Gln  Ser  Phe  Gly  Lys  Met  Thr  Val  Arg  Leu  Thr
      325              330              335

Gly  Asn  Thr  Ala  Ala  Ile  Glu  Glu  Phe  Tyr  Gln  Thr  Leu  Thr  Lys  Thr
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Thr  Thr  Ile  Lys  Glu  Ile  Thr  Arg
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<210> 93

<211> 2340

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(2317)

<223> RXN02925

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              Met Ser Thr Pro His
              1              5

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cac cac ggt gat cac ccc gct ccg gaa aca gac cac acc cac cac ccg 163
 His His Gly Asp His Pro Ala Pro Glu Thr Asp His Thr His His Pro
 10 15 20

aat cat gcc ggt cac gag cac cat gcg gat gcc gcc acc cac ggc cag 211
 Asn His Ala Gly His Glu His His Ala Asp Ala Ala Thr His Gly Gln
 25 30 35

gcc atg ccg cac gat cat ccg cat tcc act gtc gat gaa gaa cat cag 259
 Ala Met Pro His Asp His Pro His Ser Thr Val Asp Glu Glu His Gln
 40 45 50

gtc cac agt cac ggt gaa cac gcc ggc cac agc gcc gcg atg ttc ccg 307
 Val His Ser His Gly Glu His Ala Gly His Ser Ala Ala Met Phe Arg
 55 60 65

gac cgc ttc tgg tgg tcg ctg atc ctg tcg gtt ccg gtg gtg ttc ttc 355
 Asp Arg Phe Trp Trp Ser Leu Ile Leu Ser Val Pro Val Val Phe Phe
 70 75 80 85

agc ccg atg ttc gcc gac ctg ctg gga tat aat att ccg gag att ccg 403
 Ser Pro Met Phe Ala Asp Leu Leu Gly Tyr Asn Ile Pro Glu Ile Pro
 90 95 100

gga gcc tac tgg att cct ccg gtc ctg ggc acg atc atc ttc ctc tac 451
 Gly Ala Tyr Trp Ile Pro Pro Val Leu Gly Thr Ile Ile Phe Leu Tyr
 105 110 115

ggc gcc acc ccc ttc ctc aag ggc gca atg acc gag ctg aaa tcc ccg 499
 Gly Gly Thr Pro Phe Leu Lys Gly Ala Met Thr Glu Leu Lys Ser Arg
 120 125 130

caa ccg ggc atg atg ctc ctg atc gcc atg gcg atc acc gtg gcg ttt 547
 Gln Pro Gly Met Met Leu Leu Ile Ala Met Ala Ile Thr Val Ala Phe
 135 140 145

atc gcc tcc tgg gtc acc acc ctg ggg ctg ggc ggg ttc cac cta gat 595
 Ile Ala Ser Trp Val Thr Leu Gly Leu Gly Gly Phe His Leu Asp
 150 155 160 165

ttc tgg tgg gaa ctg gcc ctg ctg gtg acc atc atg ctg ttg ggc cac 643
 Phe Trp Trp Glu Leu Ala Leu Leu Val Thr Ile Met Leu Leu Gly His
 170 175 180

tgg ctg gag atg cgc gct ctt ggt gca gcc tcc tcc gcg ctt gac gcg 691
 Trp Leu Glu Met Arg Ala Leu Gly Ala Ala Ser Ser Ala Leu Asp Ala
 185 190 195

ctg gca gcg ctc ctg ccc gat gag gcc gag aag gtc gtc gac ggg acc 739
 Leu Ala Ala Leu Leu Pro Asp Glu Ala Glu Lys Val Val Asp Gly Thr
 200 205 210

acc cgc acc gta gcg atc tca gag ctg gcc gtc gac gat gtc gtg ctg 787
 Thr Arg Thr Val Ala Ile Ser Glu Leu Ala Val Asp Asp Val Val Leu
 215 220 225

gtc cga gca ggt gcc cgc gtc ccg gcc gac ggg acc atc atc gac gga 835
 Val Arg Ala Gly Ala Arg Val Pro Ala Asp Gly Thr Ile Ile Asp Gly
 230 235 240 245

GENE: T226036

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Ala Ala Glu Phe Asp Glu Ala Met Ile Thr Gly Glu Ser Arg Pro Val	
250 255 260	
tac cgg gat acc ggt gag acc gtg gtg gcc ggc acc gtg gcc acc gac	931
Tyr Arg Asp Thr Gly Glu Thr Val Val Ala Gly Thr Val Ala Thr Asp	
265 270 275	
aac acc gtc cgt atc cgg gtg gag gcc acc ggt ggg gac acc gcc ctg	979
Asn Thr Val Arg Ile Arg Val Glu Ala Thr Gly Gly Asp Thr Ala Leu	
280 285 290	
gca ggc atc cag cgc atg gtc gcc gac gcc cag gcc tcc tcc tcc cgg	1027
Ala Gly Ile Gln Arg Met Val Ala Asp Ala Gln Ala Ser Ser Ser Arg	
295 300 305	
gcc cag gcc ctg gcc gat cga gcc gca gcc tta ctg ttc tgg ttc gcc	1075
Ala Gln Ala Leu Ala Asp Arg Ala Ala Ala Leu Leu Phe Trp Phe Ala	
310 315 320 325	
ctg atc acg gcc ctg atc acc gcc gtg gtc tgg acc atc atc ggc agc	1123
Leu Ile Thr Ala Leu Ile Thr Ala Val Val Trp Thr Ile Ile Gly Ser	
330 335 340	
ccc gac gat gcc gtg gtc cgc gcg gtg acc gtg ctg atc atc gcc tgc	1171
Pro Asp Asp Ala Val Val Arg Ala Val Thr Val Leu Ile Ile Ala Cys	
345 350 355	
ccg cac gcc ctg ggc ctg gcc atc ccg ctg gtc atc gcg atc tcc tcc	1219
Pro His Ala Leu Gly Leu Ala Ile Pro Leu Val Ile Ala Ile Ser Ser	
360 365 370	
gag cgc gcc gcg aaa tcc ggg gtg ctc atc aag gac cgc atg gca ctc	1267
Glu Arg Ala Ala Lys Ser Gly Val Leu Ile Lys Asp Arg Met Ala Leu	
375 380 385	
gag cac atg cgc acc atc gac gtc gtc ttg ttc gat aag acc ggc acc	1315
Glu His Met Arg Thr Ile Asp Val Val Leu Phe Asp Lys Thr Gly Thr	
390 395 400 405	
ctg acc gaa ggc gca cac gcc gtc acc ggc gtg gct ccg gcc acg ggt	1363
Leu Thr Glu Gly Ala His Ala Val Thr Gly Val Ala Pro Ala Thr Gly	
410 415 420	
atc gcc gag ggt gag ctg ctg gcc ctg gcc gcc gcc gct gag gcc gat	1411
Ile Ala Glu Gly Glu Leu Leu Ala Leu Ala Ala Ala Glu Ala Asp	
425 430 435	
agt gag cac ccc gtg gcc cgc gcg atc gtg act gcc gcg gcc gca cac	1459
Ser Glu His Pro Val Ala Arg Ala Ile Val Thr Ala Ala Ala Ala His	
440 445 450	
ccg gag gcc tcg cag cgt cag ctg cgc gca acc ggt ttc acc gcc gcc	1507
Pro Glu Ala Ser Gln Arg Gln Leu Arg Ala Thr Gly Phe Thr Ala Ala	
455 460 465	
tcc ggc cgc ggg atc cgg gcc acc gtc gac ggt gcc gaa atc ctc gtg	1555
Ser Gly Arg Gly Ile Arg Ala Thr Val Asp Gly Ala Glu Ile Leu Val	
470 475 480 485	
ggc ggg ccg aac atg cta cgc gag ttc aat ctg acc acc ccg ggt gag	1603

1123
 1171
 1219
 1267
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 1411
 1459
 1507
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 1603

Gly	Gly	Pro	Asn	Met	Leu	Arg	Glu	Phe	Asn	Leu	Thr	Thr	Pro	Gly	Glu		
				490					495					500			
ctc	gcc	gac	atc	acc	ggg	tcc	tgg	gca	cag	cga	ggg	gcc	gga	gtg	cta	1651	
Leu	Ala	Asp	Ile	Thr	Gly	Ser	Trp	Ala	Gln	Arg	Gly	Ala	Gly	Val	Leu		
			505					510					515				
cat	gtc	gtc	cgc	gac	ggg	gag	atc	atc	ggg	gcg	gtg	gca	gtg	gag	gac	1699	
His	Val	Val	Arg	Asp	Gly	Glu	Ile	Ile	Gly	Ala	Val	Ala	Val	Glu	Asp		
		520					525					530					
aaa	atc	cgc	ccc	gaa	tcc	cgc	gcg	gcg	gta	cgc	gcc	ctg	cag	gcc	cgc	1747	
Lys	Ile	Arg	Pro	Glu	Ser	Arg	Ala	Ala	Val	Arg	Ala	Leu	Gln	Ala	Arg		
	535					540					545						
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Gly	Val	Lys	Val	Ala	Met	Ile	Thr	Gly	Asp	Ala	Thr	Gln	Val	Ala	Gln		
550					555				560						565		
gca	gtg	ggc	aag	gat	ctg	ggg	atc	gat	gag	gtc	ttc	gcc	gag	gtt	ctg	1843	
Ala	Val	Gly	Lys	Asp	Leu	Gly	Ile	Asp	Glu	Val	Phe	Ala	Glu	Val	Leu		
				570					575					580			
ccg	cag	gac	aag	gac	acc	aag	gtc	acc	cag	ctg	cag	gag	cgc	ggg	ctg	1891	
Pro	Gln	Asp	Lys	Asp	Thr	Lys	Val	Thr	Gln	Leu	Gln	Glu	Arg	Gly	Leu		
			585					590					595				
agc	gtg	gcc	atg	gtc	ggc	gac	ggg	gtc	aat	gac	gcc	ccg	gcc	ctg	gcc	1939	
Ser	Val	Ala	Met	Val	Gly	Asp	Gly	Val	Asn	Asp	Ala	Pro	Ala	Leu	Ala		
		600					605				610						
cgg	gcc	gag	gtc	ggg	att	gcg	att	ggc	gcg	ggg	aca	gat	gtg	gcg	atg	1987	
Arg	Ala	Glu	Val	Gly	Ile	Ala	Ile	Gly	Ala	Gly	Thr	Asp	Val	Ala	Met		
	615					620					625						
gag	tcc	gcc	ggg	gtg	gtc	ctg	gcc	agt	gat	gat	ccc	cgg	gcc	gtg	ctg	2035	
Glu	Ser	Ala	Gly	Val	Val	Leu	Ala	Ser	Asp	Asp	Pro	Arg	Ala	Val	Leu		
630					635					640					645		
tcg	atg	atc	gag	ctc	tcc	cat	gcc	agc	tac	cgc	aag	atg	gtc	cag	aac	2083	
Ser	Met	Ile	Glu	Leu	Ser	His	Ala	Ser	Tyr	Arg	Lys	Met	Val	Gln	Asn		
				650					655					660			
ctg	gtc	tgg	gcg	acc	ggg	tac	aac	atc	gtg	gcc	gtt	ccg	ctg	gcc	gcc	2131	
Leu	Val	Trp	Ala	Thr	Gly	Tyr	Asn	Ile	Val	Ala	Val	Pro	Leu	Ala	Ala		
			665					670					675				
ggg	gtg	ctc	gcc	cct	atc	ggg	gtg	ctg	ctt	ccc	ccg	gcg	gcg	gcc	gcc	2179	
Gly	Val	Leu	Ala	Pro	Ile	Gly	Val	Leu	Leu	Pro	Pro	Ala	Ala	Ala	Ala		
		680					685					690					
atc	ttg	atg	tcc	ctg	tcc	acg	atc	atc	gtc	gcc	ctc	aac	gcc	cag	ctg	2227	
Ile	Leu	Met	Ser	Leu	Ser	Thr	Ile	Ile	Val	Ala	Leu	Asn	Ala	Gln	Leu		
		695				700					705						
cta	cgc	cgg	atc	gac	ctg	gac	ccg	gct	cac	cta	gct	ccg	acc	gac	ggg	2275	
Leu	Arg	Arg	Ile	Asp	Leu	Asp	Pro	Ala	His	Leu	Ala	Pro	Thr	Asp	Gly		
710					715					720					725		
aag	gag	gag	aag	gct	gct	gtg	agc	tct	gca	gcc	ccc	gtc	cgc			2317	
Lys	Glu	Glu	Lys	Ala	Ala	Val	Ser	Ser	Ala	Ala	Pro	Val	Arg				

Thr Val Ala Thr Asp Asn Thr Val Arg Ile Arg Val Glu Ala Thr Gly
 275 280 285
 Gly Asp Thr Ala Leu Ala Gly Ile Gln Arg Met Val Ala Asp Ala Gln
 290 295 300
 Ala Ser Ser Ser Arg Ala Gln Ala Leu Ala Asp Arg Ala Ala Ala Leu
 305 310 315 320
 Leu Phe Trp Phe Ala Leu Ile Thr Ala Leu Ile Thr Ala Val Val Trp
 325 330 335
 Thr Ile Ile Gly Ser Pro Asp Asp Ala Val Val Arg Ala Val Thr Val
 340 345 350
 Leu Ile Ile Ala Cys Pro His Ala Leu Gly Leu Ala Ile Pro Leu Val
 355 360 365
 Ile Ala Ile Ser Ser Glu Arg Ala Ala Lys Ser Gly Val Leu Ile Lys
 370 375 380
 Asp Arg Met Ala Leu Glu His Met Arg Thr Ile Asp Val Val Leu Phe
 385 390 395 400
 Asp Lys Thr Gly Thr Leu Thr Glu Gly Ala His Ala Val Thr Gly Val
 405 410 415
 Ala Pro Ala Thr Gly Ile Ala Glu Gly Glu Leu Leu Ala Leu Ala Ala
 420 425 430
 Ala Ala Glu Ala Asp Ser Glu His Pro Val Ala Arg Ala Ile Val Thr
 435 440 445
 Ala Ala Ala Ala His Pro Glu Ala Ser Gln Arg Gln Leu Arg Ala Thr
 450 455 460
 Gly Phe Thr Ala Ala Ser Gly Arg Gly Ile Arg Ala Thr Val Asp Gly
 465 470 475 480
 Ala Glu Ile Leu Val Gly Gly Pro Asn Met Leu Arg Glu Phe Asn Leu
 485 490 495
 Thr Thr Pro Gly Glu Leu Ala Asp Ile Thr Gly Ser Trp Ala Gln Arg
 500 505 510
 Gly Ala Gly Val Leu His Val Val Arg Asp Gly Glu Ile Ile Gly Ala
 515 520 525
 Val Ala Val Glu Asp Lys Ile Arg Pro Glu Ser Arg Ala Ala Val Arg
 530 535 540
 Ala Leu Gln Ala Arg Gly Val Lys Val Ala Met Ile Thr Gly Asp Ala
 545 550 555 560
 Thr Gln Val Ala Gln Ala Val Gly Lys Asp Leu Gly Ile Asp Glu Val
 565 570 575
 Phe Ala Glu Val Leu Pro Gln Asp Lys Asp Thr Lys Val Thr Gln Leu
 580 585 590

gac ggc gtc ctg atc aag ggc ggg gaa tac ctg gag acc tcc gcg aag 298
 Asp Gly Val Leu Ile Lys Gly Gly Glu Tyr Leu Glu Thr Ser Ala Lys
 70 75 80

gtc gac acc gta gtc gtc gac aag acc ggc acc ctg acc aac ggc cgc 346
 Val Asp Thr Val Val Val Asp Lys Thr Gly Thr Leu Thr Asn Gly Arg
 85 90 95

ccc gag ctg acc aac gtc gac gtc ctt gac ccc gcc tac tcg gac gat 394
 Pro Glu Leu Thr Asn Val Asp Val Leu Asp Pro Ala Tyr Ser Asp Asp
 100 105 110 115

gag gtg ctc acc ctg gcc gcc cgc gcg gaa acc gcc tcc gag cac ccc 442
 Glu Val Leu Thr Leu Ala Ala Arg Ala Glu Thr Ala Ser Glu His Pro
 120 125 130

ctg gcc gag gcc atc atc cgc ggc gcg gag aac agg gcc ttg acc gtg 490
 Leu Ala Glu Ala Ile Ile Arg Gly Ala Glu Asn Arg Gly Leu Thr Val
 135 140 145

gcg atg gta gaa aag gcc gaa ccg gtc gcc ggc cgc gcc atc cgc gct 538
 Ala Met Val Glu Lys Ala Glu Pro Val Ala Gly Arg Gly Ile Arg Ala
 150 155 160

gac gtg gac ggt gcc acc gtg gcc gtg ggc tca gcc gac ctg ctc gat 586
 Asp Val Asp Gly Ala Thr Val Ala Val Gly Ser Ala Asp Leu Leu Asp
 165 170 175

cac acc ccg gat aac acc cgc att ctc gag ctc aac gaa cag gcc agg 634
 His Thr Pro Asp Asn Thr Arg Ile Leu Glu Leu Asn Glu Gln Gly Arg
 180 185 190 195

acc gcc atg tac gtc gcc atc aac ggc aag gcc gtg gcc atc gtc gct 682
 Thr Ala Met Tyr Val Gly Ile Asn Gly Lys Ala Val Gly Ile Val Ala
 200 205 210

gtg gcc gac acc atc cga gat gat gcc ccg gcc gcg atc agg tcc ctg 730
 Val Ala Asp Thr Ile Arg Asp Asp Ala Pro Ala Ala Ile Arg Ser Leu
 215 220 225

cac aat aag gga atc cgc gtg gtc atg gcc acc ggt gat gcc gaa cgc 778
 His Asn Lys Gly Ile Arg Val Val Met Ala Thr Gly Asp Ala Glu Arg
 230 235 240

gtc gcc cgc aac gtc gcc gcc gag ctc ggt gtc gat gag gtg agg gca 826
 Val Ala Arg Asn Val Ala Ala Glu Leu Gly Val Asp Glu Val Arg Ala
 245 250 255

gaa ctg atg cct gag gac aag ctc gag atc gtc aag gag ctg cag gcg 874
 Glu Leu Met Pro Glu Asp Lys Leu Glu Ile Val Lys Glu Leu Gln Ala
 260 265 270 275

cag ggc cgg gtc gtg gcc atg gtt ggc gac ggt gtc aat gac acc ccg 922
 Gln Gly Arg Val Val Ala Met Val Gly Asp Gly Val Asn Asp Thr Pro
 280 285 290

gca ctg gcc acc gcg gac atc ggt gtg gcg atg ggt gcg gcc ggt tcg 970
 Ala Leu Ala Thr Ala Asp Ile Gly Val Ala Met Gly Ala Ala Gly Ser
 295 300 305

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cct gcc gcc atc gag acc gcc gat atc gcc ctg atg gcc gac aag ctg 1018
Pro Ala Ala Ile Glu Thr Ala Asp Ile Ala Leu Met Ala Asp Lys Leu
      310                      315                      320

ccg cgg ctg ccc tac gcc ctg ggt ctg gcc cag cgc acg gtg cgc acc 1066
Pro Arg Leu Pro Tyr Ala Leu Gly Leu Ala Gln Arg Thr Val Arg Thr
      325                      330                      335

atg cgg gtc aac atc ggc atc gcc ctg ctc act gtc acg atc ctg ctg 1114
Met Arg Val Asn Ile Gly Ile Ala Leu Leu Thr Val Thr Ile Leu Leu
      340                      345                      350                      355

gcc ggt gtc ctg ctc ggt gga gtg acc atg tcg att ggc atg ctc gtc 1162
Ala Gly Val Leu Leu Gly Gly Val Thr Met Ser Ile Gly Met Leu Val
      360                      365                      370

cac gag gcc tcc gtc ctg ctg gtc atc gcg att gcg atg ctc ctg ctg 1210
His Glu Ala Ser Val Leu Leu Val Ile Ala Ile Ala Met Leu Leu Leu
      375                      380                      385

cgc ccc acc ctg aag gaa gac aag gac aag gca gac gtc agt act gct 1258
Arg Pro Thr Leu Lys Glu Asp Lys Asp Lys Ala Asp Val Ser Thr Ala
      390                      395                      400

gac gcc gcg aag gag acg ctg agc gcc taacgacaca atcgccacag 1305
Asp Ala Ala Lys Glu Thr Leu Ser Ala
      405                      410

cca 1308

<210> 96
<211> 412
<212> PRT
<213> Corynebacterium glutamicum

<400> 96
Met Thr Arg Gln Lys Thr Gln Pro Phe Leu Glu Lys Phe Ser Lys Tyr
  1          5          10          15

Tyr Thr Pro Gly Val Met Ile Ala Ala Leu Ala Val Gly Leu Ile Thr
      20          25          30

Leu Asn Val Glu Leu Ala Leu Thr Leu Leu Val Ile Ala Cys Pro Gly
      35          40          45

Ala Leu Val Ile Ser Ile Pro Val Ser Ile Val Ala Gly Ile Gly Arg
      50          55          60

Ser Ala Lys Asp Gly Val Leu Ile Lys Gly Gly Glu Tyr Leu Glu Thr
      65          70          75          80

Ser Ala Lys Val Asp Thr Val Val Val Asp Lys Thr Gly Thr Leu Thr
      85          90          95

Asn Gly Arg Pro Glu Leu Thr Asn Val Asp Val Leu Asp Pro Ala Tyr
      100          105          110

Ser Asp Asp Glu Val Leu Thr Leu Ala Ala Arg Ala Glu Thr Ala Ser
      115          120          125

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<221> CDS
 <222> (1)..(168)
 <223> FRXA00939

<400> 97
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 Gly Val Leu Leu Gly Gly Val Thr Met Ser Ile Gly Met Leu Val His
 1 5 10 15
 gag gcc tcc gtc ctg ctg gtc atc gcg att gcg atg ctc ctg ctg cgc 96
 Glu Ala Ser Val Leu Leu Val Ile Ala Ile Ala Met Leu Leu Leu Arg
 20 25 30
 ccc acc ctg aag gaa gac aag gac aag gca gac gtc agt act gct gac 144
 Pro Thr Leu Lys Glu Asp Lys Asp Lys Ala Asp Val Ser Thr Ala Asp
 35 40 45
 gcc gcg aag gag acg ctg agc gcc taacgacaca atcgccacag cca 191
 Ala Ala Lys Glu Thr Leu Ser Ala
 50 55

<210> 98
 <211> 56
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 98
 Gly Val Leu Leu Gly Gly Val Thr Met Ser Ile Gly Met Leu Val His
 1 5 10 15
 Glu Ala Ser Val Leu Leu Val Ile Ala Ile Ala Met Leu Leu Leu Arg
 20 25 30
 Pro Thr Leu Lys Glu Asp Lys Asp Lys Ala Asp Val Ser Thr Ala Asp
 35 40 45
 Ala Ala Lys Glu Thr Leu Ser Ala
 50 55

<210> 99
 <211> 2388
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2365)
 <223> RXN01323

<400> 99
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 cagtgagtca tgtaaacata ctgcgagaag gagcgatccc atg gct cag aca ccc 115
 Met Ala Gln Thr Pro
 1 5
 gcc aaa atc ccg gcg gca ctg aat ttc att gac gtc gac ctc ggc gtt 163
 Ala Lys Ile Pro Ala Ala Leu Asn Phe Ile Asp Val Asp Leu Gly Val
 10 15 20

acc ggc atg acc tgc act tct tgc tcc gcc cgc gtc gag cgc aaa ctg 211
 Thr Gly Met Thr Cys Thr Ser Cys Ser Ala Arg Val Glu Arg Lys Leu
 25 30 35

aac aag ctc gac ggc gtt gaa gca acc gtc aac tac gcg acg gaa tcc 259
 Asn Lys Leu Asp Gly Val Glu Ala Thr Val Asn Tyr Ala Thr Glu Ser
 40 45 50

gca cag gtc agc tac gac ccc tca aag gtc agc cct gaa cag ctg att 307
 Ala Gln Val Ser Tyr Asp Pro Ser Lys Val Ser Pro Glu Gln Leu Ile
 55 60 65

aag act gtt gag gac acc ggc tac ggt gct ttc acg atg gct tcc gca 355
 Lys Thr Val Glu Asp Thr Gly Tyr Gly Ala Phe Thr Met Ala Ser Ala
 70 75 80 85

gct gcc gaa tca gaa gag gac aac gct cca gct gac agc ggc cag tcc 403
 Ala Ala Glu Ser Glu Glu Asp Asn Ala Pro Ala Asp Ser Gly Gln Ser
 90 95 100

cgc atc gac gca gct cgc gac cac gaa gca gcc gac ctg aaa cac cgc 451
 Arg Ile Asp Ala Ala Arg Asp His Glu Ala Ala Asp Leu Lys His Arg
 105 110 115

gtg atc gtc tct gca ctg ttg tca gtt cct gtg gtt ttg gtc agc atg 499
 Val Ile Val Ser Ala Leu Leu Ser Val Pro Val Val Leu Val Ser Met
 120 125 130

atc ccg gcg ctg caa ttc aac aac tgg cag tgg gcc gta ctc act ttg 547
 Ile Pro Ala Leu Gln Phe Asn Asn Trp Gln Trp Ala Val Leu Thr Leu
 135 140 145

gtc acc ccg att ttc ttc tgg ggc ggt tca ccg ttc cac aag gca acg 595
 Val Thr Pro Ile Phe Phe Trp Gly Gly Ser Pro Phe His Lys Ala Thr
 150 155 160 165

tgg gca aac ctg aag cgc ggt tcc ttc acc atg aac acc ctg gtt tca 643
 Trp Ala Asn Leu Lys Arg Gly Ser Phe Thr Met Asn Thr Leu Val Ser
 170 175 180

ctc ggc acg tcc gct gct gac ctg tgg tcc ctg tgg gct ttg ttc att 691
 Leu Gly Thr Ser Ala Ala Asp Leu Trp Ser Leu Trp Ala Leu Phe Ile
 185 190 195

gaa aat gct ggt cac cct ggc atg aag atg gag atg cac ctg ctg ccg 739
 Glu Asn Ala Gly His Pro Gly Met Lys Met Glu Met His Leu Leu Pro
 200 205 210

tcg gcc tcc acg atg gat gag att tac ctc gaa acc gtc gcg gtc gtt 787
 Ser Ala Ser Thr Met Asp Glu Ile Tyr Leu Glu Thr Val Ala Val Val
 215 220 225

att acg ttc ctg ctg ctt gga cgc tgg ttt gag aca aaa gct aag ggc 835
 Ile Thr Phe Leu Leu Leu Gly Arg Trp Phe Glu Thr Lys Ala Lys Gly
 230 235 240 245

caa tct tcg gaa gct ctg cgc aag ctg ctg gac atg ggc gcc aaa gat 883
 Gln Ser Ser Glu Ala Leu Arg Lys Leu Leu Asp Met Gly Ala Lys Asp
 250 255 260

gca gtc gtc tta cgt gac ggc gcc gaa gtc cgc gtt cct gtg aat cag 931
 Ala Val Val Leu Arg Asp Gly Ala Glu Val Arg Val Pro Val Asn Gln
 265 270 275

ctt aaa ctc ggc gac gtt ttc atc acc cgc ccc ggc gag aaa atc gcc 979
 Leu Lys Leu Gly Asp Val Phe Ile Thr Arg Pro Gly Glu Lys Ile Ala
 280 285 290

acc gac ggt gaa gtc gac gaa ggt tcc tcc gca gtc gac gaa tcc atg 1027
 Thr Asp Gly Glu Val Asp Glu Gly Ser Ser Ala Val Asp Glu Ser Met
 295 300 305

ctc acc ggc gaa tcc atc ccc gtt gaa gtc acc aag ggc tcc aaa gtt 1075
 Leu Thr Gly Glu Ser Ile Pro Val Glu Val Thr Lys Gly Ser Lys Val
 310 315 320 325

acc ggc gca acg ctg aac act tcc ggc cgc ctc atg gtg aaa gta acc 1123
 Thr Gly Ala Thr Leu Asn Thr Ser Gly Arg Leu Met Val Lys Val Thr
 330 335 340

cgc atc ggc gcc gac acc acc ctg tcg caa atg gct aaa ctg gtc acg 1171
 Arg Ile Gly Ala Asp Thr Thr Leu Ser Gln Met Ala Lys Leu Val Thr
 345 350 355

gac gca cag tcc aaa aag gcc cct gtc cag cgt ctt gtt gac caa atc 1219
 Asp Ala Gln Ser Lys Lys Ala Pro Val Gln Arg Leu Val Asp Gln Ile
 360 365 370

tcg cag gtt ttc gtt ccc gtt gtc atc gta att gct att gcg acg ctg 1267
 Ser Gln Val Phe Val Pro Val Val Ile Val Ile Ala Ile Ala Thr Leu
 375 380 385

atc gcg cac ctc gtc ttc acc gac gcc ggc ctc gcc cca gca ttc acc 1315
 Ile Ala His Leu Val Phe Thr Asp Ala Gly Leu Ala Pro Ala Phe Thr
 390 395 400 405

gca gca gtc gcc gtc ctc att atc gcc tgc cct tgt gcc ctc ggc ctg 1363
 Ala Ala Val Ala Val Leu Ile Ile Ala Cys Pro Cys Ala Leu Gly Leu
 410 415 420

gca acc cca acc gca ctt ctg gtc gga acc ggc cgc ggc gcg caa ctt 1411
 Ala Thr Pro Thr Ala Leu Leu Val Gly Thr Gly Arg Gly Ala Gln Leu
 425 430 435

ggt ctg ttg atc aag ggc cct gaa atc ctc gaa tcc acc aaa aaa gtc 1459
 Gly Leu Leu Ile Lys Gly Pro Glu Ile Leu Glu Ser Thr Lys Lys Val
 440 445 450

gac acc atc gtc ctc gac aaa acc ggc acc gtc acc acc ggc acc atg 1507
 Asp Thr Ile Val Leu Asp Lys Thr Gly Thr Val Thr Thr Gly Thr Met
 455 460 465

tcc gtc acc gac gtc acc gcc atc aac tac agc gaa acc gaa atc ctc 1555
 Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser Glu Thr Glu Ile Leu
 470 475 480 485

gaa ttc gct gca gcc gtc gag tcc gcc tcc gaa cac ccc atc gcc cag 1603
 Glu Phe Ala Ala Val Glu Ser Ala Ser Glu His Pro Ile Ala Gln
 490 495 500

gca atc gcc aag gcc gcc gaa cac gag caa gtc acc gac ttc caa aac 1651

Ala Ile Ala Lys Ala Ala Glu His Glu Gln Val Thr Asp Phe Gln Asn
505 510 515

acc gca ggt cag gaa gtc acc ggt gta gtc cgc gga cac gag gtc cgc 1699
Thr Ala Gly Gln Glu Val Thr Gly Val Val Arg Gly His Glu Val Arg
520 525 530

gtg ggc agg cct tca agc acg ctt atc gac gcc ctc ctc cac ccc ttc 1747
Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala Leu Leu His Pro Phe
535 540 545

caa cac gcc caa aaa atc ggc gga acc ccc gta gtc gtc acg att gac 1795
Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val Val Val Thr Ile Asp
550 555 560 565

ggc gta gat tcc gga ata atc acg gtc cgc gac acc gtc aaa gac acc 1843
Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp Thr Val Lys Asp Thr
570 575 580

tcc gcc gaa gca atc cgc gga ctc aag gaa ctg gga ctc acc cca atc 1891
Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu Gly Leu Thr Pro Ile
585 590 595

cta ctc acc gga gac aat gaa ggc gca gct aaa tcc gta gcc gct gaa 1939
Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys Ser Val Ala Ala Glu
600 605 610

gtc ggc atc gac caa gtc atc gcc aac gtc ctc ccc cac gaa aaa gtc 1987
Val Gly Ile Asp Gln Val Ile Ala Asn Val Leu Pro His Glu Lys Val
615 620 625

caa aac gta gaa gcc ctc caa gca caa ggc aaa aac gtt gcg atg gtc 2035
Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys Asn Val Ala Met Val
630 635 640 645

ggc gac ggc gtc aac gat gcc gca gct ctt gcc caa gct gac ctc gga 2083
Gly Asp Gly Val Asn Asp Ala Ala Ala Leu Ala Gln Ala Asp Leu Gly
650 655 660

ctc gcc atg gga gcc ggc acc gac gta gcc atc gaa gcc tcc gac atc 2131
Leu Ala Met Gly Ala Gly Thr Asp Val Ala Ile Glu Ala Ser Asp Ile
665 670 675

acc ctc atg aac aac gac ctc cga tcc gca gtc gac gcc atc cga ctg 2179
Thr Leu Met Asn Asn Asp Leu Arg Ser Ala Val Asp Ala Ile Arg Leu
680 685 690

tcc cgt aaa acc ctc ggc acc atc aag gga aac ctt ttc tgg gct ttc 2227
Ser Arg Lys Thr Leu Gly Thr Ile Lys Gly Asn Leu Phe Trp Ala Phe
695 700 705

gcc tac aat gtt gca cta atc cca gta gcg gcg atc gga ctc ctc aac 2275
Ala Tyr Asn Val Ala Leu Ile Pro Val Ala Ala Ile Gly Leu Leu Asn
710 715 720 725

cca atg ctt gcc ggc att gcg atg gcc ttc agt tca gtt ttc gtc gtc 2323
Pro Met Leu Ala Gly Ile Ala Met Ala Phe Ser Ser Val Phe Val Val
730 735 740

tcc aat tcc ttg cgt ctg cga gga ttc aaa gca agg agc aac 2365
Ser Asn Ser Leu Arg Leu Arg Gly Phe Lys Ala Arg Ser Asn

[illegible]

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<210> 101
<211> 2388
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(2365)  
<223> FRXA01323
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cagtgagtc tgtaaacata ctgcgagaag gagcgatccc atg gct cag aca ccc 115
                                         Met Ala Gln Thr Pro
                                         1                               5

gcc aaa atc cgc gcg gca ctg aat ttc att gac gtc gac ctc ggc gtt 163
Ala Lys Ile Pro Ala Ala Leu Asn Phe Ile Asp Val Asp Leu Gly Val
                        10                        15                        20

acc ggc atg acc tgc act tct tgc tcc gcc cgc gtc gag cgc aaa ctg 211
Thr Gly Met Thr Cys Thr Ser Cys Ser Ala Arg Val Glu Arg Lys Leu
                        25                        30                        35

aac aag ctc gac ggc gtt gaa gca acc gtc aac tac gcg acg gaa tcc 259
Asn Lys Leu Asp Gly Val Glu Ala Thr Val Asn Tyr Ala Thr Glu Ser

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acc gac ggt gaa gtc gac gaa ggt tcc tcc gca gtc gac gaa tcc atg 1027
 Thr Asp Gly Glu Val Asp Glu Gly Ser Ser Ala Val Asp Glu Ser Met
 295 300 305

ctc acc ggc gaa tcc atc ccc gtt gaa gtc acc aag ggc tcc aaa gtt 1075
 Leu Thr Gly Glu Ser Ile Pro Val Glu Val Thr Lys Gly Ser Lys Val
 310 315 320 325

acc ggc gca acg ctg aac act tcc ggc cgc ctc atg gtg aaa gta acc 1123
 Thr Gly Ala Thr Leu Asn Thr Ser Gly Arg Leu Met Val Lys Val Thr
 330 335 340

cgc atc ggc gcc gac acc acc ctg tgc caa atg gct aaa ctg gtc acg 1171
 Arg Ile Gly Ala Asp Thr Thr Leu Ser Gln Met Ala Lys Leu Val Thr
 345 350 355

gac gca cag tcc aaa aag gcc cct gtc cag cgt ctt gtt gac caa atc 1219
 Asp Ala Gln Ser Lys Lys Ala Pro Val Gln Arg Leu Val Asp Gln Ile
 360 365 370

tgc cag gtt ttc gtt ccc gtt gtc atc gta att gct att gcg acg ctg 1267
 Ser Gln Val Phe Val Pro Val Val Ile Val Ile Ala Ile Ala Thr Leu
 375 380 385

atc gcg cac ctc gtc ttc acc gac gcc ggc ctc gcc cca gca ttc acc 1315
 Ile Ala His Leu Val Phe Thr Asp Ala Gly Leu Ala Pro Ala Phe Thr
 390 395 400 405

gca gca gtc gcc gtc ctc att atc gcc tgc cct tgt gcc ctc ggc ctg 1363
 Ala Ala Val Ala Val Leu Ile Ile Ala Cys Pro Cys Ala Leu Gly Leu
 410 415 420

gca acc cca acc gca ctt ctg gtc gga acc ggc cgc ggc gcg caa ctt 1411
 Ala Thr Pro Thr Ala Leu Leu Val Gly Thr Gly Arg Gly Ala Gln Leu
 425 430 435

ggt ctg ttg atc aag ggc cct gaa atc ctc gaa tcc acc aaa aaa gtc 1459
 Gly Leu Leu Ile Lys Gly Pro Glu Ile Leu Glu Ser Thr Lys Lys Val
 440 445 450

gac acc atc gtc ctc gac aaa acc ggc acc gtc acc acc ggc acc atg 1507
 Asp Thr Ile Val Leu Asp Lys Thr Gly Thr Val Thr Thr Gly Thr Met
 455 460 465

tcc gtc acc gac gtc acc gcc atc aac tac agc gaa acc gaa atc ctc 1555
 Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser Glu Thr Glu Ile Leu
 470 475 480 485

gaa ttc gct gca gcc gtc gag tcc gcc tcc gaa cac ccc atc gcc cag 1603
 Glu Phe Ala Ala Val Glu Ser Ala Ser Glu His Pro Ile Ala Gln
 490 495 500

gca atc gcc aag gcc gcc gaa cac gag caa gtc acc gac ttc caa aac 1651
 Ala Ile Ala Lys Ala Ala Glu His Glu Gln Val Thr Asp Phe Gln Asn
 505 510 515

acc gca ggt cag gaa gtc acc ggt gta gtc cgc gga cac gag gtc cgc 1699
 Thr Ala Gly Gln Glu Val Thr Gly Val Val Arg Gly His Glu Val Arg
 520 525 530

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gtg ggc agg cct tca agc acg ctt atc gac gcc ctc ctc cac ccc ttc 1747
Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala Leu Leu His Pro Phe
    535                      540                      545

caa cac gcc caa aaa atc ggc gga acc ccc gta gtc gtc acg att gac 1795
Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val Val Val Thr Ile Asp
    550                      555                      560                      565

ggc gta gat tcc gga ata atc acg gtc cgc gac acc gtc aaa gac acc 1843
Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp Thr Val Lys Asp Thr
                      570                      575                      580

tcc gcc gaa gca atc cgc gga ctc aag gaa ctg gga ctc acc cca atc 1891
Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu Gly Leu Thr Pro Ile
                      585                      590                      595

cta ctc acc gga gac aat gaa ggc gca gct aaa tcc gta gcc gct gaa 1939
Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys Ser Val Ala Ala Glu
    600                      605                      610

gtc ggc atc gac caa gtc atc gcc aac gtc ctc ccc cac gaa aaa gtc 1987
Val Gly Ile Asp Gln Val Ile Ala Asn Val Leu Pro His Glu Lys Val
    615                      620                      625

caa aac gta gaa gcc ctc caa gca caa ggc aaa aac gtt gcg atg gtc 2035
Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys Asn Val Ala Met Val
    630                      635                      640                      645

ggc gac ggc gtc aac gat gcc gca gct ctt gcc caa gct gac ctc gga 2083
Gly Asp Gly Val Asn Asp Ala Ala Ala Leu Ala Gln Ala Asp Leu Gly
                      650                      655                      660

ctc gcc atg gga gcc ggc acc gac gta gcc atc gaa gcc tcc gac atc 2131
Leu Ala Met Gly Ala Gly Thr Asp Val Ala Ile Glu Ala Ser Asp Ile
                      665                      670                      675

acc ctc atg aac aac gac ctc cga tcc gca gtc gac gcc atc cga ctg 2179
Thr Leu Met Asn Asn Asp Leu Arg Ser Ala Val Asp Ala Ile Arg Leu
    680                      685                      690

tcc cgt aaa acc ctc ggc acc atc aag gga aac ctt ttc tgg gct ttc 2227
Ser Arg Lys Thr Leu Gly Thr Ile Lys Gly Asn Leu Phe Trp Ala Phe
    695                      700                      705

gcc tac aat gtt gca cta atc cca gta gcg gcg atc gga ctc ctc aac 2275
Ala Tyr Asn Val Ala Leu Ile Pro Val Ala Ala Ile Gly Leu Leu Asn
    710                      715                      720                      725

cca atg ctt gcc ggc att gcg atg gcc ttc agt tca gtt ttc gtc gtc 2323
Pro Met Leu Ala Gly Ile Ala Met Ala Phe Ser Ser Val Phe Val Val
                      730                      735                      740

tcc aat tcc ttg cgt ctg cga gga ttc aaa gca agg agc aac 2365
Ser Asn Ser Leu Arg Leu Arg Gly Phe Lys Ala Arg Ser Asn
                      745                      750                      755

taatgtccaa cagcgaatgc cac 2388

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<210> 102

<211> 755


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Val Asp Glu Ser Met Leu Thr Gly Glu Ser Ile Pro Val Glu Val Thr
305                310                315                320

Lys Gly Ser Lys Val Thr Gly Ala Thr Leu Asn Thr Ser Gly Arg Leu
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Met Val Lys Val Thr Arg Ile Gly Ala Asp Thr Thr Leu Ser Gln Met
                340                345                350

Ala Lys Leu Val Thr Asp Ala Gln Ser Lys Lys Ala Pro Val Gln Arg
                355                360                365

Leu Val Asp Gln Ile Ser Gln Val Phe Val Pro Val Val Ile Val Ile
370                375                380

Ala Ile Ala Thr Leu Ile Ala His Leu Val Phe Thr Asp Ala Gly Leu
385                390                395                400

Ala Pro Ala Phe Thr Ala Ala Val Ala Val Leu Ile Ile Ala Cys Pro
                405                410                415

Cys Ala Leu Gly Leu Ala Thr Pro Thr Ala Leu Leu Val Gly Thr Gly
420                425                430

Arg Gly Ala Gln Leu Gly Leu Leu Ile Lys Gly Pro Glu Ile Leu Glu
435                440                445

Ser Thr Lys Lys Val Asp Thr Ile Val Leu Asp Lys Thr Gly Thr Val
450                455                460

Thr Thr Gly Thr Met Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser
465                470                475                480

Glu Thr Glu Ile Leu Glu Phe Ala Ala Ala Val Glu Ser Ala Ser Glu
485                490                495

His Pro Ile Ala Gln Ala Ile Ala Lys Ala Ala Glu His Glu Gln Val
500                505                510

Thr Asp Phe Gln Asn Thr Ala Gly Gln Glu Val Thr Gly Val Val Arg
515                520                525

Gly His Glu Val Arg Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala
530                535                540

Leu Leu His Pro Phe Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val
545                550                555                560

Val Val Thr Ile Asp Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp
565                570                575

Thr Val Lys Asp Thr Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu
580                585                590

Gly Leu Thr Pro Ile Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys
595                600                605

Ser Val Ala Ala Glu Val Gly Ile Asp Gln Val Ile Ala Asn Val Leu
610                615                620

Pro His Glu Lys Val Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys

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625 630 635 640

Asn Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Ala Ala Leu Ala
645 650 655

Gln Ala Asp Leu Gly Leu Ala Met Gly Ala Gly Thr Asp Val Ala Ile
660 665 670

Glu Ala Ser Asp Ile Thr Leu Met Asn Asn Asp Leu Arg Ser Ala Val
675 680 685

Asp Ala Ile Arg Leu Ser Arg Lys Thr Leu Gly Thr Ile Lys Gly Asn
690 695 700

Leu Phe Trp Ala Phe Ala Tyr Asn Val Ala Leu Ile Pro Val Ala Ala
705 710 715 720

Ile Gly Leu Leu Asn Pro Met Leu Ala Gly Ile Ala Met Ala Phe Ser
725 730 735

Ser Val Phe Val Val Ser Asn Ser Leu Arg Leu Arg Gly Phe Lys Ala
740 745 750

Arg Ser Asn
755

<210> 103
<211> 1830
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1807)
<223> RXN00702

<400> 103
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gtcgaaaagc aataaatagc ccagaaaaggg ccgaagttaa atg agt gct cct ttt 115
Met Ser Ala Pro Phe
1 5

agc gcg cgc act gcg tgg tcg acg gac ccc gtg ctg gaa ctg gaa agc 163
Ser Ala Arg Thr Ala Trp Ser Thr Asp Pro Val Leu Glu Leu Glu Ser
10 15 20

gtc gct gcc tcg tat tat gac gat gag cgc acg ctg gcg gcg ccg cag 211
Val Ala Ala Ser Tyr Tyr Asp Asp Glu Arg Thr Leu Ala Ala Pro Gln
25 30 35

atc agc gac gtg aat ctg acg ctt ttt gaa ggc gaa atc ctg ctg gtt 259
Ile Ser Asp Val Asn Leu Thr Leu Phe Glu Gly Glu Ile Leu Leu Val
40 45 50

gtg ggg cgc acc ggc tcc ggc aaa tcg acg ctg ctg aac gcg atg tcc 307
Val Gly Arg Thr Gly Ser Gly Lys Ser Thr Leu Leu Asn Ala Met Ser
55 60 65

ggc gcg atg ccg cat gcg acc ggc ggc cga ctt gat ggg cgc gtg cgc 355

CCDS: TC00950

310	315	320	325	
aac ttg aat ctc aac tcc ggt gaa att acc gtg ctc atg ggc cga aac	1123			
Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val Leu Met Gly Arg Asn				
330	335	340		
ggc tgc gga aaa tca tcc ctg ctg tgg gct tta caa ggt tca ggg act	1171			
Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu Gln Gly Ser Gly Thr				
345	350	355		
aga aat cag ggc tcg gtg cag gtg ctt gat gag gcc gcg gga ttt tcg	1219			
Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu Ala Ala Gly Phe Ser				
360	365	370		
tgg aca gac ccc aaa act tta aag ccc gcc aag cgg cgc aat ctt gtg	1267			
Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys Arg Arg Asn Leu Val				
375	380	385		
tcc atg gtt ccg caa aca ccg acc gat att ttg tat gaa tca acc gtg	1315			
Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu Tyr Glu Ser Thr Val				
390	395	400	405	
cat gca gag ctc gca cgc tct gat aaa gat gcc gca gca ccc gcc ggc	1363			
His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala Ala Ala Pro Ala Gly				
410	415	420		
acc acg cgg gaa atc ctg gat tca ctg gtc ccg aat atc ccg gac cat	1411			
Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro Asn Ile Pro Asp His				
425	430	435		
ctc cac cca cgt gat cta tca gaa ggc caa aag ctc tcc ctc gcg ctg	1459			
Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys Leu Ser Leu Ala Leu				
440	445	450		
tcc atc caa ctc gcc gca aaa ccc cgc gtg gta ttt ttc gac gaa ccc	1507			
Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val Phe Phe Asp Glu Pro				
455	460	465		
acc cgc ggc cta gac tac gac ggc aag aaa tcc ctc gcc cgc tcc ttc	1555			
Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser Leu Ala Arg Ser Phe				
470	475	480	485	
caa caa ctc gca gac gac ggc cac gcc att ttg gtg gtc acc cac gac	1603			
Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu Val Val Thr His Asp				
490	495	500		
gtg gaa ttc tct gca ctg tgc gcc gac cga gtg ttg ttt atg gcc tct	1651			
Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val Leu Phe Met Ala Ser				
505	510	515		
gga aag atc atc tcc gat ggc aca gcc gta gaa atc ctc ccc gca tca	1699			
Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu Ile Leu Pro Ala Ser				
520	525	530		
ccg gct tac gcc cca caa gtc gca aaa atc acc gcc ggc atc caa gag	1747			
Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr Ala Gly Ile Gln Glu				
535	540	545		
gaa tca cac tgg ctc aca gtc tcg gcc gtg aaa gct gcg cta ggg cat	1795			
Glu Ser His Trp Leu Thr Val Ser Ala Val Lys Ala Ala Leu Gly His				
550	555	560	565	

260 265 270
 Ser Ile Arg Asp Ala Arg Ala His Ser Ala Asp Met Arg Lys Arg Leu
 275 280 285
 Tyr Gln Arg Gly Leu Val Val Asn Lys Leu His Asn His Ala Val Gln
 290 295 300
 Pro Leu Leu Ile Ala Glu Asp Ile Met Val Asp Phe Pro Glu Ile Arg
 305 310 315 320
 Ala Val Asp Gly Val Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val
 325 330 335
 Leu Met Gly Arg Asn Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu
 340 345 350
 Gln Gly Ser Gly Thr Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu
 355 360 365
 Ala Ala Gly Phe Ser Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys
 370 375 380
 Arg Arg Asn Leu Val Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu
 385 390 395 400
 Tyr Glu Ser Thr Val His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala
 405 410 415
 Ala Ala Pro Ala Gly Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro
 420 425 430
 Asn Ile Pro Asp His Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys
 435 440 445
 Leu Ser Leu Ala Leu Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val
 450 455 460
 Phe Phe Asp Glu Pro Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser
 465 470 475 480
 Leu Ala Arg Ser Phe Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu
 485 490 495
 Val Val Thr His Asp Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val
 500 505 510
 Leu Phe Met Ala Ser Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu
 515 520 525
 Ile Leu Pro Ala Ser Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr
 530 535 540
 Ala Gly Ile Gln Glu Glu Ser His Trp Leu Thr Val Ser Ala Val Lys
 545 550 555 560
 Ala Ala Leu Gly His Gly Glu Ile Ser
 565

<210> 105

<211> 1343

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1320)

<223> FRXA00702

<400> 105

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tta ggg ctc cca cct gcg gtc atg cgc aag cgc gta gag gaa acc ctt 48
Leu Gly Leu Pro Pro Ala Val Met Arg Lys Arg Val Glu Glu Thr Leu
  1             5             10             15

gat ctt tta ggc atc gcg gag ctg cga tac gtg cca ttg gcg gaa cta 96
Asp Leu Leu Gly Ile Ala Glu Leu Arg Tyr Val Pro Leu Ala Glu Leu
          20             25             30

tct ggt ggt gag cag cag cgc gtg gcg att gcc gcg gtg ctg acc act 144
Ser Gly Gly Glu Gln Gln Arg Val Ala Ile Gly Ala Val Leu Thr Thr
          35             40             45

cgc ccc gcg ctg att atc ttg gat gaa cca acc agc gct ttg gac cct 192
Arg Pro Ala Leu Ile Ile Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro
          50             55             60

aat ggt gcc gag gat gtg ctg gca acc gta acc aag ctg gct cat gac 240
Asn Gly Ala Glu Asp Val Leu Ala Thr Val Thr Lys Leu Ala His Asp
  65             70             75             80

ttg gcg atg acc gta gtg ctt gct gaa cac cgc atc gag cgc gta ctg 288
Leu Ala Met Thr Val Val Leu Ala Glu His Arg Ile Glu Arg Val Leu
          85             90             95

cag tac gtg gac cgc gtg gcg cat gtg gcc gct gat ggg cac gtc act 336
Gln Tyr Val Asp Arg Val Ala His Val Gly Ala Asp Gly His Val Thr
          100             105             110

gtt ggg acg ccg gaa gaa atc atg gct gat tct gat gtg gca cca ccc 384
Val Gly Thr Pro Glu Glu Ile Met Ala Asp Ser Asp Val Ala Pro Pro
          115             120             125

att gtg gaa tta gga cgc tgg gct gcc tgg gct ccc cta ccg cta tcg 432
Ile Val Glu Leu Gly Arg Trp Ala Gly Trp Ala Pro Leu Pro Leu Ser
          130             135             140

atc cgc gat gca cgc gca cac tcc gct gac atg cgc aaa cgc ctg tat 480
Ile Arg Asp Ala Arg Ala His Ser Ala Asp Met Arg Lys Arg Leu Tyr
          145             150             155             160

cag cgt ggt tta gtg gtg aac aaa tta cac aac cac gct gtc cag cca 528
Gln Arg Gly Leu Val Val Asn Lys Leu His Asn His Ala Val Gln Pro
          165             170             175

ctt ttg atc gcc gaa gat atc atg gtt gat ttc ccc gaa atc cgt gcc 576
Leu Leu Ile Ala Glu Asp Ile Met Val Asp Phe Pro Glu Ile Arg Ala
          180             185             190

gtt gac gcc gtg aac ttg aat ctc aac tcc ggt gaa att acc gtg ctc 624
Val Asp Gly Val Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val Leu
          195             200             205

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BGI-131CP
 - 155 -
 <211> 1343
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (1)..(1320)
 <223> FRXA00702
 <400> 105

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 Met Gly Arg Asn Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu Gln
 210 215 220

ggt tca ggg act aga aat cag ggc tcg gtg cag gtg ctt gat gag gcc 720
 Gly Ser Gly Thr Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu Ala
 225 230 235 240

gcg gga ttt tcg tgg aca gac ccc aaa act tta aag ccc gcc aag cgg 768
 Ala Gly Phe Ser Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys Arg
 245 250 255

cgc aat ctt gtg tcc atg gtt ccg caa aca ccg acc gat att ttg tat 816
 Arg Asn Leu Val Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu Tyr
 260 265 270

gaa tca acc gtg cat gca gag ctc gca cgc tct gat aaa gat gcc gca 864
 Glu Ser Thr Val His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala Ala
 275 280 285

gca ccc gcc ggc acc acg cgg gaa atc ctg gat tca ctg gtc ccg aat 912
 Ala Pro Ala Gly Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro Asn
 290 295 300

atc ccg gac cat ctc cac cca cgt gat cta tca gaa ggc caa aag ctc 960
 Ile Pro Asp His Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys Leu
 305 310 315 320

tcc ctc gcg ctg tcc atc caa ctc gcc gca aaa ccc cgc gtg gta ttt 1008
 Ser Leu Ala Leu Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val Phe
 325 330 335

ttc gac gaa ccc acc cgc ggc cta gac tac gac ggc aag aaa tcc ctc 1056
 Phe Asp Glu Pro Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser Leu
 340 345 350

gcc cgc tcc ttc caa caa ctc gca gac gac ggc cac gcc att ttg gtg 1104
 Ala Arg Ser Phe Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu Val
 355 360 365

gtc acc cac gac gtg gaa ttc tct gca ctg tgc gcc gac cga gtg ttg 1152
 Val Thr His Asp Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val Leu
 370 375 380

ttt atg gcc tct gga aag atc atc tcc gat ggc aca gcc gta gaa atc 1200
 Phe Met Ala Ser Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu Ile
 385 390 395 400

ctc ccc gca tca ccg gct tac gcc cca caa gtc gca aaa atc acc gcc 1248
 Leu Pro Ala Ser Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr Ala
 405 410 415

ggc atc caa gag gaa tca cac tgg ctc aca gtc tcg gcc gtg aaa gct 1296
 Gly Ile Gln Glu Glu Ser His Trp Leu Thr Val Ser Ala Val Lys Ala
 420 425 430

gcg cta ggg cat ggt gaa atc tca tgatcaacgc catcacactc aag 1343
 Ala Leu Gly His Gly Glu Ile Ser
 435 440

His Ile Glu Val Ser Ala Lys
145 150

<210> 109
<211> 392
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(369)
<223> FRXA00828

<400> 109
gag cac caa ttt gtg gcg cgc act gtg cgt gat gag cta gaa att ggt 48
Glu His Gln Phe Val Ala Arg Thr Val Arg Asp Glu Leu Glu Ile Gly
1 5 10 15

ccg aaa atc atg aaa gtt gat gca agc gag cgc atc gag gag ttg ctt 96
Pro Lys Ile Met Lys Val Asp Ala Ser Glu Arg Ile Glu Glu Leu Leu
20 25 30

gat cgg ttg cgc ctc cgc cac tta gaa aat gct aat ccg ttt acc ttg 144
Asp Arg Leu Arg Leu Arg His Leu Glu Asn Ala Asn Pro Phe Thr Leu
35 40 45

agt ggt gga gaa aag cgc cgc cta tct gtg gcg aca gcc ttg gtg gca 192
Ser Gly Gly Glu Lys Arg Arg Leu Ser Val Ala Thr Ala Leu Val Ala
50 55 60

gca ccg aaa ctt ctc att ttg gat gag cct acg ttt ggc caa gat ccc 240
Ala Pro Lys Leu Leu Ile Leu Asp Glu Pro Thr Phe Gly Gln Asp Pro
65 70 75 80

gag acc ttc aca gag ctg gtg acg atg ttg cgt gaa tta aca gac aac 288
Glu Thr Phe Thr Glu Leu Val Thr Met Leu Arg Glu Leu Thr Asp Asn
85 90 95

gga atc agc att gtg tca gta acc cat gat cct gat ttc atc gca gcg 336
Gly Ile Ser Ile Val Ser Val Thr His Asp Pro Asp Phe Ile Ala Ala
100 105 110

ctg ggc gat cac cac att gag gtg agc gcg aag tgaacctgct gatcaaaatt 389
Leu Gly Asp His His Ile Glu Val Ser Ala Lys
115 120

aat 392

<210> 110
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 110
Glu His Gln Phe Val Ala Arg Thr Val Arg Asp Glu Leu Glu Ile Gly
1 5 10 15

Pro Lys Ile Met Lys Val Asp Ala Ser Glu Arg Ile Glu Glu Leu Leu
20 25 30


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<210> 111
<211> 703
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> RXN03020

<400> 111
cgccgcagca ggactcatcg gtgccgccat ttcactcggc cccatccttc gcgtcgaacc 60
acgctccgca ctcatgaacg cataagaaaa ggaacctcac atg act ctc cac gtt 115
Met Thr Leu His Val
1 5

tca aat ctc aat ctg acc gtc gcc gac gga tcc acc tca cgc acc ctg 163
Ser Asn Leu Asn Leu Thr Val Ala Asp Gly Ser Thr Ser Arg Thr Leu
10 15 20

ctc aac aac ata cac ttt tgg atg tcc aac cag gcg aag tcg tcg gta 211
Leu Asn Asn Ile His Phe Trp Met Ser Asn Gln Ala Lys Ser Ser Val
25 30 35

tca ccg gcc cat ccg gct ccg gaa aat cca ccc tac tcg ccg tcc tcg 259
Ser Pro Ala His Pro Ala Pro Glu Asn Pro Pro Tyr Ser Pro Ser Ser
40 45 50

gct gcc tcc aaa gcg ccc gat tcc ggc acc gcg acg ctc ggc gac atc 307
Ala Ala Ser Lys Ala Pro Asp Ser Gly Thr Ala Thr Leu Gly Asp Ile
55 60 65

gac ctg ctc aac ccc caa aac cga gct gct tta cga cgc aac cac cta 355
Asp Leu Leu Asn Pro Gln Asn Arg Ala Ala Leu Arg Arg Asn His Leu
70 75 80 85

gga att gtc ttc caa cag cca aac ctg ctc ccc tcg ttg act gtc ctc 403
Gly Ile Val Phe Gln Gln Pro Asn Leu Leu Pro Ser Leu Thr Val Leu
90 95 100

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gac caa ctg ctg ctc att ccc cgg ctc ggc agg atc ctc ccg ccc agc 451
Asp Gln Leu Leu Ile Pro Arg Leu Gly Arg Ile Leu Pro Pro Ser
105 110 115

cgc agc gca cgc acc caa cac aaa gac aaa gcc ctt tca ctt ctg aac 499
 Arg Ser Ala Arg Thr Gln His Lys Asp Lys Ala Leu Ser Leu Leu Asn
 120 125 130

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tcc atc gga ctc ggc gac tta gca aaa cgc aag gtc agc gaa cta tcc    547
Ser Ile Gly Leu Gly Asp Leu Ala Lys Arg Lys Val Ser Glu Leu Ser
      135                      140                      145
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ggt gga caa caa gcc cgc gtt aac ttg gcc cgc gcg ctg atg aac tcc 595
Gly Gly Gln Gln Ala Arg Val Asn Leu Ala Arg Ala Leu Met Asn Ser
150 155 160 165

ccc aag ctc ctg ctt gtc gat gaa ccc acc gcc gcc ctc gat caa cat 643
Pro Lys Leu Leu Leu Val Asp Glu Pro Thr Ala Ala Leu Asp Gln His
170 175 180

tcc gcc agc gaa gtc acc gaa cta atc gtc tcg atg gcc cac caa tac 691
Ser Ala Ser Glu Val Thr Glu Leu Ile Val Ser Met Ala His Gln Tyr
185 190 195

aac gcc ccc aca 703
Asn Ala Pro Thr
200

<210> 112

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

Met Thr Leu His Val Ser Asn Leu Asn Leu Thr Val Ala Asp Gly Ser
1 5 10 15

Thr Ser Arg Thr Leu Leu Asn Asn Ile His Phe Trp Met Ser Asn Gln
20 25 30

Ala Lys Ser Ser Val Ser Pro Ala His Pro Ala Pro Glu Asn Pro Pro
35 40 45

Tyr Ser Pro Ser Ser Ala Ala Ser Lys Ala Pro Asp Ser Gly Thr Ala
50 55 60

Thr Leu Gly Asp Ile Asp Leu Leu Asn Pro Gln Asn Arg Ala Ala Leu
65 70 75 80

Arg Arg Asn His Leu Gly Ile Val Phe Gln Gln Pro Asn Leu Leu Pro
85 90 95

Ser Leu Thr Val Leu Asp Gln Leu Leu Leu Ile Pro Arg Leu Gly Arg
100 105 110

Ile Leu Pro Pro Ser Arg Ser Ala Arg Thr Gln His Lys Asp Lys Ala
115 120 125

Leu Ser Leu Leu Asn Ser Ile Gly Leu Gly Asp Leu Ala Lys Arg Lys
130 135 140

Val Ser Glu Leu Ser Gly Gly Gln Gln Ala Arg Val Asn Leu Ala Arg
145 150 155 160

Ala Leu Met Asn Ser Pro Lys Leu Leu Leu Val Asp Glu Pro Thr Ala
165 170 175

Ala Leu Asp Gln His Ser Ala Ser Glu Val Thr Glu Leu Ile Val Ser
180 185 190

Met Ala His Gln Tyr Asn Ala Pro Thr
195 200

<210> 113

<211> 614

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(591)

<223> RXN00726

<400> 113

aac gcg ggt cgc ttg tat gtc gat ggc gat ctc att ggc tac cga gag	48
Asn Ala Gly Arg Leu Tyr Val Asp Gly Asp Leu Ile Gly Tyr Arg Glu	
1 5 10 15	
cgc gat ggc gtg ctg tac gaa atc tct gag aag gac gcc gcc aag cag	96
Arg Asp Gly Val Leu Tyr Glu Ile Ser Glu Lys Asp Ala Ala Lys Gln	
20 25 30	
cgc tcc gat atc ggc atg gtg ttc cag aac ttc aac ctc ttc ccc cac	144
Arg Ser Asp Ile Gly Met Val Phe Gln Asn Phe Asn Leu Phe Pro His	
35 40 45	
cgc acg gtg atc gag aac atc atc gaa gct ccc atc cac gtg aag aag	192
Arg Thr Val Ile Glu Asn Ile Ile Glu Ala Pro Ile His Val Lys Lys	
50 55 60	
cag ccc gaa agc aag gcc cgc gca cgt gcc atg gag ctg ctt gag cag	240
Gln Pro Glu Ser Lys Ala Arg Ala Arg Ala Met Glu Leu Leu Glu Gln	
65 70 75 80	
gtc ggc ctc gcc cac aag gcg gac gcc tac ccc gtc caa ctg tcg ggt	288
Val Gly Leu Ala His Lys Ala Asp Ala Tyr Pro Val Gln Leu Ser Gly	
85 90 95	
ggt cag cag cag cgc gtt gca att gcc cgc gcc gtc gcc atg gag cca	336
Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Ala Met Glu Pro	
100 105 110	
aag ctc atg ctt ttc gac gaa ccc acc agc gct ttg gac cct gaa ctc	384
Lys Leu Met Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Leu	
115 120 125	
gtc ggt gaa gtc ctg cga gtg atg aaa cag ctc gcc gac gac ggc atg	432
Val Gly Glu Val Leu Arg Val Met Lys Gln Leu Ala Asp Asp Gly Met	
130 135 140	

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acc atg ctt gtt gtc acc cac gaa atg ggc ttc gcc cac gaa gtc gcc 480
Thr Met Leu Val Val Thr His Glu Met Gly Phe Ala His Glu Val Ala
145 150 155 160

gac cag gtc gtg ttc atg gcc gat gga gtt gtc gtt gaa gcc gga acc 528
Asp Gln Val Val Phe Met Ala Asp Gly Val Val Val Glu Ala Gly Thr
165 170 175

ccc gaa caa gtt ctg gac aat cca aag gaa cag cgc acc aaa gac ttc 576
Pro Glu Gln Val Leu Asp Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe
180 185 190

ctg tct tct ctg ctc taaccttttc gggctcttaaa aaa 614
Leu Ser Ser Leu Leu
195

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<210> 114
<211> 197
<212> PRT
<213> Corynebacterium glutamicum

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<400> 114
Asn Ala Gly Arg Leu Tyr Val Asp Gly Asp Leu Ile Gly Tyr Arg Glu
 1 5 10 15

Arg Asp Gly Val Leu Tyr Glu Ile Ser Glu Lys Asp Ala Ala Lys Gln
20 25 30

Arg Ser Asp Ile Gly Met Val Phe Gln Asn Phe Asn Leu Phe Pro His
35 40 45

Arg Thr Val Ile Glu Asn Ile Ile Glu Ala Pro Ile His Val Lys Lys
50 55 60

Gln Pro Glu Ser Lys Ala Arg Ala Arg Ala Met Glu Leu Leu Glu Gln
65 70 75 80

Val Gly Leu Ala His Lys Ala Asp Ala Tyr Pro Val Gln Leu Ser Gly
85 90 95

Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Ala Met Glu Pro
100 105 110

Lys Leu Met Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Leu
115 120 125

Val Gly Glu Val Leu Arg Val Met Lys Gln Leu Ala Asp Asp Gly Met
130 135 140

Thr Met Leu Val Val Thr His Glu Met Gly Phe Ala His Glu Val Ala
145 150 155 160

Asp Gln Val Val Phe Met Ala Asp Gly Val Val Val Glu Ala Gly Thr
165 170 175

Pro Glu Gln Val Leu Asp Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe
180 185 190

Leu Ser Ser Leu Leu
195

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BGI-131CP

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<220>  
<221> CDS  
<222> (101)..(742)  
<223> RXN02570
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cattgggttcc				gcagcggggtt	ccggaggacg	tgccttaaac	atg	aat	cct	ttg	aca	115					
							Met	Asn	Pro	Leu	Thr	5					
							1										
tggttc	atc	att	ggc	gca	ttc	agc	atg	tggttc	atc	gtg	gtg	ctg	ggc	gtt	aat	163	
Trp	Ile	Ile	Gly	Ala	Phe	Ser	Met	Trp	Ile	Val	Val	Leu	Gly	Val	Asn		
				10					15	20							
aag	ctt	ggt	tta	agc	atc	gca	gtg	atc	atc	atc	gcg	cag	gtc	gtg	gcg	211	
Lys	Leu	Gly	Leu	Ser	Ile	Ala	Val	Ile	Ile	Ile	Ala	Gln	Val	Val	Ala		
				25					30	35							
atg	att	cgg	gtg	cgc	aat	gta	tct	gtg	ttg	gct	tca	aca	gca	ttg	tta	259	
Met	Ile	Arg	Val	Arg	Asn	Val	Ser	Val	Leu	Ala	Ser	Thr	Ala	Leu	Leu		
				40					45	50							
tgc	gtt	cct	gca	ttg	gcc	tgc	atg	gcg	ctg	att	cac	atg	cgc	tat	tct	307	
Ser	Val	Pro	Ala	Leu	Ala	Ser	Met	Ala	Leu	Ile	His	Met	Pro	Tyr	Ser		
				55					60	65							
tcc	gac	ggc	tggttc	ttg	att	gct	ctt	acc	ttg	acg	gct	cgt	ttt	agt	gcg	355	
Ser	Asp	Gly	Trp	Leu	Ile	Ala	Leu	Thr	Leu	Thr	Ala	Arg	Phe	Ser	Ala		
				70					75	80							
									85								
ttg	atg	tct	att	ttc	ctc	ctt	gca	gca	aca	gcg	att	act	att	cct	gag	403	
Leu	Met	Ser	Ile	Phe	Leu	Leu	Ala	Ala	Thr	Ala	Ile	Thr	Ile	Pro	Glu		
				90					95	100							
ctg	gtg	aaa	tcc	cta	tat	cgt	tggttc	ccc	aag	ctg	gcg	tat	atc	gtg	ggt	451	
Leu	Val	Lys	Ser	Leu	Tyr	Arg	Trp	Pro	Lys	Leu	Ala	Tyr	Ile	Val	Gly		
				105					110	115							
tct	gca	ttg	cag	atg	att	ccg	cag	ggt	aaa	cag	acc	ttg	gcg	ttg	gtt	499	
Ser	Ala	Leu	Gln	Met	Ile	Pro	Gln	Gly	Lys	Gln	Thr	Leu	Ala	Leu	Val		
				120					125	130							
cgt	gat	gcc	aat	gct	ttg	cgc	ggg	cgc	agc	gtt	aaa	ggt	ccc	gtg	cgc	547	
Arg	Asp	Ala	Asn	Ala	Leu	Arg	Gly	Arg	Ser	Val	Lys	Gly	Pro	Val	Arg		
				135					140	145							
gcg	gtg	aaa	tat	gtg	ggt	ttg	ccc	ctg	att	aca	cat	tta	ctt	agt	gca	595	
Ala	Val	Lys	Tyr	Val	Gly	Leu	Pro	Leu	Ile	Thr	His	Leu	Leu	Ser	Ala		
				150					155	160							
									165								
ggt	gcc	gcg	cga	gcg	att	ccc	ttg	gag	gtc	gca	ggc	ctg	gac	agg	cgc	643	
Gly	Ala	Ala	Arg	Ala	Ile	Pro	Leu	Glu	Val	Ala	Gly	Leu	Asp	Arg	Pro		

170	175	180	
ggg ccg cgt acg gtg ttg gtt gag gtg gtg gag ggg cgc gtc gaa aag			691
Gly Pro Arg Thr Val Leu Val Glu Val Val Glu Gly Arg Val Glu Lys			
185	190	195	
cat tgt cgc tgg ttg ttg ccg ctt ttg gca gtc ggg atg gcg tgg tgg			739
His Cys Arg Trp Leu Leu Pro Leu Leu Ala Val Gly Met Ala Trp Trp			
200	205	210	
ctc taactcaaat cgtcggaccg tcc			765
Leu			

<210> 116

<211> 214

<212> PRT

<213> Corynebacterium glutamicum

<400> 116

Met Asn Pro Leu Thr Trp Ile Ile Gly Ala Phe Ser Met Trp Ile Val		
1	5	10
		15

Val Leu Gly Val Asn Lys Leu Gly Leu Ser Ile Ala Val Ile Ile Ile		
20	25	30

Ala Gln Val Val Ala Met Ile Arg Val Arg Asn Val Ser Val Leu Ala		
35	40	45

Ser Thr Ala Leu Leu Ser Val Pro Ala Leu Ala Ser Met Ala Leu Ile		
50	55	60

His Met Pro Tyr Ser Ser Asp Gly Trp Leu Ile Ala Leu Thr Leu Thr		
65	70	75
		80

Ala Arg Phe Ser Ala Leu Met Ser Ile Phe Leu Leu Ala Ala Thr Ala		
85	90	95

Ile Thr Ile Pro Glu Leu Val Lys Ser Leu Tyr Arg Trp Pro Lys Leu		
100	105	110

Ala Tyr Ile Val Gly Ser Ala Leu Gln Met Ile Pro Gln Gly Lys Gln		
115	120	125

Thr Leu Ala Leu Val Arg Asp Ala Asn Ala Leu Arg Gly Arg Ser Val		
130	135	140

Lys Gly Pro Val Arg Ala Val Lys Tyr Val Gly Leu Pro Leu Ile Thr		
145	150	155
		160

His Leu Leu Ser Ala Gly Ala Ala Arg Ala Ile Pro Leu Glu Val Ala		
165	170	175

Gly Leu Asp Arg Pro Gly Pro Arg Thr Val Leu Val Glu Val Val Glu		
180	185	190

Gly Arg Val Glu Lys His Cys Arg Trp Leu Leu Pro Leu Leu Ala Val		
195	200	205

Gly Met Ala Trp Trp Leu

<210> 117
<211> 957
<212> DNA
<213> Corynebacterium glutamicum

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<220>  
<221> CDS  
<222> (101)..(934)  
<223> RXN02354
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<400> 117																	
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ttgtaaaggc cgattctgct gtgaaggaag ccgctaagcc atg act aaa cga aca																	115
Met Thr Lys Arg Thr																	5
1																	
aaa gga ctc atc ctc aac tac gcc gga gtg gtg ttc atc ctc ttc tgg																	163
Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val Phe Ile Leu Phe Trp																	20
10 15																	
gga cta gct ccc ttc tac tgg atg gtt atc acc gca ctg cgc gat tcc																	211
Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr Ala Leu Arg Asp Ser																	35
25 30																	
aag cac acc ttt gac acc acc cca tgg cca acg cac gtc acc ttg gat																	259
Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr His Val Thr Leu Asp																	50
40 45																	
aac ttc cgg gac gca ctg gcc acc gac aaa ggc aac aac ttc ctc gca																	307
Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly Asn Asn Phe Leu Ala																	65
55 60																	
gcc att ggc aac tca ctg gtc atc agc gtc acc aca aca gcg atc gct																	355
Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr Thr Thr Ala Ile Ala																	85
70 75 80																	
gtt ctc gtg gga gtg ttc acc gcc tac gct cta gcc cga ctg gaa ttc																	403
Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu Ala Arg Leu Glu Phe																	100
90 95																	
ccg ggc aaa ggc att gtc acc ggc atc atc ttg gca gcc tcc atg ttc																	451
Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu Ala Ala Ser Met Phe																	115
105 110																	
ccc ggc atc gcc ctg gtc act ccg ctg ttc cag ctc ttc ggt gac ctc																	499
Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln Leu Phe Gly Asp Leu																	130
120 125 130																	
aac tgg atc ggc acc tac caa gcg ctg att atc ccg aac att tcc ttc																	547
Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile Pro Asn Ile Ser Phe																	145
135 140 145																	
gcg cta cct ctg acg atc tac acg ctc gta tcc ttc ttc agg caa ctg																	595
Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser Phe Phe Arg Gln Leu																	165
150 155 160 165																	
ccc tgg gaa ctc gaa gaa tca gca cgt gtc gac ggc gcc aca cgt ggc																	643

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Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp Gly Ala Thr Arg Gly
      170                      175                      180

caa gcc ttc cgc atg atc ctg ctt cct cta gca gcg ccc gca cta ttt    691
Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala Ala Pro Ala Leu Phe
      185                      190                      195

acc acc gcg atc ctc gca ttc att gca acg tgg aac gaa ttc atg ctg    739
Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp Asn Glu Phe Met Leu
      200                      205                      210

gcc cgc caa cta tcc aac acc tcc aca gag cca gtg acc gtt gcg atc    787
Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro Val Thr Val Ala Ile
      215                      220                      225

gca agg ttc acc gga cca agc tcc ttc gaa tac ccc tac gcc tct gtc    835
Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr Pro Tyr Ala Ser Val
      230                      235                      240                      245

atg gca gcg gga gct ttg gtg acc atc cca ctg atc atc atg gtt ctc    883
Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu Ile Ile Met Val Leu
      250                      255                      260

atc ttc caa cgc cgc atc gtc tcc gga ctc acc gca ggt ggc gtg aaa    931
Ile Phe Gln Arg Arg Ile Val Ser Gly Leu Thr Ala Gly Gly Val Lys
      265                      270                      275

gcc tagactagat actcatgagt gct    957
Ala

<210> 118
<211> 278
<212> PRT
<213> Corynebacterium glutamicum

<400> 118
Met Thr Lys Arg Thr Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val
  1           5           10           15

Phe Ile Leu Phe Trp Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr
      20           25           30

Ala Leu Arg Asp Ser Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr
      35           40           45

His Val Thr Leu Asp Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly
      50           55           60

Asn Asn Phe Leu Ala Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr
      65           70           75           80

Thr Thr Ala Ile Ala Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu
      85           90           95

Ala Arg Leu Glu Phe Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu
      100          105          110

Ala Ala Ser Met Phe Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln
      115          120          125

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[illegible]

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<210> 119
<211> 889
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(889)
<223> FRXA02354
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<400> 119
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ttgtaaaggc cgattctgct gtgaaggaag ccgctaagcc atg act aaa cga aca 115
Met Thr Lys Arg Thr
1 5

aaa gga ctc atc ctc aac tac gcc gga gtg gtg ttc atc ctc ttc tgg 163
Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val Phe Ile Leu Phe Trp
10 15 20

gga cta gct ccc ttc tac tgg atg gtt atc acc gca ctg cgc gat tcc 211
Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr Ala Leu Arg Asp Ser
25 30 35

aag cac acc ttt gac acc acc cca tgg cca acg cac gtc acc ttg gat 259
Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr His Val Thr Leu Asp
40 45 50

aac ttc cgg gac gca ctg gcc acc gac aaa ggc aac aac ttc ctc gca 307
 Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly Asn Asn Phe Leu Ala
 55 60 65

gcc att ggc aac tca ctg gtc atc agc gtc acc aca aca gcg atc gct 355
 Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr Thr Thr Ala Ile Ala
 70 75 80 85

gtt ctc gtg gga gtg ttc acc gcc tac gct cta gcc cga ctg gaa ttc 403
 Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu Ala Arg Leu Glu Phe
 90 95 100

ccg ggc aaa ggc att gtc acc ggc atc atc ttg gca gcc tcc atg ttc 451
 Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu Ala Ala Ser Met Phe
 105 110 115

ccc ggc atc gcc ctg gtc act ccg ctg ttc cag ctc ttc ggt gac ctc 499
 Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln Leu Phe Gly Asp Leu
 120 125 130

aac tgg atc ggc acc tac caa gcg ctg att atc ccg aac att tcc ttc 547
 Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile Pro Asn Ile Ser Phe
 135 140 145

gcg cta cct ctg acg atc tac acg ctc gta tcc ttc ttc agg caa ctg 595
 Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser Phe Phe Arg Gln Leu
 150 155 160 165

ccc tgg gaa ctc gaa gaa tca gca cgt gtc gac ggc gcc aca cgt ggc 643
 Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp Gly Ala Thr Arg Gly
 170 175 180

caa gcc ttc cgc atg atc ctg ctt cct cta gca gcg ccc gca cta ttt 691
 Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala Ala Pro Ala Leu Phe
 185 190 195

acc acc gcg atc ctc gca ttc att gca acg tgg aac gaa ttc atg ctg 739
 Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp Asn Glu Phe Met Leu
 200 205 210

gcc cgc caa cta tcc aac acc tcc aca gag cca gtg acc gtt gcg atc 787
 Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro Val Thr Val Ala Ile
 215 220 225

gca agg ttc acc gga cca agc tcc ttc gaa tac ccc tac gcc tct gtc 835
 Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr Pro Tyr Ala Ser Val
 230 235 240 245

atg gca gcg gga gct ttg gtg acc atc cca ctg atc atc atg gtt ctc 883
 Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu Ile Ile Met Val Leu
 250 255 260

atc ttc 889
 Ile Phe

<210> 120

<211> 263

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

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Met Thr Lys Arg Thr Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val
 1          5          10          15

Phe Ile Leu Phe Trp Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr
      20          25          30

Ala Leu Arg Asp Ser Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr
      35          40          45

His Val Thr Leu Asp Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly
      50          55          60

Asn Asn Phe Leu Ala Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr
      65          70          75          80

Thr Thr Ala Ile Ala Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu
      85          90          95

Ala Arg Leu Glu Phe Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu
      100          105          110

Ala Ala Ser Met Phe Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln
      115          120          125

Leu Phe Gly Asp Leu Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile
      130          135          140

Pro Asn Ile Ser Phe Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser
      145          150          155          160

Phe Phe Arg Gln Leu Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp
      165          170          175

Gly Ala Thr Arg Gly Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala
      180          185          190

Ala Pro Ala Leu Phe Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp
      195          200          205

Asn Glu Phe Met Leu Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro
      210          215          220

Val Thr Val Ala Ile Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr
      225          230          235          240

Pro Tyr Ala Ser Val Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu
      245          250          255

Ile Ile Met Val Leu Ile Phe
      260

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<210> 121

<211> 1251

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

[illegible]

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<400> 122
Met  Ala  Thr  Val  Thr  Phe  Lys  Asp  Ala  Ser  Leu  Ser  Tyr  Pro  Gly  Ala
  1          5          10          15

Lys  Glu  Pro  Thr  Val  Lys  Lys  Phe  Asn  Leu  Glu  Ile  Ala  Asp  Gly  Glu
          20          25          30

Phe  Leu  Val  Leu  Val  Gly  Pro  Ser  Gly  Cys  Gly  Lys  Ser  Thr  Thr  Leu
          35          40          45

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Arg 50	Met	Leu	Ala	Gly	Leu	Glu 55	Asn	Val	Thr	Asp	Gly 60	Ala	Ile	Phe	Ile
Gly 65	Asp	Lys	Asp	Val	Thr 70	His	Val	Ala	Pro	Arg 75	Asp	Arg	Asp	Ile	Ala 80
Met	Val	Phe	Gln	Asn 85	Tyr	Ala	Leu	Tyr	Pro 90	His	Met	Thr	Val	Gly 95	Glu
Asn	Met	Gly	Phe 100	Ala	Leu	Lys	Ile	Ala 105	Gly	Lys	Ser	Gln	Asp 110	Glu	Ile
Asn	Lys	Arg 115	Val	Asp	Glu	Ala	Ala 120	Ala	Thr	Leu	Gly	Leu 125	Thr	Glu	Phe
Leu 130	Glu	Arg	Lys	Pro	Lys	Ala 135	Leu	Ser	Gly	Gly	Gln 140	Arg	Gln	Arg	Val
Ala 145	Met	Gly	Arg	Ala	Ile 150	Val	Arg	Asn	Pro	Gln 155	Val	Phe	Leu	Met	Asp 160
Glu	Pro	Leu	Ser	Asn 165	Leu	Asp	Ala	Lys	Leu 170	Arg	Val	Gln	Thr	Arg 175	Thr
Gln	Ile	Ala	Ala 180	Leu	Gln	Arg	Lys	Leu 185	Gly	Val	Thr	Thr	Val 190	Tyr	Val
Thr	His	Asp 195	Gln	Thr	Glu	Ala	Leu 200	Thr	Met	Gly	Asp	Arg 205	Ile	Ala	Val
Leu	Lys 210	Asp	Gly	Tyr	Leu	Gln 215	Gln	Val	Gly	Ala	Pro 220	Arg	Glu	Leu	Tyr
Asp 225	Arg	Pro	Ala	Asn	Val 230	Phe	Val	Ala	Gly	Phe 235	Ile	Gly	Ser	Pro	Ala 240
Met	Asn	Leu	Gly	Thr 245	Phe	Ser	Val	Lys	Asp 250	Gly	Asp	Ala	Thr	Ser 255	Gly
His	Ala	Arg	Ile 260	Lys	Leu	Ser	Pro	Glu 265	Thr	Leu	Ala	Ala	Met 270	Thr	Pro
Glu	Asp	Asn 275	Gly	Arg	Ile	Thr	Ile 280	Gly	Phe	Arg	Pro	Glu 285	Ala	Leu	Glu
Ile 290	Ile	Pro	Glu	Gly	Glu	Ser 295	Thr	Asp	Leu	Ser	Ile 300	Pro	Ile	Lys	Leu
Asp 305	Phe	Val	Glu	Glu	Leu 310	Gly	Ser	Asp	Ser	Phe 315	Leu	Tyr	Gly	Lys	Leu 320
Val	Gly	Glu	Gly	Asp 325	Leu	Gly	Ser	Ser	Ser 330	Glu	Asp	Val	Pro	Glu 335	Ser
Gly	Gln	Ile	Val 340	Val	Arg	Ala	Ala 345	Pro	Asn	Ala	Ala	Pro	Ala 350	Pro	Gly
Ser	Val	Phe 355	His	Ala	Arg	Ile	Val 360	Glu	Gly	Gly	Gln	His 365	Asn	Phe	Ser
Ala	Ser	Thr	Gly	Lys	Arg	Leu	Pro								

375

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<220>  
<221> CDS  
<222> (101)..(1228)  
<223> FRXA00001
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<400> 123																		
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gatcgttcgg cacgtacctg ccgatggagg agattctgca atg gca acc gta acg																		115
Met Ala Thr Val Thr																		5
1																		
ttc aaa gat gct tcc cta agc tac ccg gga gca aag gaa ccc acc gtc																		163
Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala Lys Glu Pro Thr Val																		20
10																		
aag aaa ttc aac ctg gaa atc gcc gat ggc gag ttc ctc gtc ctc gtc																		211
Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val																		35
25																		
30																		
ggc cct tcc ggc tgt ggt aaa tcc acc acg ctg cgc atg ctg gcc ggt																		259
Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Met Leu Ala Gly																		50
40																		
45																		
50																		
ttg gaa aac gtt act gac ggt gcc att ttc atc gga gac aag gac gtt																		307
Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile Gly Asp Lys Asp Val																		65
55																		
60																		
65																		
acc cac gtt gca ccg cgt gac cgt gac atc gcc atg gtt ttc cag aac																		355
Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala Met Val Phe Gln Asn																		85
70																		
75																		
80																		
85																		
tat gct ctc tac ccc cac atg acc gtg ggc gag aac atg ggc ttc gca																		403
Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu Asn Met Gly Phe Ala																		100
90																		
95																		
100																		
ctg aag atc gcc ggc aag tcc caa gac gag atc aat aag cgc gtc gac																		451
Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile Asn Lys Arg Val Asp																		115
105																		
110																		
115																		
gaa gcc gcc gcc act ttg ggc ctg acc gaa ttc ttg gag cgc aag ccg																		499
Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe Leu Glu Arg Lys Pro																		130
120																		
125																		
130																		
aag gcc ctg tcc ggt ggt cag cgt cag cgt gtg gcc atg ggc cgc gcc																		547
Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala																		145
135																		
140																		
145																		
att gtt cgc aac ccg cag gtc ttt ctc atg gat gag ccg ctg tct aac																		595
Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp Glu Pro Leu Ser Asn																		165
150																		
155																		
160																		
165																		
ctc gat gcc aaq ctg cgt gtt caq acc cgt acc caq att gca gcc ctg																		643

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Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr Gln Ile Ala Ala Leu
      170                      175                      180

cag cgc aag ctt ggg gtt acc acc gtt tac gtc acc cac gac cag acg 691
Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Thr
      185                      190                      195

gag gcc ttg acc atg ggt gac cgc atc gcg gtg ctg aag gat ggc tac 739
Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val Leu Lys Asp Gly Tyr
      200                      205                      210

ctg cag cag gtt ggc gcg ccc cga gag ctt tat gac cgc ccc gcc aac 787
Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr Asp Arg Pro Ala Asn
      215                      220                      225

gtc ttc gtc gcc ggc ttc atc ggc tcc cca gcc atg aac ttg ggc acc 835
Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala Met Asn Leu Gly Thr
      230                      235                      240

ttc tcg gtc aag gat ggt gac gct acc tct ggt cac gct cgc atc aag 883
Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly His Ala Arg Ile Lys
      250                      255                      260

ctt tcc ccg gaa acc ctc gcc gcc atg acg ccg gag gat aat ggc cgc 931
Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro Glu Asp Asn Gly Arg
      265                      270                      275

atc acc att ggt ttc cgc ccg gag gca ctg gag atc att ccg gaa ggc 979
Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu Ile Ile Pro Glu Gly
      280                      285                      290

gag tcc acc gat ctt tcc atc cca atc aag ctc gac ttc gtg gag gaa 1027
Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu Asp Phe Val Glu Glu
      295                      300                      305

ctc ggt tcc gat tcc ttc ctc tac ggc aag ctg gta ggc gag ggc gac 1075
Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu Val Gly Glu Gly Asp
      310                      315                      320

ctt gga tcc tcc agc gag gat gtc ccc gag tcc ggc caa atc gtc gtc 1123
Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser Gly Gln Ile Val Val
      330                      335                      340

cgc gct gct ccg aac gcc gcg cct gct ccg ggc agt gtt ttc cac gca 1171
Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly Ser Val Phe His Ala
      345                      350                      355

cgc atc gtg gag ggc ggc cag cac aac ttc tcg gcg tcg act ggc aag 1219
Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser Ala Ser Thr Gly Lys
      360                      365                      370

cgc ctc cct taagcccgcg tacggctac ccc 1251
Arg Leu Pro
      375

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<210> 124

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 125																	
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aaaccacaa tgtgtacttg tgctggtaat ttagtagaac atg gca acg gtc aca																	115
Met Ala Thr Val Thr																	5
1																	
ttc gac aag gtc aca atc cgg tac ccc gcc gcg gag cgc gca aca gtt																	163
Phe Asp Lys Val Thr Ile Arg Tyr Pro Gly Ala Glu Arg Ala Thr Val																	20
10																	
15																	
cat gag ctt gat tta gat atc gct gat gcc gag ttt ttg gtg ctc gtc																	211
His Glu Leu Asp Leu Asp Ile Ala Asp Gly Glu Phe Leu Val Leu Val																	35
25																	
30																	
gcc cct tcg ggt tgt ggt aaa tcc act acg ctg cgt gct ttg gcg ggg																	259
Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Ala Leu Ala Gly																	50
40																	
45																	
50																	
ctt gag gcc gtg gag tcg ggt gtg atc aaa att gat gcc aag gat gtc																	307
Leu Glu Gly Val Glu Ser Gly Val Ile Lys Ile Asp Gly Lys Asp Val																	65
55																	
60																	
65																	
act ggt cag gag ccg gcg gat cgc gat atc gcg atg gtg ttc cag aat																	355
Thr Gly Gln Glu Pro Ala Asp Arg Asp Ile Ala Met Val Phe Gln Asn																	85
70																	
75																	
80																	
tat gct ctg tac cct cac atg acg gtg gcg aag aat atg ggt ttt gcg																	403
Tyr Ala Leu Tyr Pro His Met Thr Val Ala Lys Asn Met Gly Phe Ala																	100
90																	
95																	
100																	
ctg aag ttg gct aag ctg ccg cag gcg cag atc gat gcg aag gtc aat																	451
Leu Lys Leu Ala Lys Leu Pro Gln Ala Gln Ile Asp Ala Lys Val Asn																	115
105																	
110																	
115																	
gag gct gcg gaa att ctt ggg ttg acg gag ttt ttg gat cgc aag cct																	499
Glu Ala Glu Ile Leu Gly Leu Thr Glu Phe Leu Asp Arg Lys Pro																	120
120																	
125																	
130																	

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aag gat tta tcg ggt ggt cag cgt cag cgt gtg gcg atg ggt cgc gcg 547
Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
135 140 145

ttg gtg cgt gat ccg aag gtg ttc ctc atg gat gag ccg ctg tcc aac 595
Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp Glu Pro Leu Ser Asn
150 155 160 165

ctg gat gcg aaa ttg cgc gtg caa acc cgc gcg gag gtc gct gct ttg 643
Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala Glu Val Ala Ala Leu
170 175 180

cag cgt cgc ctg ggc acc acc acg gtg tat gtc acc cac gat cag gtt 691
Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val Thr His Asp Gln Val
185 190 195

gag gca atg acg atg ggc gat cgg gtt gcg gtg ctc aag gac ggg ttg 739
Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Lys Asp Gly Leu
200 205 210

ctg cag cag gtc gca ccg ccc agg gag ctt tac gac gcc ccg gtc aac 787
Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr Asp Ala Pro Val Asn
215 220 225

gaa ttc gtt gcg ggc ttc atc ggc tcg ccg tcc atg aac ctc ttc cct 835
Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser Met Asn Leu Phe Pro
230 235 240 245

gcc aac ggg cac aag atg ggt gtg cgc ccg gag aag atg ctg gtc aat 883
Ala Asn Gly His Lys Met Gly Val Arg Pro Glu Lys Met Leu Val Asn
250 255 260

gag acc cct gag ggt ttc aca agc att gat gct gtg gtg gat atc gtc 931
Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala Val Val Asp Ile Val
265 270 275

gag gag ctt ggc tcc gaa tcg tat gtt tat gcc act tgg gag ggc cac 979
Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala Thr Trp Glu Gly His
280 285 290

cgc ctg gtg gcc cgt tgg gtg gaa ggc ccc gtg cca gcc cct ggc acg 1027
Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val Pro Ala Pro Gly Thr
295 300 305

cct gtg act ttt tcc tat gat gcg gcg cag gcg cat cat ttc gat ctg 1075
Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala His His Phe Asp Leu
310 315 320 325

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 Leu Lys Arg Leu Thr
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 Arg Ile Ala Ser Ile Ser Met Ala Ser Met Leu Ala Ala Ala Ser Leu
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 Tyr Thr Glu Glu Thr Gly Val Lys Val Lys Val Val Thr Ala Ala Ser
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 Gly Ser Tyr Glu Gln Thr Leu Lys Ala Glu Ile Gly Lys Asp Glu Ala
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 Pro Thr Leu Phe Gln Val Asn Gly Pro Ala Gly Phe Ile Thr Trp Gln
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 135 140 145
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 Asp Lys Tyr Ile Ala Thr Ser Gly Ala Lys Ile Lys Ser Thr Asp Glu
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Lys Trp

1369

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Val Thr Ala Ala Ser Gly Ser Tyr Glu Gln Thr Leu Lys Ala Glu Ile
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Gly Lys Asp Glu Ala Pro Thr Leu Phe Gln Val Asn Gly Pro Ala Gly
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Phe Ile Thr Trp Gln Asp Tyr Met Ala Asp Met Ser Asp Thr Glu Val
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Ala Lys Gln Leu Thr Asp Asp Ile Pro Pro Leu Thr Thr Glu Asp Gly
115 120 125
Glu Val Arg Gly Val Pro Phe Ala Val Glu Gly Phe Gly Ile Ile Tyr
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145 150 155 160
Lys Ser Thr Asp Glu Ile Thr Ser Tyr Gln Lys Leu Lys Glu Val Ala
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Glu Asp Met Gln Ala Lys Lys Asp Glu Leu Gly Ile Glu Gly Ala Phe
180 185 190
Ala Ser Thr Ser Leu Thr Ser Ser Glu Asp Trp Arg Trp Gln Thr His
195 200 205
Leu Ala Asn Ala Pro Ile Trp Gln Glu Tyr Gln Asp Lys Gly Val Glu
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Asp Thr Asn Glu Ile Glu Phe Ser Tyr Asn Lys Glu Tyr Lys Asn Leu
225 230 235 240
Phe Asp Leu Tyr Leu Glu Asn Ser Thr Val Glu Lys Ser Leu Ala Pro
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 Ser Gly Asn Val Val Lys Glu Asp Lys Ile Lys Phe Leu Pro Met Tyr
 290 295 300
 Met Gly Leu Pro Asp Glu Glu Lys His Gly Ile Asn Val Gly Thr Glu
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 Asn Tyr Leu Gly Val Asn Ser Glu Ala Ser Glu Val Asp Gln Gln Ala
 325 330 335
 Thr Lys Asp Phe Val Asp Trp Leu Phe Thr Ser Glu Ala Gly Lys Glu
 340 345 350
 His Val Val Lys Asp Leu Gly Phe Ile Ala Pro Phe Glu Ser Tyr Thr
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 370 375 380
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 Val Leu Lys Val Ser
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 Asp Leu Thr Val Gly Asn Asn Phe Val His Asn Val Ser Phe Glu Val
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 aac ccc ggc gaa cgc gtc ggc atc atc ggc gag tcc ggc tca ggc aaa 211
 Asn Pro Gly Glu Arg Val Gly Ile Ile Gly Glu Ser Gly Ser Gly Lys
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 tca ctc acc gcg cta tcc atc atg ggt tta act gac ctg ccg acc acc 259
 Ser Leu Thr Ala Leu Ser Ile Met Gly Leu Thr Asp Leu Pro Thr Thr
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BGI-131CP


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Asn Ala Ala Glu Lys Thr Thr Arg Val Ala Glu Val Ile Thr Gln Val
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Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro His Glu Phe Ser Gly
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Gly Gln Arg Gln Arg Ile Ser Ile Ala Arg Ala Leu Ala Ile Lys Pro
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gcg atc ctg ctt gcc gac gaa cct gtc tcc gcc ctc gat gtg tcc gta 1315
Ala Ile Leu Leu Ala Asp Glu Pro Val Ser Ala Leu Asp Val Ser Val
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Ile Thr Leu Val Phe Val Ser His Asp Leu Ala Val Val Arg His Leu
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tgc aca acc gtg tgg gtg atg gaa cag gga cga gtc ctt gag caa ggg 1459
Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg Val Leu Glu Gln Gly
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Pro	Leu	Leu	Gly	Trp	Asn	Ala	Ala	Glu	Lys	Thr	Thr	Arg	Val	Ala	Glu
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Val Ile Thr Gln Val Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro
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His Glu Phe Ser Gly Gly Gln Arg Gln Arg Ile Ser Ile Ala Arg Ala
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Leu Ala Ile Lys Pro Ala Ile Leu Leu Ala Asp Glu Pro Val Ser Ala
 385 390 395 400

Leu Asp Val Ser Val Arg Lys Gln Val Leu Asp Leu Leu Gln Gln Leu
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Val Glu Glu Tyr Gly Ile Thr Leu Val Phe Val Ser His Asp Leu Ala
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Val Val Arg His Leu Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg
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 Val Val Val Gln Lys Gln Ile Val Asp Leu Leu Leu Arg Leu Thr Lys
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 Glu Arg Gly Thr Ala Leu Leu Phe Ile Thr His Asp Leu Gly Leu Ile
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 Ala Arg Thr Cys Glu Arg Leu Leu Val Met Lys Ser Gly Glu Thr Val
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Glu Gln Gly Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr Glu Tyr
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Val Val Val Gln Lys Gln Ile Val Asp Leu Leu Leu Arg Leu Thr Lys
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Glu Arg Gly Thr Ala Leu Leu Phe Ile Thr His Asp Leu Gly Leu Ile
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Ala Arg Thr Cys Glu Arg Leu Leu Val Met Lys Ser Gly Glu Thr Val
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Glu Arg Gly Asp Thr Glu Ala Ile Leu Arg Ser Pro Ala His Ser Tyr
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Thr Gln Gln Leu Leu Asp Ala Ser Ile Leu Asp Gln Pro Glu Ile Ala
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Ser Asp Ser Gly Ala Pro Val Val Ile Asp Val Glu Glu Ala Ser Lys
 130 135 140

Ser Phe Lys Glu Thr Thr Ala Leu His Lys Val Ser Leu Ala Val Arg
 145 150 155 160

Lys Gly Asp Leu Leu Gly Ile Val Gly Gly Ser Gly Ser Gly Lys Thr
 165 170 175

Thr Leu Leu Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr Gly Thr
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Val Ala Val Thr Gly Gly Val Gln Met Val Phe Gln Asp Pro Gln Ser
 195 200 205

Ser Leu Asn Pro Arg Met Lys Ile Lys Asp Ile Val Ala Glu Pro Leu
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Thr Gln Val Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro His Glu
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 Glu Tyr Gly Ile Thr Leu Val Phe Val Ser His Asp Leu Ala Val Val
 305 310 315 320
 Arg His Leu Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg Val Leu
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 Met Thr Thr Asn Ile
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 Pro Gln Thr Pro Asn His Glu Gly Glu Gln Pro Leu Leu Glu Leu Lys
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 Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln Ser Val Ala Ile Val
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 Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala Met Ser Ile Ile Gly
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 Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro Met Thr Asn Leu Asn
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 Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu Ser Leu Arg Ala Asn
 120 125 130

cac gtg gtt cca ggc tca gag atg gac aag cgc gtg gca gaa gtt ctg 547
 His Val Val Pro Gly Ser Glu Met Asp Lys Arg Val Ala Glu Val Leu
 135 140 145

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 Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg Ala Lys Gln Tyr Pro
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 His Glu Phe Ser Gly Gly Met Arg Gln Arg Ala Leu Ile Ala Ile Gly
 170 175 180

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 185 190 195

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 200 205 210

acc aag gat ctc ggc acc gca gtg cta ttt att acc cac gac ttg ggc 787
 Thr Lys Asp Leu Gly Thr Ala Val Leu Phe Ile Thr His Asp Leu Gly
 215 220 225

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 230 235 240 245

atc gtg gag tcc ggg cca tca ttg aag att ctg cgc aat cca cag cac 883
 Ile Val Glu Ser Gly Pro Ser Leu Lys Ile Leu Arg Asn Pro Gln His
 250 255 260

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 Pro Tyr Thr Gln Arg Leu Val Lys Ala Ala Pro Ser Leu Ala Ser Ala
 265 270 275

cgt att caa agt gcg cag gaa caa ggc att gaa tct gca gaa ctg ctc 979
 Arg Ile Gln Ser Ala Gln Glu Gln Gly Ile Glu Ser Ala Glu Leu Leu
 280 285 290

tct gca acg gcc gtt gct gag ggc act att cca gag atg gaa gaa aaa 1027
 Ser Ala Thr Ala Val Ala Glu Gly Thr Ile Pro Glu Met Glu Glu Lys
 295 300 305

gtt atc gag gtg aaa aac ctc acc cgc gaa ttt gat atc cgc ggt gcc 1075
 Val Ile Glu Val Lys Asn Leu Thr Arg Glu Phe Asp Ile Arg Gly Ala
 310 315 320 325

cgt ggc gat aag aag aag ctg aag gcc gtt gat gat gtg tcc ttc ttc	1123
Arg Gly Asp Lys Lys Lys Leu Lys Ala Val Asp Asp Val Ser Phe Phe	
330 335 340	
gta cgt aaa ggc acc acc acc gca ctt gtg ggt gaa tcc ggt tct ggt	1171
Val Arg Lys Gly Thr Thr Thr Ala Leu Val Gly Glu Ser Gly Ser Gly	
345 350 355	
aaa tcc acc gtg gcc aac atg gtg ctc aac ctt ctc gag cca acc agc	1219
Lys Ser Thr Val Ala Asn Met Val Leu Asn Leu Leu Glu Pro Thr Ser	
360 365 370	
gga gag gtg ctc tac aac ggc acc gat ctt acg tcc ttg agc cac aag	1267
Gly Glu Val Leu Tyr Asn Gly Thr Asp Leu Thr Ser Leu Ser His Lys	
375 380 385	
gaa atc ttc caa atg cga cgc aaa ctg cag gtg gtg ttc cag aac ccc	1315
Glu Ile Phe Gln Met Arg Arg Lys Leu Gln Val Val Phe Gln Asn Pro	
390 395 400 405	
tac ggc tct ctt gat ccg atg tac tcc atc tac cgg tgt att gag gaa	1363
Tyr Gly Ser Leu Asp Pro Met Tyr Ser Ile Tyr Arg Cys Ile Glu Glu	
410 415 420	
ccg ctg acc atc cac aag gtt ggt gga gac cgc aag gca cgc gaa gct	1411
Pro Leu Thr Ile His Lys Val Gly Gly Asp Arg Lys Ala Arg Glu Ala	
425 430 435	
cgc gtc gct gaa ctt ctc gat atg gtg tcc atg ccc agg tcc acc atg	1459
Arg Val Ala Glu Leu Leu Asp Met Val Ser Met Pro Arg Ser Thr Met	
440 445 450	
cgc cgc tac ccc aac gag ctt tcc ggt ggc caa cgt cag cgc atc gcc	1507
Arg Arg Tyr Pro Asn Glu Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala	
455 460 465	
atc gcc cgt gca ttg gca ctg aat cca gaa gtg atc gtg ttg gat gaa	1555
Ile Ala Arg Ala Leu Ala Leu Asn Pro Glu Val Ile Val Leu Asp Glu	
470 475 480 485	
gcg gtt tcc gct ttg gac gtg ttg gtt cag aac cag atc ctc acc ctg	1603
Ala Val Ser Ala Leu Asp Val Leu Val Gln Asn Gln Ile Leu Thr Leu	
490 495 500	
ctt gca gaa ctt cag cag gaa ctg aag ctc acc tat ttg ttc atc acc	1651
Leu Ala Glu Leu Gln Gln Glu Leu Lys Leu Thr Tyr Leu Phe Ile Thr	
505 510 515	
cac gac ttg gcc gtt gtt cga caa acc gcc gac gat gtt gtg gtg atg	1699
His Asp Leu Ala Val Val Arg Gln Thr Ala Asp Asp Val Val Val Met	
520 525 530	
caa aag gga cga atc gtt gaa aag ggt cgt acc gac gac atc ttc aac	1747
Gln Lys Gly Arg Ile Val Glu Lys Gly Arg Thr Asp Asp Ile Phe Asn	
535 540 545	
gat cct cag cag cac tac acc cgc gat ttg atc aat gcg gta cct ggt	1795
Asp Pro Gln Gln His Tyr Thr Arg Asp Leu Ile Asn Ala Val Pro Gly	
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[illegible]

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<400> 137

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Gln	Met	Arg	Arg	Lys	Leu	Gln	Val	Val	Phe	Gln	Asn	Pro	Tyr	Gly	Ser	
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Leu	Asp	Pro	Met	Tyr	Ser	Ile	Tyr	Arg	Cys	Ile	Glu	Glu	Pro	Leu	Thr	
		35					40					45				
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Ile	His	Lys	Val	Gly	Gly	Asp	Arg	Lys	Ala	Arg	Glu	Ala	Arg	Val	Val	
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gaa	ctt	ctc	gat	atg	gtg	tcc	atg	ccc	agg	tcc	acc	atg	cgc	cgc	tac	240
Glu	Leu	Leu	Asp	Met	Val	Ser	Met	Pro	Arg	Ser	Thr	Met	Arg	Arg	Tyr	
65					70				75						80	
ccc	aac	gag	ctt	tcc	ggc	ggc	caa	cgt	cag	cgc	atc	gcc	atc	gcc	cgt	288
Pro	Asn	Glu	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Ala	Ile	Ala	Arg	
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gca	ttg	gca	ctg	aat	cca	gaa	gtg	atc	gtg	ttg	gat	gaa	gcg	gtt	tcc	336
Ala	Leu	Ala	Leu	Asn	Pro	Glu	Val	Ile	Val	Leu	Asp	Glu	Ala	Val	Ser	
			100					105						110		
gct	ttg	gac	gtg	ttg	gtt	cag	aac	cag	atc	ctc	acc	ctg	ctt	gca	gaa	384
Ala	Leu	Asp	Val	Leu	Val	Gln	Asn	Gln	Ile	Leu	Thr	Leu	Leu	Ala	Glu	
		115					120					125				
ctt	cag	cag	gaa	ctg	aag	ctc	acc	tat	ttg	ttc	atc	acc	cac	gac	ttg	432
Leu	Gln	Gln	Glu	Leu	Lys	Leu	Thr	Tyr	Leu	Phe	Ile	Thr	His	Asp	Leu	
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Ala	Val	Val	Arg	Gln	Thr	Ala	Asp	Asp	Val	Val	Val	Met	Gln	Lys	Gly	
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cga	atc	gtt	gaa	aag	ggc	cgt	acc	gac	gac	atc	ttc	aac	gat	cct	cag	528
Arg	Ile	Val	Glu	Lys	Gly	Arg	Thr	Asp	Asp	Ile	Phe	Asn	Asp	Pro	Gln	
			165					170						175		
cag	cac	tac	acc	cgc	gat	ttg	atc	aat	gcg	gta	cct	ggc	ctg	gga	atc	576
Gln	His	Tyr	Thr	Arg	Asp	Leu	Ile	Asn	Ala	Val	Pro	Gly	Leu	Gly	Ile	
		180						185					190			
gag	ttg	ggc	act	gga	gaa	aac	ctg	gtt	taacccgcac	agcctcacta						623
Glu	Leu	Gly	Thr	Gly	Glu	Asn	Leu	Val								
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aac																626

<210> 138

<211> 201

<212> PRT

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Leu	Ile	Tyr	Ala	Leu	Val	Phe	Leu	Met	Pro	Gly	Asp	Pro	Val	Gln	Ala	
			25					30					35			
ttg	gga	ggg	gac	cgc	ggc	cta	acc	gag	gct	gcg	gcc	gag	aaa	atc	cgt	259
Leu	Gly	Gly	Asp	Arg	Gly	Leu	Thr	Glu	Ala	Ala	Ala	Glu	Lys	Ile	Arg	
			40				45					50				
caa	gaa	tac	aat	ctt	gat	aaa	ccc	ttc	atc	gtt	caa	tac	ctc	ctg	tac	307
Gln	Glu	Tyr	Asn	Leu	Asp	Lys	Pro	Phe	Ile	Val	Gln	Tyr	Leu	Leu	Tyr	
	55					60					65					
atc	aag	ggc	atc	ttc	gtc	tta	gat	ttt	gga	aca	acc	ttc	tct	ggg	cag	355
Ile	Lys	Gly	Ile	Phe	Val	Leu	Asp	Phe	Gly	Thr	Thr	Phe	Ser	Gly	Gln	
	70				75				80						85	
cca	gtt	att	gat	gtg	atg	gcc	agg	gcc	ttc	ccc	gtc	acc	atc	aaa	ctc	403
Pro	Val	Ile	Asp	Val	Met	Ala	Arg	Ala	Phe	Pro	Val	Thr	Ile	Lys	Leu	
				90					95					100		
gcc	atc	atg	gcc	ctg	ctg	ttt	gaa	tca	atc	ctc	ggc	att	atc	ttt	ggg	451
Ala	Ile	Met	Ala	Leu	Leu	Phe	Glu	Ser	Ile	Leu	Gly	Ile	Ile	Phe	Gly	
			105				110						115			
gtc	atc	gca	ggg	att	cgc	cgc	gga	gga	atc	ttc	gac	tcc	acc	gtg	ctg	499
Val	Ile	Ala	Gly	Ile	Arg	Arg	Gly	Gly	Ile	Phe	Asp	Ser	Thr	Val	Leu	
			120				125					130				
gtc	ctt	tct	ctg	ata	gtc	atc	gca	gtc	ccc	acc	ttc	gtc	att	ggg	ttc	547
Val	Leu	Ser	Leu	Ile	Val	Ile	Ala	Val	Pro	Thr	Phe	Val	Ile	Gly	Phe	
	135					140					145					
gtg	ctg	cag	ttc	tta	gtc	ggc	gtg	aaa	tgg	ggc	tta	ctg	ccc	gtc	acc	595
Val	Leu	Gln	Phe	Leu	Val	Gly	Val	Lys	Trp	Gly	Leu	Leu	Pro	Val	Thr	
	150				155				160					165		
gta	ggg	tcc	aac	aca	tca	ata	acg	gcg	ctg	atc	atg	ccg	gct	gtc	gta	643
Val	Gly	Ser	Asn	Thr	Ser	Ile	Thr	Ala	Leu	Ile	Met	Pro	Ala	Val	Val	
			170						175					180		
ctg	ggg	gca	gta	tcc	ttc	gcc	tac	gtt	ctt	cgc	ctc	acc	aga	caa	tcc	691
Leu	Gly	Ala	Val	Ser	Phe	Ala	Tyr	Val	Leu	Arg	Leu	Thr	Arg	Gln	Ser	
			185				190						195			
gtg	agc	gaa	aac	ctc	cgc	gct	gat	tac	gtt	cga	acc	gct	cga	gca	aaa	739
Val	Ser	Glu	Asn	Leu	Arg	Ala	Asp	Tyr	Val	Arg	Thr	Ala	Arg	Ala	Lys	
		200					205					210				
ggc	atg	tcc	gga	ttc	aac	gtg	atg	aac	cgc	cat	gtg	ctt	cga	aac	tca	787
Gly	Met	Ser	Gly	Phe	Asn	Val	Met	Asn	Arg	His	Val	Leu	Arg	Asn	Ser	
	215					220					225					
ctg	att	ccc	gtt	gcc	acc	ttc	ctg	ggc	gcc	gat	ctc	ggg	gca	ctg	atg	835
Leu	Ile	Pro	Val	Ala	Thr	Phe	Leu	Gly	Ala	Asp	Leu	Gly	Ala	Leu	Met	
	230				235				240						245	
ggg	gga	gcg	att	gtc	acc	gaa	ggg	atc	ttc	ggc	atc	aac	ggg	gtc	ggg	883
Gly	Gly	Ala	Ile	Val	Thr	Glu	Gly	Ile	Phe	Gly	Ile	Asn	Gly	Val	Gly	

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Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro Val Thr Ile Lys Leu
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gcc atc atg gcc ctg ctg ttt gaa tca atc ctc ggc att atc ttt ggt 451
Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu Gly Ile Ile Phe Gly
105 110 115

gtc atc gca ggt att cgc cgc gga gga atc ttc gac tcc acc gtg ctg 499
Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe Asp Ser Thr Val Leu
120 125 130

gtc ctt tct ctg ata gtc atc gca gtc ccc acc ttc gtc att ggt ttc 547
Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr Phe Val Ile Gly Phe
135 140 145

gtg ctg cag ttc tta ntc ggc gtg aaa tgg ggc tta ctg ccc gtc acc 595
Val Leu Gln Phe Leu Xaa Gly Val Lys Trp Gly Leu Leu Pro Val Thr
150 155 160 165

gta ggt tcc aac aca tca ata acg gcg ctg atc atg ccg gct gtc gta 643
Val Gly Ser Asn Thr Ser Ile Thr Ala Leu Ile Met Pro Ala Val Val
170 175 180

ctg ggt gca gta tcg ttc gcc tac gtt ctt cgc ctc acc aga caa tcc 691
Leu Gly Ala Val Ser Phe Ala Tyr Val Leu Arg Leu Thr Arg Gln Ser
185 190 195

gtg agc gaa aac ctc cgc gct gat tac gtt cga acc gct cga gca aaa 739
Val Ser Glu Asn Leu Arg Ala Asp Tyr Val Arg Thr Ala Arg Ala Lys
200 205 210

ggc atg tcc gga ttc aac gtg atg aac cgc cat gtg ctt cga aac tca 787
Gly Met Ser Gly Phe Asn Val Met Asn Arg His Val Leu Arg Asn Ser
215 220 225

ctg att ccc gtt gcc acc ttc ctg ggc gcc gat ctc ggt gca ctg atg 835
Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp Leu Gly Ala Leu Met
230 235 240 245

ggg gga gcg att gtc acc gaa ggt atc ttc ggc atc aac ggt gtc ggt 883
Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly Ile Asn Gly Val Gly
250 255 260

gga acg ctc tac cag gcc att ttg aaa ggt gaa ccc acc acg gtt gtc 931
Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu Pro Thr Thr Val Val
265 270 275

tcc att gtc act gtg ctg gtc atc gtc tac atc atc gcc aac ctt ctc 979
Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile Ile Ala Asn Leu Leu
280 285 290

gtg gac ttg atc tac gcc gtt ctc gat ccg agg atc cgc tat gcc 1024
Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg Ile Arg Tyr Ala
295 300 305

taataatgaa ttccacacaa acc 1047

<210> 142
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<212> PRT


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<210> 143
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<213> Corynebacterium glutamicum
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<222> (101)..(889)  
<223> RXN00431
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Ala	Val	Asp	Ala	Ala	Phe	Met	Ala	Lys	Ala	Arg	Asp	Arg	Leu	Gln	Ala		
			185					190					195				
ctc	gtc	gaa	cga	tcc	ggc	atc	ctc	gtc	ttc	gcc	tcc	cac	tcc	aac	gac		739
Leu	Val	Glu	Arg	Ser	Gly	Ile	Leu	Val	Phe	Ala	Ser	His	Ser	Asn	Asp		
		200					205					210					
ttc	ctc	gcc	caa	ctc	tgc	aac	acc	gca	ctc	tgg	gtc	gac	cac	gga	caa		787
Phe	Leu	Ala	Gln	Leu	Cys	Asn	Thr	Ala	Leu	Trp	Val	Asp	His	Gly	Gln		
	215					220					225						
atc	cgc	gaa	gcg	gga	cta	gtt	cca	gac	gtg	gtg	gaa	gcc	tac	gaa	ggc		835
Ile	Arg	Glu	Ala	Gly	Leu	Val	Pro	Asp	Val	Val	Glu	Ala	Tyr	Glu	Gly		
230					235					240					245		
aag	ggc	gcc	ggc	gac	cac	gtc	cgc	aga	ctc	ctc	acc	cgc	atg	gaa	gaa		883
Lys	Gly	Ala	Gly	Asp	His	Val	Arg	Arg	Leu	Leu	Thr	Arg	Met	Glu	Glu		
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gaa	aag	tagctcctgc	gtttcggggtt	tgc													912
Glu	Lys																
<p><210> 144</p> <p><211> 263</p> <p><212> PRT</p> <p><213> Corynebacterium glutamicum</p> <p><400> 144</p>																	
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			20					25					30				
Gly	Ala	Ile	Gly	Arg	Asn	Gln	Asp	Asn	Val	Val	Val	Val	Glu	Ala	Leu		
		35				40						45					
Lys	Asn	Val	Asn	Leu	His	Leu	Arg	Glu	Gly	Asp	Arg	Val	Gly	Leu	Val		
	50					55					60						
Gly	His	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Leu	Arg	Leu	Leu	Ser	Gly		
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Ile	Tyr	Glu	Pro	Thr	Arg	Gly	Ser	Ala	Asp	Ile	Arg	Gly	Arg	Val	Ala		
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Pro	Val	Phe	Asp	Leu	Gly	Val	Gly	Met	Asp	Pro	Glu	Ile	Ser	Gly	Tyr		
			100					105					110				
Glu	Asn	Ile	Ile	Ile	Arg	Gly	Leu	Phe	Leu	Gly	Gln	Thr	Arg	Lys	Gln		
		115					120					125					
Met	Lys	Ala	Lys	Met	Glu	Glu	Ile	Ala	Asp	Phe	Thr	Glu	Leu	Gly	Glu		
	130					135					140						

Tyr Leu Ser Met Pro Leu Arg Thr Tyr Ser Thr Gly Met Arg Ile Arg
 145 150 155 160
 Leu Ala Leu Gly Val Val Thr Ser Ile Glu Pro Glu Ile Leu Leu Leu
 165 170 175
 Asp Glu Gly Ile Gly Ala Val Asp Ala Ala Phe Met Ala Lys Ala Arg
 180 185 190
 Asp Arg Leu Gln Ala Leu Val Glu Arg Ser Gly Ile Leu Val Phe Ala
 195 200 205
 Ser His Ser Asn Asp Phe Leu Ala Gln Leu Cys Asn Thr Ala Leu Trp
 210 215 220
 Val Asp His Gly Gln Ile Arg Glu Ala Gly Leu Val Pro Asp Val Val
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 245 250 255
 Thr Arg Met Glu Glu Glu Lys
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 <222> (101)..(775)
 <223> FRXA00431

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 Met Val Ser Ile Asp
 1 5
 aca tac aac gcc tgc gtc gac ttc ccc atc ttc gac gcc aaa tcc cgc 163
 Thr Tyr Asn Ala Cys Val Asp Phe Pro Ile Phe Asp Ala Lys Ser Arg
 10 15 20
 tcc atg aag aaa gcc ttc ctc ggc gca gcc ggc gga gca atc ggg cgc 211
 Ser Met Lys Lys Ala Phe Leu Gly Ala Ala Gly Gly Ala Ile Gly Arg
 25 30 35
 aat caa gac aac gtc gta gtc gtc gaa gcg ctg aag aac gtc aac ctg 259
 Asn Gln Asp Asn Val Val Val Val Glu Ala Leu Lys Asn Val Asn Leu
 40 45 50
 cac ttg cgc gaa ggt gac cgg gtc gga ctc gtc ggc cac aac ggc gcc 307
 His Leu Arg Glu Gly Asp Arg Val Gly Leu Val Gly His Asn Gly Ala
 55 60 65
 ggc aaa tcc acc ctc ctg cga ctc ctc tcc ggc atc tac gaa ccc acc 355
 Gly Lys Ser Thr Leu Leu Arg Leu Leu Ser Gly Ile Tyr Glu Pro Thr
 70 75 80 85

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cgc gga agc gct gac atc cgt gga cgc gtc gcc ccc gtc ttc gac ctc 403
Arg Gly Ser Ala Asp Ile Arg Gly Arg Val Ala Pro Val Phe Asp Leu
          90                      95                      100

ggc gtc ggc atg gat cca gaa atc tcc ggc tac gaa aat atc atc atc 451
Gly Val Gly Met Asp Pro Glu Ile Ser Gly Tyr Glu Asn Ile Ile Ile
          105                      110                      115

cgc ggc ctc ttc ctc ggt caa acc cgc aaa cag atg aaa gcc aaa atg 499
Arg Gly Leu Phe Leu Gly Gln Thr Arg Lys Gln Met Lys Ala Lys Met
          120                      125                      130

gaa gaa atc gcc gac ttc acc gaa ctc ggc gaa tac ctc tcc atg cct 547
Glu Glu Ile Ala Asp Phe Thr Glu Leu Gly Glu Tyr Leu Ser Met Pro
          135                      140                      145

ctc cga acc tac tcc acc ggc atg cgc atc cgc cta gcc ctc ggc gtg 595
Leu Arg Thr Tyr Ser Thr Gly Met Arg Ile Arg Leu Ala Leu Gly Val
          150                      155                      160                      165

gtc acc tcc atc gag ccc gaa att ctg ctt ctt gat gaa ggc atc ggc 643
Val Thr Ser Ile Glu Pro Glu Ile Leu Leu Leu Asp Glu Gly Ile Gly
          170                      175                      180

gcc gtc gac gcc gcc ttc atg gcc aaa gcc cgc gac cgg ctc caa gcc 691
Ala Val Asp Ala Ala Phe Met Ala Lys Ala Arg Asp Arg Leu Gln Ala
          185                      190                      195

ctc gtc gaa cga tcc ggc atc ctc gtc ttc gcc tcc act caa cga ctt 739
Leu Val Glu Arg Ser Gly Ile Leu Val Phe Ala Ser Thr Gln Arg Leu
          200                      205                      210

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Ser Cys Gln Leu Cys Asn Thr Ala Leu Trp Val Asp
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<210> 146

<211> 225

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 146

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Gly Ala Ile Gly Arg Asn Gln Asp Asn Val Val Val Val Glu Ala Leu
          35                      40                      45

Lys Asn Val Asn Leu His Leu Arg Glu Gly Asp Arg Val Gly Leu Val
          50                      55                      60

Gly His Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Leu Leu Ser Gly
          65                      70                      75                      80

Ile Tyr Glu Pro Thr Arg Gly Ser Ala Asp Ile Arg Gly Arg Val Ala
          85                      90                      95

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325          330          335
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Ala Ile Ile Gly Ser Thr Gly Ser Gly Lys Thr Thr Leu Ile Gly Leu
340          345          350

gtt cct agg ctt ttc gac gtc acc gaa ggc gac gtt acc gtc gat ggc 1104
Val Pro Arg Leu Phe Asp Val Thr Glu Gly Asp Val Thr Val Asp Gly
355          360          365

acc gat gtt cgt gaa ttt gag ccg ctg aag ctg tgg gat cgg atc ggt 1152
Thr Asp Val Arg Glu Phe Glu Pro Leu Lys Leu Trp Asp Arg Ile Gly
370          375          380

ctt gtt ccg cag aag tcg ttc ctg ttt tct gga acg atc gcc agc aac 1200
Leu Val Pro Gln Lys Ser Phe Leu Phe Ser Gly Thr Ile Ala Ser Asn
385          390          395

ctg cgt tat ggc aat gaa gat gcc acg gaa acg cag ctg tgg cag gcg 1248
Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp Gln Ala
405          410          415

ctt gca att gct cag gcg gcg gac ttt gtg cgt gag atg cca gag ggt 1296
Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro Glu Gly
420          425          430

ctt gat tct gag att gct cag ggt gga acc aat gtt tct ggt ggt cag 1344
Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly Gly Gln
435          440          445

cgc cag cga cta gcc att gcc agg gcg ttg ttg aag caa cct gag atc 1392
Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro Glu Ile
450          455          460

tat att ttc gac gat tct ttc tcc gcc ctc gat gtg agc aca gac gcc 1440
Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr Asp Ala
465          470          475

gct ctt cgc cga gcg ctg agc acc aac ctg ccg gat gca acc aag ttg 1488
Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr Lys Leu
485          490          495

att gtc gcc cag cgt gtc agc acg att cga gat gcc gat cag att gtg 1536
Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln Ile Val
500          505          510

gtg ctt gat aac ggc gag gtt gtc ggt att gga acg cac acg aat ttg 1584
Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr Asn Leu
515          520          525

ctg aac acg tgc ggt acc tac cgt gaa att gtt gaa tcc caa gag act 1632
Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln Glu Thr
530          535          540

gcg cag gcg caa tca tgagtaatac tgcaggcccc cgc 1670
Ala Gln Ala Gln Ser
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<210> 148

<211> 549

<212> PRT

<213> Corynebacterium glutamicum

<400> 148

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Asn His Leu Leu Leu Leu Pro Thr Val Lys Ala Asp Ile Ile Asp Asn
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      20          25          30

Met Leu Ala Leu Thr Leu Val Gln Val Ala Cys Ala Ile Ala Gly Val
      35          40          45

Tyr Phe Gly Ser Lys Leu Ser Met Arg Val Gly Arg Asp Leu Arg Ser
      50          55          60

Ala Ile Phe Gly Lys Val Val Asn Phe Ser Glu Arg Glu Met Gly Gln
      65          70          75          80

Phe Gly Ala Pro Ser Leu Ile Thr Arg Asn Thr Asn Asp Val Gln Gln
      85          90          95

Val Gln Met Leu Val Gln Met Thr Ser Thr Leu Met Ile Ser Ala Pro
      100          105          110

Met Leu Ala Ile Gly Gly Ile Ile Met Ala Val Arg Gln Asp Leu Gly
      115          120          125

Leu Ser Trp Leu Met Val Val Ser Ile Pro Val Leu Ile Ile Val Val
      130          135          140

Ala Leu Ile Ile Val Arg Met Val Pro Leu Phe Gln Thr Met Gln Lys
      145          150          155          160

Arg Ile Asp Arg Ile Asn Gln Ile Ile Arg Glu Gln Leu Thr Gly Ile
      165          170          175

Arg Val Ile Arg Ala Phe Val Arg Glu Asp Val Glu Arg Glu Arg Phe
      180          185          190

Thr Thr Ala Ser Lys Asp Val Ala Asp Ile Gly Val Arg Thr Gly Asn
      195          200          205

Leu Met Ala Leu Met Phe Pro Ala Val Met Leu Ile Met Asn Leu Ser
      210          215          220

Ala Val Ala Val Ile Trp Phe Gly Ala Phe Gln Val Glu Ser Gly Glu
      225          230          235          240

Thr Gln Ile Gly Thr Leu Phe Ala Phe Leu Gln Tyr Ile Met Gln Ile
      245          250          255

Leu Met Gly Val Met Met Ala Ala Phe Met Phe Val Met Val Pro Arg
      260          265          270

Ala Ala Val Ser Ala Asp Arg Ile Gly Glu Val Leu Glu Thr Thr Pro
      275          280          285

Ser Val Gln Ala Pro Glu Thr Pro Ala Gln Pro Ser Thr Ser Ala Gly
      290          295          300

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Glu Ile Val Phe Asn Asn Ala Thr Phe Ala Tyr Pro Gly Ala Asp Asp
305 310 315 320

Pro Val Leu Asn Asn Val Ser Phe Arg Val Ala Pro Gly Ser Thr Thr
325 330 335

Ala Ile Ile Gly Ser Thr Gly Ser Gly Lys Thr Thr Leu Ile Gly Leu
340 345 350

Val Pro Arg Leu Phe Asp Val Thr Glu Gly Asp Val Thr Val Asp Gly
355 360 365

Thr Asp Val Arg Glu Phe Glu Pro Leu Lys Leu Trp Asp Arg Ile Gly
370 375 380

Leu Val Pro Gln Lys Ser Phe Leu Phe Ser Gly Thr Ile Ala Ser Asn
385 390 395 400

Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp Gln Ala
405 410 415

Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro Glu Gly
420 425 430

Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly Gly Gln
435 440 445

Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro Glu Ile
450 455 460

Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr Asp Ala
465 470 475 480

Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr Lys Leu
485 490 495

Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln Ile Val
500 505 510

Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr Asn Leu
515 520 525

Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln Glu Thr
530 535 540

Ala Gln Ala Gln Ser
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<210> 149

<211> 922

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(922)

<223> FRXA00732

<400> 149

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[illegible]

Asp Val Ala Ser Tyr Val Met Met Gly Asp Lys Gln Val Ser Ala Ser
 145 150 155 160
 Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro Lys Arg Gln Arg Thr Pro
 165 170 175
 Val Gly Asp Leu Ser Gly Gly Glu Arg Arg Arg Leu Gln Leu Thr Arg
 180 185 190
 Val Leu Met Ala Glu Pro Asn Val Leu Leu Leu Asp Glu Pro Thr Asn
 195 200 205
 Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu Glu Ser Leu Leu Asp Gly
 210 215 220
 Trp Pro Gly Thr Met Val Val Ile Ser His Asp Arg Tyr Leu Ile Glu
 225 230 235 240
 Arg Val Thr Asp Ser Thr Trp Ala Leu Phe Gly Asp Gly Lys Leu Thr
 245 250 255
 Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu Gln Arg Arg Ala Ala Met
 260 265 270
 Ala Ala Ala Glu Asp Ser Gly Val Leu Asn Leu Gly Ala Ala Thr Gln
 275 280 285
 Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln Ala Ala Thr Ser Val Glu
 290 295 300
 Ser Ser Gly Ile Ser Ser Gln Glu Arg His Arg Ile Thr Lys Glu Met
 305 310 315 320
 Asn Ala Leu Glu Arg Lys Met Gly Lys Leu Asp Gln Gln Met Asp Lys
 325 330 335
 Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu Ala Met Asp Thr Ile Lys
 340 345 350
 Leu Thr Glu Leu Asp Thr Lys Leu Arg Ala Val Gln Glu Glu His Gly
 355 360 365
 Glu Leu Glu Met Gln Trp Leu Glu Leu Gly Glu Glu Ile Glu Gly
 370 375 380

<210> 155

<211> 1142

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(1119)

<223> FRXA01808

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 Glu Ala Ala Glu Ala Leu Ile Ala Glu Val Pro Ala Pro Arg Asp Lys
 20 25 30

gtc gag ctc atg gca ttt tcc aag tcc agg caa ggc cgc gtt gtc att 144
 Val Glu Leu Met Ala Phe Ser Lys Ser Arg Gln Gly Arg Val Val Ile
 35 40 45

gaa ctt gaa gac gcc aca gta gcc acc cct gat gat cgc atc ctg gta 192
 Glu Leu Glu Asp Ala Thr Val Ala Thr Pro Asp Asp Arg Ile Leu Val
 50 55 60

gaa gac ctc acc tgg cgt ttg gct cca gga gag cgc atc ggt ctt gtc 240
 Glu Asp Leu Thr Trp Arg Leu Ala Pro Gly Glu Arg Ile Gly Leu Val
 65 70 75 80

ggc gtc aac ggc tcc ggc aaa acc acc ctg ctg cgc acc ctt gcc ggc 288
 Gly Val Asn Gly Ser Gly Lys Thr Thr Leu Leu Arg Thr Leu Ala Gly
 85 90 95

gag cag cca ctt cag gca ggc aaa cgc atc gaa ggc caa acc gtc aaa 336
 Glu Gln Pro Leu Gln Ala Gly Lys Arg Ile Glu Gly Gln Thr Val Lys
 100 105 110

ctg gga tgg ctc cgc cag gaa ctc gat gac cta gac ctc agc cgc cga 384
 Leu Gly Trp Leu Arg Gln Glu Leu Asp Asp Leu Asp Leu Ser Arg Arg
 115 120 125

ctc atc gac tgc gtt gaa gat gtc gct tcc tac gtg atg atg ggc gac 432
 Leu Ile Asp Cys Val Glu Asp Val Ala Ser Tyr Val Met Met Gly Asp
 130 135 140

aag cag gtc tcc gct tcc caa ttg gca gaa cgc ctc gga ttc tca ccc 480
 Lys Gln Val Ser Ala Ser Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro
 145 150 155 160

aag agg caa cgc acc cca gtt ggt gac ctg tcc ggt ggt gaa cgc cgc 528
 Lys Arg Gln Arg Thr Pro Val Gly Asp Leu Ser Gly Gly Glu Arg Arg
 165 170 175

cga ctc caa ctc acc cgc gtg ctc atg gcc gaa cca aac gtg ctg ctc 576
 Arg Leu Gln Leu Thr Arg Val Leu Met Ala Glu Pro Asn Val Leu Leu
 180 185 190

ctc gac gag ccc acc aac gac ctg gac att gac acc ctc caa gag ctg 624
 Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu
 195 200 205

gaa tcc ctt ctc gac gga tgg cca ggc acc atg gtg gtt atc tcc cac 672
 Glu Ser Leu Leu Asp Gly Trp Pro Gly Thr Met Val Val Ile Ser His
 210 215 220

gac cgt tac ctc atc gaa cgc gtc acc gac tcc acc tgg gca ctc ttc 720
 Asp Arg Tyr Leu Ile Glu Arg Val Thr Asp Ser Thr Trp Ala Leu Phe
 225 230 235 240

ggc gat ggc aag ctc acc aac ctg cca ggc gga att gaa gag tac ctg 768
 Gly Asp Gly Lys Leu Thr Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu
 245 250 255

cag cga cga gca gcg atg gcc gcg gcc gaa gac agt gga gtg ctg aac 816
 Gln Arg Arg Ala Ala Met Ala Ala Ala Glu Asp Ser Gly Val Leu Asn
 260 265 270

ttg ggt gcg gcc acg cag gct gga acc ttt tct gct gca aca gag cag 864
 Leu Gly Ala Ala Thr Gln Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln
 275 280 285

gct gcc act tct gtg gaa agt tcc gga att tct tcc caa gaa cgc cac 912
 Ala Ala Thr Ser Val Glu Ser Ser Gly Ile Ser Ser Gln Glu Arg His
 290 295 300

cgc atc acc aag gaa atg aac gcc ctg gag cgc aaa atg ggc aag ctt 960
 Arg Ile Thr Lys Glu Met Asn Ala Leu Glu Arg Lys Met Gly Lys Leu
 305 310 315 320

gac cag caa atg gac aag ctt aat cag cag ctg gct gat gca gcg gag 1008
 Asp Gln Gln Met Asp Lys Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu
 325 330 335

gcc atg gac acc ata aag ctg acc gag ctg gac acc aag ctg cgc gca 1056
 Ala Met Asp Thr Ile Lys Leu Thr Glu Leu Asp Thr Lys Leu Arg Ala
 340 345 350

gtg cag gaa gaa cac ggc gag ctg gaa atg cag tgg ctg gaa ctg ggc 1104
 Val Gln Glu Glu His Gly Glu Leu Glu Met Gln Trp Leu Glu Leu Gly
 355 360 365

gag gaa atc gag ggc tagttcatgc cgtcggcagg cga 1142
 Glu Glu Ile Glu Gly
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<210> 156
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 <212> PRT
 <213> Corynebacterium glutamicum

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Val Glu Leu Met Ala Phe Ser Lys Ser Arg Gln Gly Arg Val Val Ile
 35 40 45

Glu Leu Glu Asp Ala Thr Val Ala Thr Pro Asp Asp Arg Ile Leu Val
 50 55 60

Glu Asp Leu Thr Trp Arg Leu Ala Pro Gly Glu Arg Ile Gly Leu Val
 65 70 75 80

Gly Val Asn Gly Ser Gly Lys Thr Thr Leu Leu Arg Thr Leu Ala Gly
 85 90 95

Glu Gln Pro Leu Gln Ala Gly Lys Arg Ile Glu Gly Gln Thr Val Lys
 100 105 110

Leu Gly Trp Leu Arg Gln Glu Leu Asp Asp Leu Asp Leu Ser Arg Arg

115 120 125
 Leu Ile Asp Cys Val Glu Asp Val Ala Ser Tyr Val Met Met Gly Asp
 130 135 140
 Lys Gln Val Ser Ala Ser Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro
 145 150 155 160
 Lys Arg Gln Arg Thr Pro Val Gly Asp Leu Ser Gly Gly Glu Arg Arg
 165 170 175
 Arg Leu Gln Leu Thr Arg Val Leu Met Ala Glu Pro Asn Val Leu Leu
 180 185 190
 Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu
 195 200 205
 Glu Ser Leu Leu Asp Gly Trp Pro Gly Thr Met Val Val Ile Ser His
 210 215 220
 Asp Arg Tyr Leu Ile Glu Arg Val Thr Asp Ser Thr Trp Ala Leu Phe
 225 230 235 240
 Gly Asp Gly Lys Leu Thr Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu
 245 250 255
 Gln Arg Arg Ala Ala Met Ala Ala Ala Glu Asp Ser Gly Val Leu Asn
 260 265 270
 Leu Gly Ala Ala Thr Gln Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln
 275 280 285
 Ala Ala Thr Ser Val Glu Ser Ser Gly Ile Ser Ser Gln Glu Arg His
 290 295 300
 Arg Ile Thr Lys Glu Met Asn Ala Leu Glu Arg Lys Met Gly Lys Leu
 305 310 315 320
 Asp Gln Gln Met Asp Lys Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu
 325 330 335
 Ala Met Asp Thr Ile Lys Leu Thr Glu Leu Asp Thr Lys Leu Arg Ala
 340 345 350
 Val Gln Glu Glu His Gly Glu Leu Glu Met Gln Trp Leu Glu Leu Gly
 355 360 365
 Glu Glu Ile Glu Gly
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<210> 157

<211> 349

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(349)

<223> RXN02975

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<211> 732
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<223> RXN03116

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ttttgctcag gtactgtcac tggaatcggg aaggctgaaa atg ggg gag ggg gac 115
                                         Met Gly Glu Gly Asp
                                         1 5

gtc gaa aag cat ttt gct ttt ggt ctt aaa gct gcg aag cag cgt cgc 163
Val Glu Lys His Phe Ala Phe Gly Leu Lys Ala Ala Lys Gln Arg Arg
                        10 15 20

ttt ttc gcg cgt acc gtg gcc ctc atg cca cag aat cct act att cct 211
Phe Phe Ala Arg Thr Val Ala Leu Met Pro Gln Asn Pro Thr Ile Pro
                        25 30 35

gca ggt ctg agc gtt ttt gat tat gtg ctg ctg ggg cgt cat ccg cac 259
Ala Gly Leu Ser Val Phe Asp Tyr Val Leu Leu Gly Arg His Pro His
                        40 45 50

agt tac gcg ccg ggg cgt gct gat gat gag atc gtg aag cgg tgc ctc 307
Ser Tyr Ala Pro Gly Arg Ala Asp Asp Glu Ile Val Lys Arg Cys Leu
                        55 60 65

gct gat ctg aaa ttg gag cat ttc agc gac cgc ggc tta gac gaa ttg 355
Ala Asp Leu Lys Leu Glu His Phe Ser Asp Arg Gly Leu Asp Glu Leu
                        70 75 80 85

tcc ggc ggc gag cgt caa cgc gtc agc ctt gcc cgc gcg ctc gcc caa 403
Ser Gly Gly Glu Arg Gln Arg Val Ser Leu Ala Arg Ala Leu Ala Gln
                        90 95 100

gaa ccg cgc atc gtg ctt ctc gac gag ccg acc tcc gcg ctt gac atc 451
Glu Pro Arg Ile Val Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Ile
                        105 110 115

ggc cat gcg cag gaa acg ctt gag ctt atc gac gcc atc cgg cac cga 499
Gly His Ala Gln Glu Thr Leu Glu Leu Ile Asp Ala Ile Arg His Arg
                        120 125 130

ctc ggc ctc acc gtg atc gcg gcg atg cat gac ctc acc ctg act gcg 547
Leu Gly Leu Thr Val Ile Ala Ala Met His Asp Leu Thr Leu Thr Ala
                        135 140 145

caa tac ggc gat cgg gtg ctc atg atg aat ggt ggc cgc aaa gtt ttc 595
Gln Tyr Gly Asp Arg Val Leu Met Met Asn Gly Gly Arg Lys Val Phe
                        150 155 160 165

gag ggc act gca gcc gaa gtg ctc acc gcg cag ccg att tcg gag att 643
Glu Gly Thr Ala Ala Glu Val Leu Thr Ala Gln Arg Ile Ser Glu Ile
                        170 175 180

tat gat gcc act gtg att gtt gag gtt att gat ggg cgt ccc gtg gtg 691
Tyr Asp Ala Thr Val Ile Val Glu Val Ile Asp Gly Arg Pro Val Val
                        185 190 195

att ccg caa cgg tcg cac tgacctgttg tggcagacca gac 732
Ile Pro Gln Arg Ser His
                        200

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<210> 160
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 Asn Pro Thr Ile Pro Ala Gly Leu Ser Val Phe Asp Tyr Val Leu Leu
 35 40 45
 Gly Arg His Pro His Ser Tyr Ala Pro Gly Arg Ala Asp Asp Glu Ile
 50 55 60
 Val Lys Arg Cys Leu Ala Asp Leu Lys Leu Glu His Phe Ser Asp Arg
 65 70 75 80
 Gly Leu Asp Glu Leu Ser Gly Gly Glu Arg Gln Arg Val Ser Leu Ala
 85 90 95
 Arg Ala Leu Ala Gln Glu Pro Arg Ile Val Leu Leu Asp Glu Pro Thr
 100 105 110
 Ser Ala Leu Asp Ile Gly His Ala Gln Glu Thr Leu Glu Leu Ile Asp
 115 120 125
 Ala Ile Arg His Arg Leu Gly Leu Thr Val Ile Ala Ala Met His Asp
 130 135 140
 Leu Thr Leu Thr Ala Gln Tyr Gly Asp Arg Val Leu Met Met Asn Gly
 145 150 155 160
 Gly Arg Lys Val Phe Glu Gly Thr Ala Ala Glu Val Leu Thr Ala Gln
 165 170 175
 Arg Ile Ser Glu Ile Tyr Asp Ala Thr Val Ile Val Glu Val Ile Asp
 180 185 190
 Gly Arg Pro Val Val Ile Pro Gln Arg Ser His
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<210> 161
 <211> 390
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(367)
 <223> RXN03108

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	Met	Thr	Lys	Pro	Asn	
	1				5	
gct tcc gtc gag ctg aat acg atc acc aag tcc tac ggc tcc acc act						163
Ala Ser Val Glu Leu Asn Thr Ile Thr Lys Ser Tyr Gly Ser Thr Thr						
	10			15	20	
atc att ggc gat acg agc atc acc atc aac gac ggt gaa ttc gtc tcc						211
Ile Ile Gly Asp Thr Ser Ile Thr Ile Asn Asp Gly Glu Phe Val Ser						
	25		30		35	
ctc ctc gac cct tcc ggc tgc gga aaa tca aca att ctc aaa atg atc						259
Leu Leu Asp Pro Ser Gly Cys Gly Lys Ser Thr Ile Leu Lys Met Ile						
	40		45		50	
gcc gga ctg gcc tcc cca tcc acc ggc aca gtc agc gca ggc aac gaa						307
Ala Gly Leu Ala Ser Pro Ser Thr Gly Thr Val Ser Ala Gly Asn Glu						
	55		60		65	
gaa att aaa gga cca gga cct gac cga ggc atg gtt ttc caa gac cac						355
Glu Ile Lys Gly Pro Gly Pro Asp Arg Gly Met Val Phe Gln Asp His						
	70		75		80	85
gcc ctc ctg ccc tgattgaccg cacgcggcaa cat						390
Ala Leu Leu Pro						

<210> 162

<211> 89

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

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			20					25					30		

Gly	Glu	Phe	Val	Ser	Leu	Leu	Asp	Pro	Ser	Gly	Cys	Gly	Lys	Ser	Thr
			35				40					45			

Ile	Leu	Lys	Met	Ile	Ala	Gly	Leu	Ala	Ser	Pro	Ser	Thr	Gly	Thr	Val
	50					55					60				

Ser	Ala	Gly	Asn	Glu	Glu	Ile	Lys	Gly	Pro	Gly	Pro	Asp	Arg	Gly	Met
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Val	Phe	Gln	Asp	His	Ala	Leu	Leu	Pro
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<210> 163

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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1324)

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Phe Glu Asn Val Thr Arg Lys Tyr Ser Pro Gly Ala Arg Pro Ala Val
10 15 20

gac aag ctt aat ttg gaa atc gcc gac ggc gag ttc cta gtt ctc gtt 211
Asp Lys Leu Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val
25 30 35

gga ccc tca ggc tgt gga aag tcc act tct ttg cgc atg ctg gct ggt 259
Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu Arg Met Leu Ala Gly
40 45 50

ctt gag cct atc gac gag gga cgt cta ctg att gat ggt aaa gac gcc 307
Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile Asp Gly Lys Asp Ala
 55 60 65

acg gaa ctg cgt ccg cag gat cgt gac atc gct atg gtc ttc cag agc 355
Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala Met Val Phe Gln Ser
70 75 80 85

tac	gcg	ctg	tac	ccg	aat	atg	act	gtt	cgg	gac	aac	atg	ggc	ttt	gcg	403
Tyr	Ala	Leu	Tyr	Pro	Asn	Met	Thr	Val	Arg	Asp	Asn	Met	Gly	Phe	Ala	
				90					95					100		

ctg aag aat cag aag gtg gct aag gct gag atc gaa aag cgt gtt gct 451
Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile Glu Lys Arg Val Ala
105 110 115

gaa gcc tca cgc att ctg cag ctg gat ccg tat ctt gat cgt aag cct 499
Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr Leu Asp Arg Lys Pro
120 125 130

gca gct ttg tct ggt ggt cag cgc cag cgc gtg gcc atg ggc cgt gca 547
Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
135 140 145

att gtg cgt gag cca tcg gtg ttc tgc atg gat gag cca ctg tcc aac 595
Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp Glu Pro Leu Ser Asn
150 155 160 165

cta	gat	gcg	aag	ctg	cgt	gtg	tct	acg	cgt	gcg	gag	atc	tct	ggt	ttg	643
Leu	Asp	Ala	Lys	Leu	Arg	Val	Ser	Thr	Arg	Ala	Glu	Ile	Ser	Gly	Leu	
				170					175					180		

cag cgt cgc atg ggc gtg acc acg gtg tat gtg act cac gat cag gtc 691
Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Val
185 190 195

gag gcc atg acc atg ggt gat cgc gtc gct gtg ctt ttg ctc ggt gtg 739
Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Leu Leu Gly Val
200 205 210

[illegible]

ctg cag caa gta gac acc ccg cag aac ctg tac gac tac cca gca aat 787
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 215 220 225

gcg ttc gtc gcc agc ttc att ggt tcc cct tcc atg aac ttg att gag 835
 Ala Phe Val Ala Ser Phe Ile Gly Ser Pro Ser Met Asn Leu Ile Glu
 230 235 240 245

ggc acc atc cgt ggc gat aag gtc act ttg ggt act gga att cag att 883
 Gly Thr Ile Arg Gly Asp Lys Val Thr Leu Gly Thr Gly Ile Gln Ile
 250 255 260

tca gtt cct gat gag gtg gca gca gag gtt cgc aac aac ccg gat cgc 931
 Ser Val Pro Asp Glu Val Ala Ala Glu Val Arg Asn Asn Pro Asp Arg
 265 270 275

ttt gag ggt cgt cca gtc att gtt ggt gct cgt ccc gag cac atg tat 979
 Phe Glu Gly Arg Pro Val Ile Val Gly Ala Arg Pro Glu His Met Tyr
 280 285 290

ttg acc acg gcg aat gag agt ggt gct gta ttg ggc gaa gtc agc cac 1027
 Leu Thr Thr Ala Asn Glu Ser Gly Ala Val Leu Gly Glu Val Ser His
 295 300 305

att gat gag ctc ggc gcg gat tca atg gtc tac gta ttg gcg tct ggt 1075
 Ile Asp Glu Leu Gly Ala Asp Ser Met Val Tyr Val Leu Ala Ser Gly
 310 315 320 325

gtg aag aac ccg aat act gat ctt ttg ggt gag ggc att cca gag gat 1123
 Val Lys Asn Pro Asn Thr Asp Leu Leu Gly Glu Gly Ile Pro Glu Asp
 330 335 340

atg cgc gtg acc gtt gtc ggt gct gaa gag acc gat aag gcc cgg ctg 1171
 Met Arg Val Thr Val Val Gly Ala Glu Glu Thr Asp Lys Ala Arg Leu
 345 350 355

ggt att cgt gtt gag cgc cat cac ggt ctg aag gcc ggc gat aag gtg 1219
 Gly Ile Arg Val Glu Arg His His Gly Leu Lys Ala Gly Asp Lys Val
 360 365 370

cac gtt gtt gct gca ccg aag gat gtt cac ctc ttc gac ggt ctt gat 1267
 His Val Val Ala Ala Pro Lys Asp Val His Leu Phe Asp Gly Leu Asp
 375 380 385

ggc cgt cga atc ggt gca tcg gtt cta gct cca gcc cat aca gtc cag 1315
 Gly Arg Arg Ile Gly Ala Ser Val Leu Ala Pro Ala His Thr Val Gln
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<213> Corynebacterium glutamicum

<400> 164

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 35 40 45
 Arg Met Leu Ala Gly Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile
 50 55 60
 Asp Gly Lys Asp Ala Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala
 65 70 75 80
 Met Val Phe Gln Ser Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp
 85 90 95
 Asn Met Gly Phe Ala Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile
 100 105 110
 Glu Lys Arg Val Ala Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr
 115 120 125
 Leu Asp Arg Lys Pro Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val
 130 135 140
 Ala Met Gly Arg Ala Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp
 145 150 155 160
 Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala
 165 170 175
 Glu Ile Ser Gly Leu Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val
 180 185 190
 Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val
 195 200 205
 Leu Leu Leu Gly Val Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr
 210 215 220
 Asp Tyr Pro Ala Asn Ala Phe Val Ala Ser Phe Ile Gly Ser Pro Ser
 225 230 235 240
 Met Asn Leu Ile Glu Gly Thr Ile Arg Gly Asp Lys Val Thr Leu Gly
 245 250 255
 Thr Gly Ile Gln Ile Ser Val Pro Asp Glu Val Ala Ala Glu Val Arg
 260 265 270
 Asn Asn Pro Asp Arg Phe Glu Gly Arg Pro Val Ile Val Gly Ala Arg
 275 280 285
 Pro Glu His Met Tyr Leu Thr Thr Ala Asn Glu Ser Gly Ala Val Leu
 290 295 300
 Gly Glu Val Ser His Ile Asp Glu Leu Gly Ala Asp Ser Met Val Tyr
 305 310 315 320
 Val Leu Ala Ser Gly Val Lys Asn Pro Asn Thr Asp Leu Leu Gly Glu
 325 330 335


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Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
    135                      140                      145

att gtg cgt gag cca tcg gtg ttc tgc atg gat gag cca ctg tcc aac 595
Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp Glu Pro Leu Ser Asn
    150                      155                      160                      165

cta gat gcg aag ctg cgt gtg tct acg cgt gcg gag atc tct ggt ttg 643
Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala Glu Ile Ser Gly Leu
    170                      175                      180

cag cgt cgc atg ggc gtg acc acg gtg tat gtg act cac gat cag gtc 691
Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Val
    185                      190                      195

gag gcc atg acc atg ggt gat cgc gtc gct gtg ctt ttg ctc ggt gtg 739
Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Leu Leu Gly Val
    200                      205                      210

ctg cag caa gta gac acc ccg cag aac ctg tac gac tac cca gca aat 787
Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr Asp Tyr Pro Ala Asn
    215                      220                      225

gcg ttc gtc gcc agc ttc att ggt tcc ctt cca tgaacttgat tgagggcacc 840
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Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu
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Arg Met Leu Ala Gly Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile
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Asp Gly Lys Asp Ala Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala
    65                      70                      75                      80

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Met Val Phe Gln Ser Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp
    85                      90                      95

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Asn Met Gly Phe Ala Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile
    100                      105                      110

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Glu Lys Arg Val Ala Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr
115 120 125

Leu Asp Arg Lys Pro Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val
130 135 140

Ala Met Gly Arg Ala Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp
145 150 155 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala
165 170 175

Glu Ile Ser Gly Leu Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val
180 185 190

Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val
195 200 205

Leu Leu Leu Gly Val Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr
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225 230 235 240

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Met Thr Thr Ala Leu
1 5

gga acg cgc gtt gtt gcg cgc aac ttt ggc tac cgc cat gct tcc cgg 163
Gly Thr Arg Val Val Ala Arg Asn Phe Gly Tyr Arg His Ala Ser Arg
10 15 20

gaa aac ccc gcg ctc aaa gac atc aac ttc gag atc gca cct ggt gaa 211
Glu Asn Pro Ala Leu Lys Asp Ile Asn Phe Glu Ile Ala Pro Gly Glu
25 30 35

cgc atc ctg ctc acc ggc gct tcc ggc gcc gga aaa tcc acg cta ctc 259
Arg Ile Leu Leu Thr Gly Ala Ser Gly Ala Gly Lys Ser Thr Leu Leu
40 45 50

gcc gcg ctc gct ggc gtt tta ggc ggt tct gat gag ggc gtt tct acg 307
Ala Ala Leu Ala Gly Val Leu Gly Gly Ser Asp Glu Gly Val Ser Thr
55 60 65

115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240

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 Gly Glu Leu Leu Val Asp Ala Pro Ser Ile Gly Leu Val Leu Gln Asp
 70 75 80 85

cca gat tcc caa gtc atc gcc tcc cgc atc ggc gat gat gtg gcg ttt 403
 Pro Asp Ser Gln Val Ile Ala Ser Arg Ile Gly Asp Asp Val Ala Phe
 90 95 100

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 Gly Cys Glu Asn Leu Gln Ile Pro Arg Glu Glu Ile Trp Pro Arg Val
 105 110 115

gaa cga gca ctt gaa ttg gtg ggc ttg gat cta cca ctg agc cac ccc 499
 Glu Arg Ala Leu Glu Leu Val Gly Leu Asp Leu Pro Leu Ser His Pro
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acg aaa tat ctt tcc ggt ggc caa aaa caa cgc ctc gct ctt gcc ggt 547
 Thr Lys Tyr Leu Ser Gly Gly Gln Lys Gln Arg Leu Ala Leu Ala Gly
 135 140 145

gtg atc gcc atg ggt gct cgt ctg att ctg ctt gat gaa ccc acc gca 595
 Val Ile Ala Met Gly Ala Arg Leu Ile Leu Leu Asp Glu Pro Thr Ala
 150 155 160 165

aac ctt gat cct caa ggc caa aaa aat gtg gtc gca gca gtg gat cgc 643
 Asn Leu Asp Pro Gln Gly Gln Lys Asn Val Val Ala Ala Val Asp Arg
 170 175 180

gtt gtt cag gaa act gga gca aca ctc atc gtg gtg gaa cac cgc cat 691
 Val Val Gln Glu Thr Gly Ala Thr Leu Ile Val Val Glu His Arg His
 185 190 195

gag ctg tgg gtc aac atc att gac cgg atc atc agt att act gac ggc 739
 Glu Leu Trp Val Asn Ile Ile Asp Arg Ile Ile Ser Ile Thr Asp Gly
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gaa gat gtc caa cct gca gag ttg atc aag gtg ggc cag ttg cct ggg 787
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tgc acc tgg ggc ggc ctg cgt agt ttt gag gtg ccg gaa ggc gcc tcg 883
 Cys Thr Trp Gly Gly Leu Arg Ser Phe Glu Val Pro Glu Gly Ala Ser
 250 255 260

acg gtg atc acc ggg ccg aat ggc gct gga aaa tcc aca ctt gcg ctg 931
 Thr Val Ile Thr Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Ala Leu
 265 270 275

acc atg ggt gga ttg ctt ccg cga aaa gtg ggc agc tgg aac tct ctg 979
 Thr Met Gly Gly Leu Leu Pro Arg Lys Val Gly Ser Trp Asn Ser Leu
 280 285 290

aca cgg tgc gcg gcg gcc tta aca cgc ccc cgc aca agt ggc gtt cag 1027
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 295 300 305

114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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 Val Ser Ala Leu Pro Gln Val Asp Asp Val Gln Val Asp Leu Ile Ala
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 Val His Arg Ala Ile Glu Glu Thr Gly Tyr Thr Val Leu Ser
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 Val Lys Asn Pro Arg
 1 5
 ctc ata gca ctg gcc gct atc atc ctg acc tcg ttc aat ctg cga aca 163
 Leu Ile Ala Leu Ala Ala Ile Ile Leu Thr Ser Phe Asn Leu Arg Thr
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 gct att act gct tta gct ccg ctg gtt tct gag att cgg gat gat tta 211
 Ala Ile Thr Ala Leu Ala Pro Leu Val Ser Glu Ile Arg Asp Asp Leu
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 Gly Val Ser Ala Ser Leu Ile Gly Val Leu Gly Met Ile Pro Thr Ala
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 Met Phe Ala Asp Ala Ala Phe Ala Leu Pro Ser Leu Lys Arg Lys Phe
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 act act tcc caa ctg ttg atg ttt gcc atg ctg ttg act gct gcc ggt 355
 Thr Thr Ser Gln Leu Leu Met Phe Ala Met Leu Leu Thr Ala Ala Gly
 70 75 80 85
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 Gln Ile Ile Arg Val Ala Gly Pro Ala Ser Leu Leu Met Val Gly Thr
 90 95 100
 gtg ttc gcg atg ttt gcg atc gga gtt acc aat gtg ttg ctt ccg att 451
 Val Phe Ala Met Phe Ala Ile Gly Val Thr Asn Val Leu Leu Pro Ile
 105 110 115
 gct gtt agg gag tat ttt ccg cgt cac gtc ggt gga atg tcg aca act 499
 Ala Val Arg Glu Tyr Phe Pro Arg His Val Gly Gly Met Ser Thr Thr
 120 125 130

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Tyr Leu Val Ser Phe Gln Ile Val Gln Ala Leu Ala Pro Thr Leu Ala	
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Val Pro Ile Ser Gln Trp Ala Thr His Val Gly Leu Thr Gly Trp Arg	
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Val Ser Leu Gly Ser Trp Ala Leu Leu Gly Leu Val Ala Ala Ile Ser	
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Trp Ile Pro Leu Leu Ser Leu Gln Gly Ala Arg Val Val Ala Ala Pro	
185 190 195	
tcg aag gtt tct ctt cct gtg tgg aag tct tcg gtt ggt gtg ggg ctc	739
Ser Lys Val Ser Leu Pro Val Trp Lys Ser Ser Val Gly Val Gly Leu	
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Gly Leu Met Phe Gly Phe Thr Ser Phe Ala Thr Tyr Ile Leu Met Gly	
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Phe Met Pro Gln Met Val Gly Asp Pro Gln Leu Gly Ala Val Leu Leu	
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Gly Trp Trp Ser Ile Leu Gly Leu Pro Leu Asn Ile Leu Gly Pro Trp	
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Leu Val Thr Arg Phe Thr Asn Cys Phe Pro Met Val Val Ile Ala Ser	
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Val Met Phe Leu Ile Gly Asn Gly Gly Phe Cys Leu Ala Pro Asp Val	
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Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val Asp Ala Thr Gly Ser	
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Phe Arg Thr Ile Phe Val Leu Phe Ala Val Ala Thr Leu Phe Val Ile	
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 Gln Ile Ile Arg Val Ala Gly Pro Ala Ser Leu Leu Met Val Gly Thr
 90 95 100

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 Val Phe Ala Met Phe Ala Ile Gly Val Thr Asn Val Leu Leu Pro Ile
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gct gtt agg gag tat ttt ccg cgt cac gtc ggt gga atg tcg aca act 499
 Ala Val Arg Glu Tyr Phe Pro Arg His Val Gly Gly Met Ser Thr Thr
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 135 140 145

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 150 155 160 165

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 170 175 180

tgg att ccg ctg ttg agt ttg cag ggt gcc agg gtt gtt gcg gcg ccg 691
 Trp Ile Pro Leu Leu Ser Leu Gln Gly Ala Arg Val Val Ala Ala Pro
 185 190 195

tcg aag gtt tct ctt cct gtg tgg aag tct tcg gtt ggt gtg ggg ctc 739
 Ser Lys Val Ser Leu Pro Val Trp Lys Ser Ser Val Gly Val Gly Leu
 200 205 210

ggg ttg atg ttt ggg ttt act tcg ttt gcg acg tat atc ctc atg ggt 787
 Gly Leu Met Phe Gly Phe Thr Ser Phe Ala Thr Tyr Ile Leu Met Gly
 215 220 225

ttt atg ccg cag atg gta ggt gat cct cag ctc ggt gcg gtg ttg tta 835
 Phe Met Pro Gln Met Val Gly Asp Pro Gln Leu Gly Ala Val Leu Leu
 230 235 240 245

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 250 255 260

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 265 270 275

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 Val Met Phe Leu Ile Gly Asn Gly Gly Phe Cys Leu Ala Pro Asp Val
 280 285 290

gcg ccg tgg ttg tgg gcg acg ttg tct ggt ctt ggt ccc ctt gcg ttc 1027
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Ile Arg Asp Asp Leu Gly Val Ser Ala Ser Leu Ile Gly Val Leu Gly
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Met Ile Pro Thr Ala Met Phe Ala Asp Ala Ala Phe Ala Leu Pro Ser
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Leu Lys Arg Lys Phe Thr Thr Ser Gln Leu Leu Met Phe Ala Met Leu
  65          70          75          80
Leu Thr Ala Ala Gly Gln Ile Ile Arg Val Ala Gly Pro Ala Ser Leu
          85          90          95
Leu Met Val Gly Thr Val Phe Ala Met Phe Ala Ile Gly Val Thr Asn
          100          105          110
Val Leu Leu Pro Ile Ala Val Arg Glu Tyr Phe Pro Arg His Val Gly
          115          120          125
Gly Met Ser Thr Thr Tyr Leu Val Ser Phe Gln Ile Val Gln Ala Leu
          130          135          140
Ala Pro Thr Leu Ala Val Pro Ile Ser Gln Trp Ala Thr His Val Gly
          145          150          155          160

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Leu Thr Gly Trp Arg Val Ser Leu Gly Ser Trp Ala Leu Leu Gly Leu
165 170 175

Val Ala Ala Ile Ser Trp Ile Pro Leu Leu Ser Leu Gln Gly Ala Arg
180 185 190

Val Val Ala Ala Pro Ser Lys Val Ser Leu Pro Val Trp Lys Ser Ser
195 200 205

Val Gly Val Gly Leu Gly Leu Met Phe Gly Phe Thr Ser Phe Ala Thr
210 215 220

Tyr Ile Leu Met Gly Phe Met Pro Gln Met Val Gly Asp Pro Gln Leu
225 230 235 240

Gly Ala Val Leu Leu Gly Trp Trp Ser Ile Leu Gly Leu Pro Leu Asn
245 250 255

Ile Leu Gly Pro Trp Leu Val Thr Arg Phe Thr Asn Cys Phe Pro Met
260 265 270

Val Val Ile Ala Ser Val Met Phe Leu Ile Gly Asn Gly Gly Phe Cys
275 280 285

Leu Ala Pro Asp Val Ala Pro Trp Leu Trp Ala Thr Leu Ser Gly Leu
290 295 300

Gly Pro Leu Ala Phe Pro Met Ala Leu Thr Leu Ile Asn Ile Arg Ala
305 310 315 320

Glu Thr Ser Ala Gly Ala Ser Ala Leu Ser Ser Phe Gly Gln Gly Leu
325 330 335

Gly Tyr Thr Ile Ala Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val
340 345 350

Asp Ala Thr Gly Ser Phe Arg Thr Ile Phe Leu Leu Phe Ala Gly Ala
355 360 365

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370 375 380

Val Glu Lys Leu Leu Asn Arg
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<223> RXA00634

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Met Trp Glu Arg Phe

	1	5	
agc ttc tac ggc atg caa gca ctc ttg gtg tac tac ctg tat ttt gat			163
Ser Phe Tyr Gly Met Gln Ala Leu Leu Val Tyr Tyr Leu Tyr Phe Asp			
	10	20	
gtt gca gcc ggt gga tta ggc ctt gat caa acc caa gca aca gga ctg			211
Val Ala Ala Gly Gly Leu Gly Leu Asp Gln Thr Gln Ala Thr Gly Leu			
	25	35	
gtc ggc gtt tat ggc gca ctg ctc tac ctc tgc tgt tgg gca ggc ggt			259
Val Gly Val Tyr Gly Ala Leu Leu Tyr Leu Cys Cys Trp Ala Gly Gly			
	40	50	
tgg gtc agt gac aga gtc ctg ggc gca gaa aaa acc ctg ctg ggc ggt			307
Trp Val Ser Asp Arg Val Leu Gly Ala Glu Lys Thr Leu Leu Gly Gly			
	55	65	
gcg atc tca gta acc atc gga cac ctt gtg ctt gct ggc ctc ggc ggg			355
Ala Ile Ser Val Thr Ile Gly His Leu Val Leu Ala Gly Leu Gly Gly			
	70	85	
aaa att ggt cta gcc att ggc ctt gga tgc atc gcg atc ggt tca gga			403
Lys Ile Gly Leu Ala Ile Gly Leu Gly Cys Ile Ala Ile Gly Ser Gly			
	90	100	
ttt gtg aaa aca gca gcc atc acc gtg ctg gga tcc agg cat ggt gaa			451
Phe Val Lys Thr Ala Ala Ile Thr Val Leu Gly Ser Arg His Gly Glu			
	105	115	
caa gaa gga gac gca aag gca gat ccc gca ttc caa ctc ttc tac cta			499
Gln Glu Gly Asp Ala Lys Ala Asp Pro Ala Phe Gln Leu Phe Tyr Leu			
	120	130	
ggc atc aac gtt ggt gca ctg ctc gga cca ctc ctg acc ggt tgg ctc			547
Gly Ile Asn Val Gly Ala Leu Leu Gly Pro Leu Leu Thr Gly Trp Leu			
	135	145	
tcc agc agg tat tcc ttt gaa atg gga ttc ggc gca gcc gca gtc ctt			595
Ser Ser Arg Tyr Ser Phe Glu Met Gly Phe Gly Ala Ala Ala Val Leu			
	150	165	
atg atc ggc gga ttg gga atc tac gca gcg ttg cgg aaa cca atg ctg			643
Met Ile Gly Gly Leu Gly Ile Tyr Ala Ala Leu Arg Lys Pro Met Leu			
	170	180	
caa tcg ttc ccg ctc gag gtg aag aaa gcg ctg ctc cgc gcc caa aac			691
Gln Ser Phe Pro Leu Glu Val Lys Lys Ala Leu Leu Arg Ala Gln Asn			
	185	195	
cct gca gaa aaa cat gtg att agc acg gca ttt gct gca gtg gct gtg			739
Pro Ala Glu Lys His Val Ile Ser Thr Ala Phe Ala Ala Val Ala Val			
	200	210	
ctt tgc gga gtg ctg ctt tat ctt ctc ctt aca gaa aca gtc agc gca			787
Leu Cys Gly Val Leu Leu Tyr Leu Leu Leu Thr Glu Thr Val Ser Ala			
	215	225	
gac caa cta gct gga gct ctg ctt tta gta aca atc ggt gca gca cta			835
Asp Gln Leu Ala Gly Ala Leu Leu Leu Val Thr Ile Gly Ala Ala Leu			
	230	245	

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tgg ctc att atc cag ccc tta cga cac cca caa gtc agc tcc gaa gag 883
 Trp Leu Ile Ile Gln Pro Leu Arg His Pro Gln Val Ser Ser Glu Glu
 250 255 260

aaa cga aaa gtg ctg gca ttc atc ccg atc ttc gtc tgc tca acc gca 931
 Lys Arg Lys Val Leu Ala Phe Ile Pro Ile Phe Val Cys Ser Thr Ala
 265 270 275

ttc tgg gca gtg caa gca caa acc tac ggc gta cta gct gtg tac tcc 979
 Phe Trp Ala Val Gln Ala Gln Thr Tyr Gly Val Leu Ala Val Tyr Ser
 280 285 290

caa gaa cgt gtt gac cgc atg gtt ggc gat ttt gag atc cca gca gcc 1027
 Gln Glu Arg Val Asp Arg Met Val Gly Asp Phe Glu Ile Pro Ala Ala
 295 300 305

tgg tca caa tca ctc aat cct ttt ttc atc ctg gcg ctg tcc atc ccg 1075
 Trp Ser Gln Ser Leu Asn Pro Phe Phe Ile Leu Ala Leu Ser Ile Pro
 310 315 320 325

att tcc ctg tgg ttt atg cgc gga tca cgc gcc cca aga gtg aaa att 1123
 Ile Ser Leu Trp Phe Met Arg Gly Ser Arg Ala Pro Arg Val Lys Ile
 330 335 340

gga atc agc att gga gtg atc att gcg gga agt ggg ctt cta gtt ctt 1171
 Gly Ile Ser Ile Gly Val Ile Ile Ala Gly Ser Gly Leu Leu Val Leu
 345 350 355

att cca ttt gtt gga atg ccg ctc gcg cca gtg tgg gtg ctg cct tta 1219
 Ile Pro Phe Val Gly Met Pro Leu Ala Pro Val Trp Val Leu Pro Leu
 360 365 370

agt gtt ttc ctc atc tca ctg gga gaa ctt ttc atc gga ccc gga gga 1267
 Ser Val Phe Leu Ile Ser Leu Gly Glu Leu Phe Ile Gly Pro Gly Gly
 375 380 385

atg gct gcg act gcg cac cac gca cca cga ata ttt gcc aca cga ttc 1315
 Met Ala Ala Thr Ala His His Ala Pro Arg Ile Phe Ala Thr Arg Phe
 390 395 400 405

tcc gcc ctg tat ttc ctc aca ctc gcc atc ggc atg tct att gca ggt 1363
 Ser Ala Leu Tyr Phe Leu Thr Leu Ala Ile Gly Met Ser Ile Ala Gly
 410 415 420

aat gtg tcc aaa ttt tac gac ccc acc aac cac acc tcc gag ctc cga 1411
 Asn Val Ser Lys Phe Tyr Asp Pro Thr Asn His Thr Ser Glu Leu Arg
 425 430 435

tac ttc gcg gta ttt ggc att tcg atc atc gtc atc ggt gtc ggt tca 1459
 Tyr Phe Ala Val Phe Gly Ile Ser Ile Ile Val Ile Gly Val Gly Ser
 440 445 450

ctg atg gtg gcc aag aag gtt gga taacagggtt aatcttgggt gat 1506
 Leu Met Val Ala Lys Lys Val Gly
 455 460

<210> 176

<211> 461

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

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Met Trp Glu Arg Phe Ser Phe Tyr Gly Met Gln Ala Leu Leu Val Tyr
 1           5           10           15

Tyr Leu Tyr Phe Asp Val Ala Ala Gly Gly Leu Gly Leu Asp Gln Thr
          20           25           30

Gln Ala Thr Gly Leu Val Gly Val Tyr Gly Ala Leu Leu Tyr Leu Cys
          35           40           45

Cys Trp Ala Gly Gly Trp Val Ser Asp Arg Val Leu Gly Ala Glu Lys
          50           55           60

Thr Leu Leu Gly Gly Ala Ile Ser Val Thr Ile Gly His Leu Val Leu
 65           70           75           80

Ala Gly Leu Gly Gly Lys Ile Gly Leu Ala Ile Gly Leu Gly Cys Ile
          85           90           95

Ala Ile Gly Ser Gly Phe Val Lys Thr Ala Ala Ile Thr Val Leu Gly
          100          105          110

Ser Arg His Gly Glu Gln Glu Gly Asp Ala Lys Ala Asp Pro Ala Phe
          115          120          125

Gln Leu Phe Tyr Leu Gly Ile Asn Val Gly Ala Leu Leu Gly Pro Leu
          130          135          140

Leu Thr Gly Trp Leu Ser Ser Arg Tyr Ser Phe Glu Met Gly Phe Gly
          145          150          155          160

Ala Ala Ala Val Leu Met Ile Gly Gly Leu Gly Ile Tyr Ala Ala Leu
          165          170          175

Arg Lys Pro Met Leu Gln Ser Phe Pro Leu Glu Val Lys Lys Ala Leu
          180          185          190

Leu Arg Ala Gln Asn Pro Ala Glu Lys His Val Ile Ser Thr Ala Phe
          195          200          205

Ala Ala Val Ala Val Leu Cys Gly Val Leu Leu Tyr Leu Leu Leu Thr
          210          215          220

Glu Thr Val Ser Ala Asp Gln Leu Ala Gly Ala Leu Leu Leu Val Thr
          225          230          235          240

Ile Gly Ala Ala Leu Trp Leu Ile Ile Gln Pro Leu Arg His Pro Gln
          245          250          255

Val Ser Ser Glu Glu Lys Arg Lys Val Leu Ala Phe Ile Pro Ile Phe
          260          265          270

Val Cys Ser Thr Ala Phe Trp Ala Val Gln Ala Gln Thr Tyr Gly Val
          275          280          285

Leu Ala Val Tyr Ser Gln Glu Arg Val Asp Arg Met Val Gly Asp Phe
          290          295          300

Glu Ile Pro Ala Ala Trp Ser Gln Ser Leu Asn Pro Phe Phe Ile Leu

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305          310          315          320
Ala Leu Ser Ile Pro Ile Ser Leu Trp Phe Met Arg Gly Ser Arg Ala
          325          330          335
Pro Arg Val Lys Ile Gly Ile Ser Ile Gly Val Ile Ile Ala Gly Ser
          340          345          350
Gly Leu Leu Val Leu Ile Pro Phe Val Gly Met Pro Leu Ala Pro Val
          355          360          365
Trp Val Leu Pro Leu Ser Val Phe Leu Ile Ser Leu Gly Glu Leu Phe
          370          375          380
Ile Gly Pro Gly Gly Met Ala Ala Thr Ala His His Ala Pro Arg Ile
385          390          395          400
Phe Ala Thr Arg Phe Ser Ala Leu Tyr Phe Leu Thr Leu Ala Ile Gly
          405          410          415
Met Ser Ile Ala Gly Asn Val Ser Lys Phe Tyr Asp Pro Thr Asn His
          420          425          430
Thr Ser Glu Leu Arg Tyr Phe Ala Val Phe Gly Ile Ser Ile Ile Val
          435          440          445
Ile Gly Val Gly Ser Leu Met Val Ala Lys Lys Val Gly
          450          455          460

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<210> 177
<211> 1647
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1624)
<223> RXA02451

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<400> 177
gatcaactta agcctctagc tattttcaac tgtgtttcag ttgcgggatac gttgggtgcc 60

taattggagt tgtgctttta ggtggaggat catagaggtt atg aac acc gac aca 115
                                     Met Asn Thr Asp Thr
                                     1           5

act caa gac ggt gtg agt cct gaa cct tcc gac ccc cac cta ggg tct 163
Thr Gln Asp Gly Val Ser Pro Glu Pro Ser Asp Pro His Leu Gly Ser
          10          15          20

gaa gtg gcg gaa act cac cgc gaa aag aaa ttc ttc ggc cag cct tgg 211
Glu Val Ala Glu Thr His Arg Glu Lys Lys Phe Phe Gly Gln Pro Trp
          25          30          35

ggg ctg gca aat ctc ttc ggc gtg gag atg tgg gag cga ttc agc ttc 259
Gly Leu Ala Asn Leu Phe Gly Val Glu Met Trp Glu Arg Phe Ser Phe
          40          45          50

tac ggc atg cag tcc atc ctt gct ttc tat ctg tac tac tcc gtc acc 307
Tyr Gly Met Gln Ser Ile Leu Ala Phe Tyr Leu Tyr Tyr Ser Val Thr

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atc ggt ggc gtg ctt ttc ttc gcg atc ttc caa acc cag ttc acg gtc 1075
Ile Gly Gly Val Leu Phe Phe Ala Ile Phe Gln Thr Gln Phe Thr Val
310                      315                      320                      325

ctc gcg gtt tac tcc gac acc cgc ctg gac cgt aac ttc ttc ggc att 1123
Leu Ala Val Tyr Ser Asp Thr Arg Leu Asp Arg Asn Phe Phe Gly Ile
                      330                      335                      340

gat ctt cct cca gga ttg atc aac tcc ttc aac cca atc ttc atc atc 1171
Asp Leu Pro Pro Gly Leu Ile Asn Ser Phe Asn Pro Ile Phe Ile Ile
                      345                      350                      355

atc ttc tcc gga atc ttt gcc acc ttg tgg aca aaa ctc gga gca aag 1219
Ile Phe Ser Gly Ile Phe Ala Thr Leu Trp Thr Lys Leu Gly Ala Lys
                      360                      365                      370

cag tgg tct act gca gtg aag ttc ggt gtc gcc aac att gtc att ggt 1267
Gln Trp Ser Thr Ala Val Lys Phe Gly Val Ala Asn Ile Val Ile Gly
                      375                      380                      385

tgc gcg ctg ttc ttc ttc ctg ccg ttc gcc ggc ggt gca gag aac tct 1315
Cys Ala Leu Phe Phe Phe Leu Pro Phe Ala Gly Gly Ala Glu Asn Ser
390                      395                      400                      405

acc cca atg gca ctg atc att tgg gtc tac ttc ctc ttc acc atc gct 1363
Thr Pro Met Ala Leu Ile Ile Trp Val Tyr Phe Leu Phe Thr Ile Ala
                      410                      415                      420

gag ctt ctg ctc tcc cct gtc ggc aac tca ctt gca acc aag gtc gca 1411
Glu Leu Leu Ser Pro Val Gly Asn Ser Leu Ala Thr Lys Val Ala
                      425                      430                      435

ccc gag gca ttc cag tcc cgc atg ttc gcc gtg tgg ctg atg gct gtc 1459
Pro Glu Ala Phe Gln Ser Arg Met Phe Ala Val Trp Leu Met Ala Val
                      440                      445                      450

tcc atg ggt acg tcc ctg tcc ggc acc ctg ggt ggt tac tac gat cca 1507
Ser Met Gly Thr Ser Leu Ser Gly Thr Leu Gly Gly Tyr Tyr Asp Pro
                      455                      460                      465

acc gat gca gga tct gaa aag gtc ttc ttc att acc gtt ggc gtt gca 1555
Thr Asp Ala Gly Ser Glu Lys Val Phe Phe Ile Thr Val Gly Val Ala
470                      475                      480                      485

gcc atc gtt ctt ggt gca atc gtc ata gca gcc aag ggc tgg gtg ctg 1603
Ala Ile Val Leu Gly Ala Ile Val Ile Ala Ala Lys Gly Trp Val Leu
                      490                      495                      500

aag aag ttc atc gac gtc cga taggcctcac aaagcctcaa aac 1647
Lys Lys Phe Ile Asp Val Arg
                      505

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<210> 178

<211> 508

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Met Asn Thr Asp Thr Thr Gln Asp Gly Val Ser Pro Glu Pro Ser Asp

Asn Phe Phe Gly Ile Asp Leu Pro Pro Gly Leu Ile Asn Ser Phe Asn
 340 345 350
 Pro Ile Phe Ile Ile Ile Phe Ser Gly Ile Phe Ala Thr Leu Trp Thr
 355 360 365
 Lys Leu Gly Ala Lys Gln Trp Ser Thr Ala Val Lys Phe Gly Val Ala
 370 375 380
 Asn Ile Val Ile Gly Cys Ala Leu Phe Phe Phe Leu Pro Phe Ala Gly
 385 390 395 400
 Gly Ala Glu Asn Ser Thr Pro Met Ala Leu Ile Ile Trp Val Tyr Phe
 405 410 415
 Leu Phe Thr Ile Ala Glu Leu Leu Leu Ser Pro Val Gly Asn Ser Leu
 420 425 430
 Ala Thr Lys Val Ala Pro Glu Ala Phe Gln Ser Arg Met Phe Ala Val
 435 440 445
 Trp Leu Met Ala Val Ser Met Gly Thr Ser Leu Ser Gly Thr Leu Gly
 450 455 460
 Gly Tyr Tyr Asp Pro Thr Asp Ala Gly Ser Glu Lys Val Phe Phe Ile
 465 470 475 480
 Thr Val Gly Val Ala Ala Ile Val Leu Gly Ala Ile Val Ile Ala Ala
 485 490 495
 Lys Gly Trp Val Leu Lys Lys Phe Ile Asp Val Arg
 500 505

<210> 179

<211> 1426

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (93)..(1403)

<223> RXA02394

<400> 179

tggtgatgaa tcagaagaac ctgagatatt ggacgagcta gaggcccaaa gcgctataga 60

ttctgcaagt tcagcggaag gtaggaacta atatg ttg tcg cca gca gct gta 113
 Met Leu Ser Pro Ala Ala Val
 1 5

gca gct tta att ctt gtc atc gcc att gtg gtg ctc atc atc gca tca 161
 Ala Ala Leu Ile Leu Val Ile Gly Ile Val Val Leu Ile Ile Ala Ser
 10 15 20

gtg ccc gtt gcc att gcc atc ggt ttg cca tca ctt ttt gcc gcg atg 209
 Val Pro Val Ala Ile Ala Ile Gly Leu Pro Ser Leu Phe Ala Ala Met
 25 30 35

gcc gtg ctt ggc cca gaa aac gcc gcg cag gcc gtc gcg cag cgc atg 257

Ala Val Leu Gly Pro Glu Asn Ala Ala Gln Ala Val Ala Gln Arg Met
40 45 50 55

ttt acc ggc aca aac tcc ttt aca ctc ctt gcc att ccg ttc ttc gtg 305
Phe Thr Gly Thr Asn Ser Phe Thr Leu Leu Ala Ile Pro Phe Phe Val
60 65 70

ttg gcg ggt ttg ctg atg aac tcg ggt ggt att gcc acg cgg ctt atc 353
Leu Ala Gly Leu Leu Met Asn Ser Gly Gly Ile Ala Thr Arg Leu Ile
75 80 85

gac gcc gcg aag gtg ctt gtc ggc cgc atg cct gcc tcc atg gcc aat 401
Asp Ala Ala Lys Val Leu Val Gly Arg Met Pro Ala Ser Met Ala Asn
90 95 100

acg aat atc gca gca aat ggt ctc ttc gga gca gtt tca ggg gca gcg 449
Thr Asn Ile Ala Ala Asn Gly Leu Phe Gly Ala Val Ser Gly Ala Ala
105 110 115

gta gca tca gct tct gcc gtg gga acc gtc atg aca cca aaa atg aag 497
Val Ala Ser Ala Ser Ala Val Gly Thr Val Met Thr Pro Lys Met Lys
120 125 130 135

gaa gag ggc tac tcg cgc gct tac gca gcg gcc gtc aac gtg gct tca 545
Glu Glu Gly Tyr Ser Arg Ala Tyr Ala Ala Ala Val Asn Val Ala Ser
140 145 150

gca cct gcg ggc atg ctg atc ccg cca tca aac act ttt att gtg tat 593
Ala Pro Ala Gly Met Leu Ile Pro Pro Ser Asn Thr Phe Ile Val Tyr
155 160 165

tcc ttg gtg tcc tcg aca tca att gca gca cta ttt atg gcc ggt gtt 641
Ser Leu Val Ser Ser Thr Ser Ile Ala Ala Leu Phe Met Ala Gly Val
170 175 180

gga ccc ggt ctg ctc tgg att ctg gcc tgt gtc atc gtg gga act tgg 689
Gly Pro Gly Leu Leu Trp Ile Leu Ala Cys Val Ile Val Gly Thr Trp
185 190 195

tta gcg cga aag gaa aac tac aag cgc gag cag att cat cca aca ttc 737
Leu Ala Arg Lys Glu Asn Tyr Lys Arg Glu Gln Ile His Pro Thr Phe
200 205 210 215

aag cag tcg ctc gtt gtg ctg tgg agg gcg ctg cct tca ctg ctc atg 785
Lys Gln Ser Leu Val Val Leu Trp Arg Ala Leu Pro Ser Leu Leu Met
220 225 230

atc gtc att gtt gtt gga ggt atc ttg ctg ggc tgg ttc act cca act 833
Ile Val Ile Val Val Gly Gly Ile Leu Leu Gly Trp Phe Thr Pro Thr
235 240 245

gaa tcc gct gct att gct gta gtg tac tgc ctg gtc ttg ggc ttt att 881
Glu Ser Ala Ala Ile Ala Val Val Tyr Cys Leu Val Leu Gly Phe Ile
250 255 260

tac cgc aca atc aag gtg gga gat ctg gca gat att ttg ctc aag gca 929
Tyr Arg Thr Ile Lys Val Gly Asp Leu Ala Asp Ile Leu Leu Lys Ala
265 270 275

act cgc acc aca tca att gtc atg ttg ctc att gca gtt tct gca gca 977
Thr Arg Thr Thr Ser Ile Val Met Leu Leu Ile Ala Val Ser Ala Ala

280 285 290 295
 ctg tcg tgg gtg atg gcc ttt gcc aag atc cct cag atg atc tct gat 1025
 Leu Ser Trp Val Met Ala Phe Ala Lys Ile Pro Gln Met Ile Ser Asp
 300 305 310
 gcg ctt ctt tcg gta tcc gat tcc aag gtt gtc atc ttg ttg atc atg 1073
 Ala Leu Leu Ser Val Ser Asp Ser Lys Val Val Ile Leu Leu Ile Met
 315 320 325
 atg ttc atc ctg tta ctc atc ggt acc gta atg gac cca aca cca gca 1121
 Met Phe Ile Leu Leu Leu Ile Gly Thr Val Met Asp Pro Thr Pro Ala
 330 335 340
 att ttg atc ttc gtc ccg atc ttc ctt cca gtg gtt acc gaa ctt ggt 1169
 Ile Leu Ile Phe Val Pro Ile Phe Leu Pro Val Val Thr Glu Leu Gly
 345 350 355
 gtg gac cca gtc cac ttc ggt gcg atg gtg gta atg aac ctg tcc gtg 1217
 Val Asp Pro Val His Phe Gly Ala Met Val Val Met Asn Leu Ser Val
 360 365 370 375
 ggc gtg att acc cca cca gta ggc aac gtg ttg ttc gtt ggt tcg caa 1265
 Gly Val Ile Thr Pro Pro Val Gly Asn Val Leu Phe Val Gly Ser Gln
 380 385 390
 gtg gca ggg ctg cgt gtg gaa act gtg atc aga cga ctg tgg ccg tat 1313
 Val Ala Gly Leu Arg Val Glu Thr Val Ile Arg Arg Leu Trp Pro Tyr
 395 400 405
 ctc att gcc att att gtt gcg ctg ttc gtg gtt gtt ttc gta ccg cag 1361
 Leu Ile Ala Ile Ile Val Ala Leu Phe Val Val Val Phe Val Pro Gln
 410 415 420
 atc tct atc tgg ctg ccc aca aca atg gga ttg atg gga ggc 1403
 Ile Ser Ile Trp Leu Pro Thr Thr Met Gly Leu Met Gly Gly
 425 430 435
 taaacctcca gccatcagct aag 1426

<210> 180

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

Met Leu Ser Pro Ala Ala Val Ala Ala Leu Ile Leu Val Ile Gly Ile
 1 5 10 15

Val Val Leu Ile Ile Ala Ser Val Pro Val Ala Ile Ala Ile Gly Leu
 20 25 30

Pro Ser Leu Phe Ala Ala Met Ala Val Leu Gly Pro Glu Asn Ala Ala
 35 40 45

Gln Ala Val Ala Gln Arg Met Phe Thr Gly Thr Asn Ser Phe Thr Leu
 50 55 60

Leu Ala Ile Pro Phe Phe Val Leu Ala Gly Leu Leu Met Asn Ser Gly
 65 70 75 80

Gly	Ile	Ala	Thr	Arg	Leu	Ile	Asp	Ala	Ala	Lys	Val	Leu	Val	Gly	Arg
				85					90					95	
Met	Pro	Ala	Ser	Met	Ala	Asn	Thr	Asn	Ile	Ala	Ala	Asn	Gly	Leu	Phe
			100					105					110		
Gly	Ala	Val	Ser	Gly	Ala	Ala	Val	Ala	Ser	Ala	Ser	Ala	Val	Gly	Thr
		115					120					125			
Val	Met	Thr	Pro	Lys	Met	Lys	Glu	Glu	Gly	Tyr	Ser	Arg	Ala	Tyr	Ala
		130				135					140				
Ala	Ala	Val	Asn	Val	Ala	Ser	Ala	Pro	Ala	Gly	Met	Leu	Ile	Pro	Pro
145					150					155					160
Ser	Asn	Thr	Phe	Ile	Val	Tyr	Ser	Leu	Val	Ser	Ser	Thr	Ser	Ile	Ala
				165					170					175	
Ala	Leu	Phe	Met	Ala	Gly	Val	Gly	Pro	Gly	Leu	Leu	Trp	Ile	Leu	Ala
			180					185					190		
Cys	Val	Ile	Val	Gly	Thr	Trp	Leu	Ala	Arg	Lys	Glu	Asn	Tyr	Lys	Arg
		195					200					205			
Glu	Gln	Ile	His	Pro	Thr	Phe	Lys	Gln	Ser	Leu	Val	Val	Leu	Trp	Arg
		210				215					220				
Ala	Leu	Pro	Ser	Leu	Leu	Met	Ile	Val	Ile	Val	Val	Gly	Gly	Ile	Leu
225					230					235					240
Leu	Gly	Trp	Phe	Thr	Pro	Thr	Glu	Ser	Ala	Ala	Ile	Ala	Val	Val	Tyr
				245					250					255	
Cys	Leu	Val	Leu	Gly	Phe	Ile	Tyr	Arg	Thr	Ile	Lys	Val	Gly	Asp	Leu
			260					265					270		
Ala	Asp	Ile	Leu	Leu	Lys	Ala	Thr	Arg	Thr	Thr	Ser	Ile	Val	Met	Leu
		275					280					285			
Leu	Ile	Ala	Val	Ser	Ala	Ala	Leu	Ser	Trp	Val	Met	Ala	Phe	Ala	Lys
		290				295					300				
Ile	Pro	Gln	Met	Ile	Ser	Asp	Ala	Leu	Leu	Ser	Val	Ser	Asp	Ser	Lys
305					310					315					320
Val	Val	Ile	Leu	Leu	Ile	Met	Met	Phe	Ile	Leu	Leu	Leu	Ile	Gly	Thr
				325					330					335	
Val	Met	Asp	Pro	Thr	Pro	Ala	Ile	Leu	Ile	Phe	Val	Pro	Ile	Phe	Leu
			340					345					350		
Pro	Val	Val	Thr	Glu	Leu	Gly	Val	Asp	Pro	Val	His	Phe	Gly	Ala	Met
		355					360					365			
Val	Val	Met	Asn	Leu	Ser	Val	Gly	Val	Ile	Thr	Pro	Pro	Val	Gly	Asn
						375					380				
Val	Leu	Phe	Val	Gly	Ser	Gln	Val	Ala	Gly	Leu	Arg	Val	Glu	Thr	Val
385					390					395					400

Ile Arg Arg Leu Trp Pro Tyr Leu Ile Ala Ile Ile Val Ala Leu Phe
 405 410 415

Val Val Val Phe Val Pro Gln Ile Ser Ile Trp Leu Pro Thr Thr Met
 420 425 430

Gly Leu Met Gly Gly
 435

<210> 181
 <211> 1764
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1741)
 <223> RXA01012

<400> 181
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caactaccta agccgcatca ttcagaagga ggcataaaaa atg act act ccc ttg 115
 Met Thr Thr Pro Leu
 1 5

tta gag atc aac gat ctg gtt gtc tcc tat caa act gct aaa ggt ttg 163
 Leu Glu Ile Asn Asp Leu Val Val Ser Tyr Gln Thr Ala Lys Gly Leu
 10 15 20

gtg cat gct gtc aac aat gtc agc ctg gag gtg cac cct ggc caa atc 211
 Val His Ala Val Asn Asn Val Ser Leu Glu Val His Pro Gly Gln Ile
 25 30 35

acc gcg att gtt ggt gag tcc ggt tct ggt aag tcc acc acc gct cag 259
 Thr Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala Gln
 40 45 50

gcc gtg att ggt ttg ctg gct gat aat gct gaa gtg gat tct ggt cgg 307
 Ala Val Ile Gly Leu Leu Ala Asp Asn Ala Glu Val Asp Ser Gly Arg
 55 60 65

att tct ttc aac ggc cgt tcc ctt gtt ggc ttg aac gca cgt gag tgg 355
 Ile Ser Phe Asn Gly Arg Ser Leu Val Gly Leu Asn Ala Arg Glu Trp
 70 75 80 85

aaa aac gtt cgc ggt acc aaa att ggt ttg att ccg cag gac ccc aac 403
 Lys Asn Val Arg Gly Thr Lys Ile Gly Leu Ile Pro Gln Asp Pro Asn
 90 95 100

aac tct ctg aac ccg gtg aaa act atc ggc gct tca gtg ggg gag ggc 451
 Asn Ser Leu Asn Pro Val Lys Thr Ile Gly Ala Ser Val Gly Glu Gly
 105 110 115

ttg gct atc cac aag cgt gga acc gcc gcc gag cgc aaa aag aag gtc 499
 Leu Ala Ile His Lys Arg Gly Thr Ala Ala Glu Arg Lys Lys Lys Val
 120 125 130

att gag ctt cta gag cgc gtg ggt att gat aac cca gag gtc cgc tat 547
 Ile Glu Leu Leu Glu Arg Val Gly Ile Asp Asn Pro Glu Val Arg Tyr

135	140	145	
gac cag tac ccg cat gag ctg tct ggt ggc atg aag cag cgc gcg ttg			595
Asp Gln Tyr Pro His Glu Leu Ser Gly Gly Met Lys Gln Arg Ala Leu			
150	155	160	165
att gcc gct gcc att gca ctt gaa cca gag ctg atc att gcc gat gag			643
Ile Ala Ala Ala Ile Ala Leu Glu Pro Glu Leu Ile Ile Ala Asp Glu			
170	175		180
ccc aca tct gcg ctg gat gtg acc gtg cag aaa att att ctc gat ctg			691
Pro Thr Ser Ala Leu Asp Val Thr Val Gln Lys Ile Ile Leu Asp Leu			
185	190		195
ctg gaa gac atg cag cgt gaa ttg ggc atg ggt att ttg ttc att act			739
Leu Glu Asp Met Gln Arg Glu Leu Gly Met Gly Ile Leu Phe Ile Thr			
200	205		210
cac gat cta gcc gtg gca ggc gat cgg gcg gat cgc atc gtc gtc atg			787
His Asp Leu Ala Val Ala Gly Asp Arg Ala Asp Arg Ile Val Val Met			
215	220		225
caa aaa ggc gag gtg cgc gaa agt ggt tac gcg gct tcg gtc ttg acc			835
Gln Lys Gly Glu Val Arg Glu Ser Gly Tyr Ala Ala Ser Val Leu Thr			
230	235		240
gac ccc cag cat gag tat tcc aag aag ttg ctt gcc gac gcg ccc tcc			883
Asp Pro Gln His Glu Tyr Ser Lys Lys Leu Leu Ala Asp Ala Pro Ser			
250	255		260
ctc acc atc ggc gag atc ccc acg cga gtt ccg gcc gta gat ccg gag			931
Leu Thr Ile Gly Glu Ile Pro Thr Arg Val Pro Ala Val Asp Pro Glu			
265	270		275
gta gcg cag gcc aaa ggc ccg ctt ctg gta gtg gat aaa ttc cgc aag			979
Val Ala Gln Ala Lys Gly Pro Leu Leu Val Val Asp Lys Phe Arg Lys			
280	285		290
gaa cac caa cga ggc aaa gaa gga gca ttt gtt gcc gca aat gat att			1027
Glu His Gln Arg Gly Lys Glu Gly Ala Phe Val Ala Ala Asn Asp Ile			
295	300		305
tcc ttc gaa gta ctg cct ggc acc acg cat gcc atc gtc ggt gaa tcc			1075
Ser Phe Glu Val Leu Pro Gly Thr Thr His Ala Ile Val Gly Glu Ser			
310	315		320
ggt tct ggt aaa acc acg ctt ggc cgc gcg atc gcg atg ttt aat acg			1123
Gly Ser Gly Lys Thr Thr Leu Gly Arg Ala Ile Ala Met Phe Asn Thr			
330	335		340
ccg acc tct ggt tcc att tca gta agt ggc aag gac atc acc aac ctg			1171
Pro Thr Ser Gly Ser Ile Ser Val Ser Gly Lys Asp Ile Thr Asn Leu			
345	350		355
tcc aag gcc cag cag cgg gaa ctg cgc cag caa atc cag ctg gtg tac			1219
Ser Lys Ala Gln Gln Arg Glu Leu Arg Gln Gln Ile Gln Leu Val Tyr			
360	365		370
caa aac ccg tat tct tcc ctg gat cct cgc caa acc att ggc tcc acc			1267
Gln Asn Pro Tyr Ser Ser Leu Asp Pro Arg Gln Thr Ile Gly Ser Thr			
375	380		385


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atc gcg gaa cct ctg cgc aat ttc acc aag gtg agc aag cag gaa gcc 1315
Ile Ala Glu Pro Leu Arg Asn Phe Thr Lys Val Ser Lys Gln Glu Ala
390                      395                      400                      405

gac gaa aag gtg gca cac tac ctg gaa ctg gtg gcg ctt gac ccg gct 1363
Asp Glu Lys Val Ala His Tyr Leu Glu Leu Val Ala Leu Asp Pro Ala
                      410                      415                      420

ctt gcc acc cgt cgc cca cgt gag ctc tct ggt ggt cag cgc cag cgc 1411
Leu Ala Thr Arg Arg Pro Arg Glu Leu Ser Gly Gly Gln Arg Gln Arg
                      425                      430                      435

gtc gcc att gct cgt gcc atg att ttg gaa cct gaa ttg gtg gtt ttc 1459
Val Ala Ile Ala Arg Ala Met Ile Leu Glu Pro Glu Leu Val Val Phe
                      440                      445                      450

gac gaa gcc gta tcc gcg ttg gat gtg act gtg cag gca caa atc ctg 1507
Asp Glu Ala Val Ser Ala Leu Asp Val Thr Val Gln Ala Gln Ile Leu
                      455                      460                      465

cgc ctg ctc gac gat ctg caa cga gag cta ggc ttg act tac gtg ttt 1555
Arg Leu Leu Asp Asp Leu Gln Arg Glu Leu Gly Leu Thr Tyr Val Phe
470                      475                      480                      485

att tcc cac gac ctg gct gtg gtc cgt gaa atc tct gac act gtg tct 1603
Ile Ser His Asp Leu Ala Val Val Arg Glu Ile Ser Asp Thr Val Ser
                      490                      495                      500

gtg atg agt cgc ggc aac cag gtg gaa ctt gga aaa acc gca gaa gta 1651
Val Met Ser Arg Gly Asn Gln Val Glu Leu Gly Lys Thr Ala Glu Val
                      505                      510                      515

ttt aac aac ccg caa acc gat ttc act cgc cga ctc atc gac gcg atc 1699
Phe Asn Asn Pro Gln Thr Asp Phe Thr Arg Arg Leu Ile Asp Ala Ile
                      520                      525                      530

cca gga tcg cgc tat cgt ggt ggc gaa ctc aat ctt gga cta 1741
Pro Gly Ser Arg Tyr Arg Gly Gly Glu Leu Asn Leu Gly Leu
                      535                      540                      545

taggagcaga tcttaaaaat gtc 1764

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<210> 182

<211> 547

<212> PRT

<213> Corynebacterium glutamicum

<400> 182

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Met Thr Thr Pro Leu Leu Glu Ile Asn Asp Leu Val Val Ser Tyr Gln
  1                      5                      10                      15

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Thr Ala Lys Gly Leu Val His Ala Val Asn Asn Val Ser Leu Glu Val
      20                      25                      30

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His Pro Gly Gln Ile Thr Ala Ile Val Gly Glu Ser Gly Ser Gly Lys
      35                      40                      45

```

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Ser Thr Thr Ala Gln Ala Val Ile Gly Leu Leu Ala Asp Asn Ala Glu
      50                      55                      60

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Val 65	Asp	Ser	Gly	Arg	Ile 70	Ser	Phe	Asn	Gly	Arg 75	Ser	Leu	Val	Gly	Leu 80
Asn	Ala	Arg	Glu	Trp 85	Lys	Asn	Val	Arg	Gly 90	Thr	Lys	Ile	Gly	Leu 95	Ile
Pro	Gln	Asp	Pro 100	Asn	Asn	Ser	Leu	Asn 105	Pro	Val	Lys	Thr	Ile 110	Gly	Ala
Ser	Val	Gly 115	Glu	Gly	Leu	Ala	Ile 120	His	Lys	Arg	Gly	Thr 125	Ala	Ala	Glu
Arg	Lys 130	Lys	Lys	Val	Ile	Glu 135	Leu	Leu	Glu	Arg	Val 140	Gly	Ile	Asp	Asn
Pro 145	Glu	Val	Arg	Tyr 150	Asp	Gln	Tyr	Pro	His 155	Glu	Leu	Ser	Gly	Gly	Met 160
Lys	Gln	Arg	Ala	Leu 165	Ile	Ala	Ala	Ala	Ile 170	Ala	Leu	Glu	Pro	Glu 175	Leu
Ile	Ile	Ala	Asp 180	Glu	Pro	Thr	Ser	Ala 185	Leu	Asp	Val	Thr	Val 190	Gln	Lys
Ile	Ile 195	Leu	Asp	Leu	Leu	Glu	Asp 200	Met	Gln	Arg	Glu 205	Leu	Gly	Met	Gly
Ile 210	Leu	Phe	Ile	Thr	His	Asp 215	Leu	Ala	Val	Ala 220	Gly	Asp	Arg	Ala	Asp
Arg 225	Ile	Val	Val	Met	Gln 230	Lys	Gly	Glu	Val	Arg 235	Glu	Ser	Gly	Tyr	Ala 240
Ala	Ser	Val	Leu 245	Thr	Asp	Pro	Gln	His	Glu 250	Tyr	Ser	Lys	Lys	Leu 255	Leu
Ala	Asp	Ala	Pro 260	Ser	Leu	Thr	Ile	Gly 265	Glu	Ile	Pro	Thr	Arg 270	Val	Pro
Ala	Val 275	Asp	Pro	Glu	Val	Ala	Gln 280	Ala	Lys	Gly	Pro	Leu 285	Leu	Val	Val
Asp 290	Lys	Phe	Arg	Lys	Glu	His 295	Gln	Arg	Gly	Lys	Glu 300	Gly	Ala	Phe	Val
Ala 305	Ala	Asn	Asp	Ile	Ser 310	Phe	Glu	Val	Leu	Pro 315	Gly	Thr	Thr	His	Ala 320
Ile	Val	Gly	Glu 325	Ser	Gly	Ser	Gly	Lys	Thr 330	Thr	Leu	Gly	Arg	Ala 335	Ile
Ala	Met	Phe 340	Asn	Thr	Pro	Thr	Ser	Gly 345	Ser	Ile	Ser	Val	Ser 350	Gly	Lys
Asp	Ile 355	Thr	Asn	Leu	Ser	Lys	Ala 360	Gln	Gln	Arg	Glu 365	Leu	Arg	Gln	Gln
Ile 370	Gln	Leu	Val	Tyr	Gln 375	Asn	Pro	Tyr	Ser	Ser 380	Leu	Asp	Pro	Arg	Gln

40 45 50
 ttc atc ctc ggc atg ctc aaa ggc gac ttg gga acc tct agc ggt ggc 307
 Phe Ile Leu Gly Met Leu Lys Gly Asp Leu Gly Thr Ser Ser Gly Gly
 55 60 65
 gta gct gtt acc gac att gtt gcc cgc gct ttc ccc atc acc ctg cag 355
 Val Ala Val Thr Asp Ile Val Ala Arg Ala Phe Pro Ile Thr Leu Gln
 70 75 80 85
 cta aca ttc tgg gga ctc atc atc gct gtt gta gtg gcg ttg atc ctc 403
 Leu Thr Phe Trp Gly Leu Ile Ile Ala Val Val Val Ala Leu Ile Leu
 90 95 100
 ggt gtc atc gcc gct cta tac cga gac cgc tgg cct gac cag ttg att 451
 Gly Val Ile Ala Ala Leu Tyr Arg Asp Arg Trp Pro Asp Gln Leu Ile
 105 110 115
 cgc gtg gtc tcc att gcg gct ctt gct act cct tca ttc tgg ttg gct 499
 Arg Val Val Ser Ile Ala Ala Leu Ala Thr Pro Ser Phe Trp Leu Ala
 120 125 130
 atc ttg ctg atc cag tgg ttg ggt act atc cct gga gcc tgg ggt ttc 547
 Ile Leu Leu Ile Gln Trp Leu Gly Thr Ile Pro Gly Ala Trp Gly Phe
 135 140 145
 ttc cca gca ctt gtc acc cgg tgg gtc cca ttc agc gaa gat ccc gcc 595
 Phe Pro Ala Leu Val Thr Arg Trp Val Pro Phe Ser Glu Asp Pro Ala
 150 155 160 165
 acc tac ttc aac aac atc gca ctt cag cga ttg cgt tgg cag tcc ccg 643
 Thr Tyr Phe Asn Asn Ile Ala Leu Gln Arg Leu Arg Trp Gln Ser Pro
 170 175 180
 ttg cag gtt ctt tgg ccc gcg ttg ttc gta cct cca tgg tgg aag aac 691
 Leu Gln Val Leu Trp Pro Ala Leu Phe Val Pro Pro Trp Trp Lys Asn
 185 190 195
 tgg aca agg act acg tcc gca cag caa tgg gtg cag gat ccc caa aac 739
 Trp Thr Arg Thr Thr Ser Ala Gln Gln Ser Val Gln Asp Pro Gln Asn
 200 205 210
 tgaagttgtt gcccgcaatg ttc 762

<210> 184

<211> 213

<212> PRT

<213> Corynebacterium glutamicum

<400> 184

Met Ile Ile Gly Val Thr Leu Leu Val Phe Ile Val Met Ser Phe Ser
 1 5 10 15

Pro Ala Asp Pro Ala Arg Leu Ala Leu Gly Glu Ser Ala Ser Pro Glu
 20 25 30

Ala Leu Glu Ala Tyr Arg Glu Ala Asn Gly Leu Asn Asp Pro Met Met
 35 40 45

Val Arg Tyr Phe Asp Phe Ile Leu Gly Met Leu Lys Gly Asp Leu Gly

BGI-131CP

Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Shapiro-Wilk	Normality
Age	34.5	10.2	22	55	0.15	2.85	0.98	0.95
Gender	1.2	0.4	1	2	0.05	2.95	0.99	0.98
Marital Status	1.8	0.4	1	2	0.05	2.95	0.99	0.98
Education	12.5	1.5	9	16	0.15	2.85	0.98	0.95
Income	1500	500	500	3000	0.15	2.85	0.98	0.95
Occupation	1.5	0.5	1	3	0.05	2.95	0.99	0.98
Health Status	1.2	0.4	1	2	0.05	2.95	0.99	0.98
Stress Level	2.5	0.8	1	4	0.15	2.85	0.98	0.95
Life Satisfaction	3.5	0.5	1	5	0.15	2.85	0.98	0.95
Resilience	2.8	0.6	1	4	0.15	2.85	0.98	0.95
Optimism	3.2	0.5	1	4	0.15	2.85	0.98	0.95
Emotional Stability	2.5	0.4	1	4	0.15	2.85	0.98	0.95
Self-Esteem	3.0	0.5	1	4	0.15	2.85	0.98	0.95
Life Satisfaction	3.5	0.5	1	5	0.15	2.85	0.98	0.95
Resilience	2.8	0.6	1	4	0.15	2.85	0.98	0.95
Optimism	3.2	0.5	1	4	0.15	2.85	0.98	0.95
Emotional Stability	2.5	0.4	1	4	0.15	2.85	0.98	0.95
Self-Esteem	3.0	0.5	1	4	0.15	2.85	0.98	0.95

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gtc tac ctc gtc caa ggt gtc acc ctc acc gtt gcc atc gcc ttc atc 259
Val Tyr Leu Val Gln Gly Val Thr Leu Thr Val Ala Ile Ala Phe Ile
40 45 50

atc gtc aat atc gcc gtg gac ctg ctc tac gtc ctg gtc aat cca cgt 307
 Ile Val Asn Ile Ala Val Asp Leu Leu Tyr Val Leu Val Asn Pro Arg
 55 60 65

att agg agc atc tagatgcgcc gtaaactaac cac 342
 Ile Arg Ser Ile
 70

<210> 186

<211> 73

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

Val Ile Gly Leu Arg Val Gly Ser Leu Met Gly Gly Ala Val Ile Ile
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Glu Ile Ile Phe Asn Ile Gln Ala Met Gly Gln Leu Ile Leu Asp Gly
 20 25 30

Val Thr Arg Asn Asp Val Tyr Leu Val Gln Gly Val Thr Leu Thr Val
 35 40 45

Ala Ile Ala Phe Ile Ile Val Asn Ile Ala Val Asp Leu Leu Tyr Val
 50 55 60

Leu Val Asn Pro Arg Ile Arg Ser Ile
 65 70

<210> 187

<211> 1089

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1066)

<223> RXA02034

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aattgtcggtt gattggtcgg aaagaatccg gggtagcgca gtg agt aaa aca atc 115
 Val Ser Lys Thr Ile
 1 5

gct tgg act gtg ctg cgg tac acc ctg act ttt gtg atc gcc agc atc 163
 Ala Trp Thr Val Leu Arg Tyr Thr Leu Thr Phe Val Ile Ala Ser Ile
 10 15 20

atc att ttt gtg ctg att cga gtc atc ccc ggt gac ccc gcc gct gtt 211
 Ile Ile Phe Val Leu Ile Arg Val Ile Pro Gly Asp Pro Ala Ala Val
 25 30 35

gcc ctg gga att acc gcg aca cca gaa gca atc gct gcg ttg caa tca 259
 Ala Leu Gly Ile Thr Ala Thr Pro Glu Ala Ile Ala Ala Leu Gln Ser
 40 45 50

GeneBank

caa tta ggt act gat caa ccg ctt ttc caa cag tac ttt tcc tgg ata 307
 Gln Leu Gly Thr Asp Gln Pro Leu Phe Gln Gln Tyr Phe Ser Trp Ile
 55 60 65

ggt gga atg ctc act ggc gat ttc ggc acc tcg ctg agc tct ggc caa 355
 Gly Gly Met Leu Thr Gly Asp Phe Gly Thr Ser Leu Ser Ser Gly Gln
 70 75 80 85

gac ctt tcc ccc atc att ttt gac cgc tta caa gtg agc ctc att ttg 403
 Asp Leu Ser Pro Ile Ile Phe Asp Arg Leu Gln Val Ser Leu Ile Leu
 90 95 100

gtg gga tgc tcc att gtg ttg tcg ttg ctc att gcc att cca ctt ggt 451
 Val Gly Cys Ser Ile Val Leu Ser Leu Leu Ile Ala Ile Pro Leu Gly
 105 110 115

gtg ctt tcg gcc cgg cgc ggt ggc gtg atc att tcc ggc atc agc cag 499
 Val Leu Ser Ala Arg Arg Gly Gly Val Ile Ile Ser Gly Ile Ser Gln
 120 125 130

att ggc att gcg atc cct agt ttc ctc gcc ggt att ttg ttg gtc gct 547
 Ile Gly Ile Ala Ile Pro Ser Phe Leu Ala Gly Ile Leu Leu Val Ala
 135 140 145

gtc ttc gcc gtt ggt ttg ggg tgg ctg ccc gcc aat ggc tgg att ccg 595
 Val Phe Ala Val Gly Leu Gly Trp Leu Pro Ala Asn Gly Trp Ile Pro
 150 155 160 165

ccg tcg gaa aac ttt gga ggt ttc tta gcc agg ctg atc ctc ccg gtt 643
 Pro Ser Glu Asn Phe Gly Gly Phe Leu Ala Arg Leu Ile Leu Pro Val
 170 175 180

ctg gct ctt act gct gtt caa gca gca att ttg acc cgc tat gtc cgc 691
 Leu Ala Leu Thr Ala Val Gln Ala Ala Ile Leu Thr Arg Tyr Val Arg
 185 190 195

tct gca gta atg gat gta atg ggg caa gat ttc atg cgc acc gcg agg 739
 Ser Ala Val Met Asp Val Met Gly Gln Asp Phe Met Arg Thr Ala Arg
 200 205 210

tcg aaa ggt atg agc ttc aac cgc gcg ttg atc atc cac ggt ctt cgg 787
 Ser Lys Gly Met Ser Phe Asn Arg Ala Leu Ile Ile His Gly Leu Arg
 215 220 225

aat gct gct ctt cct gtc ctt acc gtc act ggt ttg cag cta aca acc 835
 Asn Ala Ala Leu Pro Val Leu Thr Val Thr Gly Leu Gln Leu Thr Thr
 230 235 240 245

ttg gtt atc ggc gcc gtg gtg att gaa caa gtc ttt gtc atc ccc gga 883
 Leu Val Ile Gly Ala Val Val Ile Glu Gln Val Phe Val Ile Pro Gly
 250 255 260

atc ggt tcg atg ctg ctg gag tcc gtg tcc aac cgt gat ctc atc gct 931
 Ile Gly Ser Met Leu Leu Glu Ser Val Ser Asn Arg Asp Leu Ile Ala
 265 270 275

gtg caa tct att gtc atg ctg ctg gtg gcg ttc acg ttg ctg gtt aat 979
 Val Gln Ser Ile Val Met Leu Leu Val Ala Phe Thr Leu Leu Val Asn
 280 285 290

ttg gtg gtt gat ctg ctg tat cag gtg gtt gat cca aga gtc ggt gct 1027

Ile His Gly Leu Arg Asn Ala Ala Leu Pro Val Leu Thr Val Thr Gly
225 230 235 240

[illegible]

Leu Gln Leu Thr Thr Leu Val Ile Gly Ala Val Val Ile Glu Gln Val
 245 250 255
 Phe Val Ile Pro Gly Ile Gly Ser Met Leu Leu Glu Ser Val Ser Asn
 260 265 270
 Arg Asp Leu Ile Ala Val Gln Ser Ile Val Met Leu Leu Val Ala Phe
 275 280 285
 Thr Leu Leu Val Asn Leu Val Val Asp Leu Leu Tyr Gln Val Val Asp
 290 295 300
 Pro Arg Val Gly Ala Val Gly Val Ala Ser Thr Lys Val Pro Gly Ser
 305 310 315 320
 Val Ala

<210> 189
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <221> CDS
 <222> (1)..(795)
 <223> RXA01013

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 Leu Gly Asn Pro Trp Thr Arg Pro Ala Ala Val Ile Ser Ile Val Val
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 ctc gcc gtt gcg gtg ctg atg gca ctt gtt cct gga ctg ttt acc tcc 96
 Leu Ala Val Ala Val Leu Met Ala Leu Val Pro Gly Leu Phe Thr Ser
 20 25 30
 cag gat ccg ttc act ggc gat gat gtg gcg ctg ctt ggg cca agt ggc 144
 Gln Asp Pro Phe Thr Gly Asp Asp Val Ala Leu Leu Gly Pro Ser Gly
 35 40 45
 acc cac tgg ttt ggt acc gat tcc gtg gga cgc gat ctc tac agt cgt 192
 Thr His Trp Phe Gly Thr Asp Ser Val Gly Arg Asp Leu Tyr Ser Arg
 50 55 60
 gtt gtt tac ggc gcg agg gaa acc ctg ctc ggt gca ctg atc gca gtg 240
 Val Val Tyr Gly Ala Arg Glu Thr Leu Leu Gly Ala Leu Ile Ala Val
 65 70 75 80
 ctg gtt ggt ctg atc gtg gga acc ctg atc gga ctg ctc gca ggt gca 288
 Leu Val Gly Leu Ile Val Gly Thr Leu Ile Gly Leu Leu Ala Gly Ala
 85 90 95
 cag cgc ggt tgg gtt gac act gta tta atg cgt ttc gtg gat gtg ctg 336
 Gln Arg Gly Trp Val Asp Thr Val Leu Met Arg Phe Val Asp Val Leu
 100 105 110
 ttg tcc atc ccg gca ctg ctg ctc agc ttg act gtc att atc ctt ttg 384
 Leu Ser Ile Pro Ala Leu Leu Leu Ser Leu Thr Val Ile Ile Leu Leu
 115 120 125

48 96 144 192 240 288 336 384

[illegible]

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<222> (101)..(910)  
<223> RXN02933
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ggttccaggg agcgtggcctt aagtgacaac gatcaaaaac atg ccc ctt tca ggg 115
Met Pro Leu Ser Gly
1 5

aaa atc ggc ggc ttc atc gtt gcc gtt gta ttt gtt ctt gct gcg ctg 163
Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe Val Leu Ala Ala Leu
10 15 20

tct ttc att tgg act ccg ttt gat cca gtt caa gct ttc cca cag gag 211
Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln Ala Phe Pro Gln Glu
25 30 35

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<210> 193
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(889)
 <223> FRXA02033

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 ggttccaggg agcgtggctt aagtgacaac gatcaaaaac atg ccc ott tca ggg 115
 Met Pro Leu Ser Gly
 1 5
 aaa atc ggc ggc ttc atc gtt gcc gtt gta ttt gtt ctt gct gcg ctg 163
 Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe Val Leu Ala Ala Leu
 10 15 20
 tct ttc att tgg act ccg ttt gat cca gtt caa gct ttc cca cag gag 211
 Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln Ala Phe Pro Gln Glu
 25 30 35
 cgc ott gag gga agt tct ttg agg cac ctg ttg gga acg gat cgt tat 259
 Arg Leu Glu Gly Ser Ser Leu Arg His Leu Leu Gly Thr Asp Arg Tyr
 40 45 50
 ggt cgc gat gtt tta tcc cag atc atg gtt ggt tcc cgc gtc acg ttg 307
 Gly Arg Asp Val Leu Ser Gln Ile Met Val Gly Ser Arg Val Thr Leu
 55 60 65
 ttg gtg ggc atc att gcg gtg gcg atc gca gca tta atc ggc acg cca 355
 Leu Val Gly Ile Ile Ala Val Ala Ile Ala Ala Leu Ile Gly Thr Pro
 70 75 80 85
 ctg ggt att gct gcg gga atg cgc cgt ggc atg gtg gaa acc ttt gtc 403
 Leu Gly Ile Ala Ala Gly Met Arg Arg Gly Met Val Glu Thr Phe Val
 90 95 100
 atg cgt ggt gcc gat tta atg ttg gcg ttc cca gca ctg ttg ttg gcg 451
 Met Arg Gly Ala Asp Leu Met Leu Ala Phe Pro Ala Leu Leu Leu Ala
 105 110 115
 att att tcc ggc gcc gtt ttc ggc gcc tcc acg tgg tcc gcg atg gtc 499
 Ile Ile Ser Gly Ala Val Phe Gly Ala Ser Thr Trp Ser Ala Met Val
 120 125 130
 gcg atc ggc atc gca ggc atc cct agt ttt gcc cgc gtg gct cgt gca 547
 Ala Ile Gly Ile Ala Gly Ile Pro Ser Phe Ala Arg Val Ala Arg Ala
 135 140 145
 ggc aca ttg cag gtg acc agt cag gat ttc atc gca gct gct cgg cta 595
 Gly Thr Leu Gln Val Thr Ser Gln Asp Phe Ile Ala Ala Ala Arg Leu
 150 155 160 165
 tca aaa gta agt tcc gcc cgg atc gcg ctt cgc cat att ttg ccc aac 643
 Ser Lys Val Ser Ser Ala Arg Ile Ala Leu Arg His Ile Leu Pro Asn
 170 175 180

Ala Ala Ala Arg Leu Ser Lys Val Ser Ser Ala Arg Ile Ala Leu Arg
 165 170 175

His Ile Leu Pro Asn Ile Thr Ser Met Leu Ile Val Gln Ala Ser Val
 180 185 190

Ala Phe Ala Leu Ala Ile Leu Ala Glu Ala Ala Leu Ser Phe Leu Gly
 195 200 205

Leu Gly Thr Thr Pro Pro Asp Pro Ser Trp Gly Arg Met Leu Gln Thr
 210 215 220

Ala Gln Ala Ser Ile Gly Val Thr Pro Met Leu Ala Val Trp Pro Gly
 225 230 235 240

Ala Ala Ile Ala Leu Thr Val Leu Gly Phe Asn Leu Phe Gly Asp Gly
 245 250 255

Leu Arg Asp Ala Ile Asp Pro
 260

<210> 195
 <211> 958
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(958)
 <223> RXA01006

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cattgaccat tccagcgacc attccagtga ggaggactaa atg act acc tgc cag 115
 Met Thr Thr Ser Gln
 1 5

att ctg cgc cgc atc ggc caa gcc gtc ttg gtc ttg ttg gtc acc ttt 163
 Ile Leu Arg Arg Ile Gly Gln Ala Val Leu Val Leu Leu Val Thr Phe
 10 15 20

acc ttg gcg ttc atc atg ctt tcc gcc ctc cct ggc gat gct gtg tcc 211
 Thr Leu Ala Phe Ile Met Leu Ser Ala Leu Pro Gly Asp Ala Val Ser
 25 30 35

gcc cgc tat tcc agc cct gat ttg ggt ctg tca cct gag cag atc gca 259
 Ala Arg Tyr Ser Ser Pro Asp Leu Gly Leu Ser Pro Glu Gln Ile Ala
 40 45 50

cag atc cgt gaa tcc tat ggt gcc gat gaa tcc ctg atc gct cag tac 307
 Gln Ile Arg Glu Ser Tyr Gly Ala Asp Glu Ser Leu Ile Ala Gln Tyr
 55 60 65

ttc tcc acc ttg ggt ggc ttc ctt gta ggt aac ttc ggt tac tcc gta 355
 Phe Ser Thr Leu Gly Gly Phe Leu Val Gly Asn Phe Gly Tyr Ser Val
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caa acc gga act gcc gtg gca acc cag ctg gca gaa gcc cta cca ggc 403
 Gln Thr Gly Thr Ala Val Ala Thr Gln Leu Ala Glu Ala Leu Pro Gly


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          90          95          100
acc ttg acc ttg gct att ttg gca ttc ttg ctc gca gcc att ttg gca 451
Thr Leu Thr Leu Ala Ile Leu Ala Phe Leu Leu Ala Ala Ile Leu Ala
          105          110          115

ctg gtt att tcc att ctt gcc acc atg gat cgc ttt gca tgg atc aag 499
Leu Val Ile Ser Ile Leu Ala Thr Met Asp Arg Phe Ala Trp Ile Lys
          120          125          130

ggc atc ttc cag gct ctg cct cca ttc ttt gtg tcc ctt cca agt ttc 547
Gly Ile Phe Gln Ala Leu Pro Pro Phe Phe Val Ser Leu Pro Ser Phe
          135          140          145

tgg ttg ggc atc atc ttg atc cag atc gtg tcc ttc cgc ctt ggt tgg 595
Trp Leu Gly Ile Ile Leu Ile Gln Ile Val Ser Phe Arg Leu Gly Trp
          150          155          160

gtc ccc gtt att ggg acc acc ccg gca caa gga ctg atc ctg ccg acc 643
Val Pro Val Ile Gly Thr Thr Pro Ala Gln Gly Leu Ile Leu Pro Thr
          170          175          180

atc acc ttg tcc atc cca att acc gct ccg ctt gca cag gtg ctc atc 691
Ile Thr Leu Ser Ile Pro Ile Thr Ala Pro Leu Ala Gln Val Leu Ile
          185          190          195

cgc tcg att gaa gag gtc aag gca caa ccg ttc atc gcg gct gtt cgt 739
Arg Ser Ile Glu Glu Val Lys Ala Gln Pro Phe Ile Ala Ala Val Arg
          200          205          210

gct cgc ggt gcg ggt gaa atg tgg atc ttc ttc cgc aac atc att cgc 787
Ala Arg Gly Ala Gly Glu Met Trp Ile Phe Phe Arg Asn Ile Ile Arg
          215          220          225

aac gcc ctt ttg cca acc ctg acg att gcc ggc atc ttg ttt ggt gaa 835
Asn Ala Leu Leu Pro Thr Leu Thr Ile Ala Gly Ile Leu Phe Gly Glu
          230          235          240

cta gtc ggt ggg gcc gtg gtc acc gag gca gtg ttc ggc cgc gct gga 883
Leu Val Gly Gly Ala Val Val Thr Glu Ala Val Phe Gly Arg Ala Gly
          250          255          260

ctt ggc caa atg acc gtc aac gca gtg gcc aac cgc gat atg cca gtg 931
Leu Gly Gln Met Thr Val Asn Ala Val Ala Asn Arg Asp Met Pro Val
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atg ctt gcc atc gtg gtg atc gca gct 958
Met Leu Ala Ile Val Val Ile Ala Ala
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<210> 196

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

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Leu Leu Val Thr Phe Thr Leu Ala Phe Ile Met Leu Ser Ala Leu Pro

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                20                25                30
Gly Asp Ala Val Ser Ala Arg Tyr Ser Ser Pro Asp Leu Gly Leu Ser
      35                40                45
Pro Glu Gln Ile Ala Gln Ile Arg Glu Ser Tyr Gly Ala Asp Glu Ser
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Leu Ile Ala Gln Tyr Phe Ser Thr Leu Gly Gly Phe Leu Val Gly Asn
      65                70                75                80
Phe Gly Tyr Ser Val Gln Thr Gly Thr Ala Val Ala Thr Gln Leu Ala
      85                90                95
Glu Ala Leu Pro Gly Thr Leu Thr Leu Ala Ile Leu Ala Phe Leu Leu
      100               105               110
Ala Ala Ile Leu Ala Leu Val Ile Ser Ile Leu Ala Thr Met Asp Arg
      115               120               125
Phe Ala Trp Ile Lys Gly Ile Phe Gln Ala Leu Pro Pro Phe Phe Val
      130               135               140
Ser Leu Pro Ser Phe Trp Leu Gly Ile Ile Leu Ile Gln Ile Val Ser
      145               150               155               160
Phe Arg Leu Gly Trp Val Pro Val Ile Gly Thr Thr Pro Ala Gln Gly
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Leu Ile Leu Pro Thr Ile Thr Leu Ser Ile Pro Ile Thr Ala Pro Leu
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Ala Gln Val Leu Ile Arg Ser Ile Glu Glu Val Lys Ala Gln Pro Phe
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Ile Ala Ala Val Arg Ala Arg Gly Ala Gly Glu Met Trp Ile Phe Phe
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Arg Asn Ile Ile Arg Asn Ala Leu Leu Pro Thr Leu Thr Ile Ala Gly
      225               230               235               240
Ile Leu Phe Gly Glu Leu Val Gly Gly Ala Val Val Thr Glu Ala Val
      245               250               255
Phe Gly Arg Ala Gly Leu Gly Gln Met Thr Val Asn Ala Val Ala Asn
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Arg Asp Met Pro Val Met Leu Ala Ile Val Val Ile Ala Ala
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<210> 197

<211> 1482

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1459)

<223> RXA02312

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gca gag act gag aat ccc acc aag acg ctt cct cgg gca atc aac tcc 787
Ala Glu Thr Glu Asn Pro Thr Lys Thr Leu Pro Arg Ala Ile Asn Ser

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215 220 225
 att ccc atc cgc atc gtg gtg ttc tat gtt ttg gcg ttg gct gtc atc 835
 Ile Pro Ile Arg Ile Val Val Phe Tyr Val Leu Ala Leu Ala Val Ile
 230 235 240 245

 atg atg gtc acc cca tgg gat cag gtc cgt gct gac aac agc cca ttc 883
 Met Met Val Thr Pro Trp Asp Gln Val Arg Ala Asp Asn Ser Pro Phe
 250 255 260

 gtg cag atg ttc gcg ctg gca gga atc cca gcg gcg gca ggc atc att 931
 Val Gln Met Phe Ala Leu Ala Gly Ile Pro Ala Ala Ala Gly Ile Ile
 265 270 275

 aac ttt gtg gtc atc act tct gca gcg tcg tct gcc aac agt ggt att 979
 Asn Phe Val Val Ile Thr Ser Ala Ala Ser Ser Ala Asn Ser Gly Ile
 280 285 290

 ttc tcc acc tcc cgc atg ttg tat gga ttg tct ttg gaa ggc gca gct 1027
 Phe Ser Thr Ser Arg Met Leu Tyr Gly Leu Ser Leu Glu Gly Ala Ala
 295 300 305

 ccg aaa cgg tgg agc cgg ttg tcc aag aac ttg gtg cca gcc agg gga 1075
 Pro Lys Arg Trp Ser Arg Leu Ser Lys Asn Leu Val Pro Ala Arg Gly
 310 315 320 325

 ttg act ttt tct gtg att tgc ctc att cca gcg gtg ggt ttg ctg tac 1123
 Leu Thr Phe Ser Val Ile Cys Leu Ile Pro Ala Val Gly Leu Leu Tyr
 330 335 340

 gct ggc ggc act gtc atc gag gca ttc aca ctg atc acc acg gtt tct 1171
 Ala Gly Gly Thr Val Ile Glu Ala Phe Thr Leu Ile Thr Thr Val Ser
 345 350 355

 tcg gtg ttg ttc atg gtg gtg tgg tcc tac att ttg gtg gct tat atc 1219
 Ser Val Leu Phe Met Val Val Trp Ser Tyr Ile Leu Val Ala Tyr Ile
 360 365 370

 gtc tac cgc cgc aac agc ccg gaa tta cac aaa aag tcg att ttc aaa 1267
 Val Tyr Arg Arg Asn Ser Pro Glu Leu His Lys Lys Ser Ile Phe Lys
 375 380 385

 atg cct ggc ggc gtg gtc atg gca gtt gtg gtg ttg gtg ttc ttc gca 1315
 Met Pro Gly Gly Val Val Met Ala Val Val Val Leu Val Phe Phe Ala
 390 395 400 405

 gcg atg ttg gtg gtg ctg tcc ctg gag ccg gat acc cgt gca gcg ctc 1363
 Ala Met Leu Val Val Leu Ser Leu Glu Pro Asp Thr Arg Ala Ala Leu
 410 415 420

 atc gcg acg cca gtg tgg ttc atc att ttg ggt atc ggt tgg ttg tcc 1411
 Ile Ala Thr Pro Val Trp Phe Ile Ile Leu Gly Ile Gly Trp Leu Ser
 425 430 435

 atc ggt gga gct aag ggc gct aag cat cgc agc caa ata acc tcc cac 1459
 Ile Gly Gly Ala Lys Gly Ala Lys His Arg Ser Gln Ile Thr Ser His
 440 445 450

 taaagctcct gggttagact cga 1482

[illegible]

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<212> DNA
<213> *Corynebacterium glutamicum*

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<222> (101)..(1219)  
<223> RXA00090
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											gtg	gcc	gtg	gat	aaa		115
											Val	Ala	Val	Asp	Lys		
											1				5		
gat att gaa aac cgc acc tca gac ctt tct cga tgg gaa act atg gag																	163
Asp	Ile	Glu	Asn	Arg	Thr	Ser	Asp	Leu	Ser	Arg	Trp	Glu	Thr	Met	Glu		
				10					15					20			
gaa tca gca acg gtc gag gga cgc acc gat gtc gaa cta gca tca gcg																	211
Glu	Ser	Ala	Thr	Val	Glu	Gly	Arg	Thr	Asp	Val	Glu	Leu	Ala	Ser	Ala		
			25					30					35				
ccg agc aaa cga cgc acc tca ggt gca ttc caa aca gcg cgc gcc aag																	259
Pro	Ser	Lys	Arg	Arg	Thr	Ser	Gly	Ala	Phe	Gln	Thr	Ala	Arg	Ala	Lys		
		40					45					50					

gca ctt gtc gga ccg atg aca ttc ctc gga ttc ttg gtc gcg acc ttg 1027
 Ala Leu Val Gly Pro Met Thr Phe Leu Gly Phe Leu Val Ala Thr Leu
 295 300 305

gca tat caa ttc gcc gac act tac gac cac cga tac atc ctt ccg atg 1075
 Ala Tyr Gln Phe Ala Asp Thr Tyr Asp His Arg Tyr Ile Leu Pro Met
 310 315 320 325

tcc gca ctc atc gga ttc gtc gta ctc agc ggc gct tac ttt gtc atg 1123
 Ser Ala Leu Ile Gly Phe Val Val Leu Ser Gly Ala Tyr Phe Val Met
 330 335 340

aac cac gtg ttc cgc gca caa ggc gtc gtg tcc atc att att gag atg 1171
 Asn His Val Phe Arg Ala Gln Gly Val Val Ser Ile Ile Ile Glu Met
 345 350 355

gtc ggc ggt acc gtc ttc ctc atc gtc atc ctc aga aag ggc aga ctg 1219
 Val Gly Gly Thr Val Phe Leu Ile Val Ile Leu Arg Lys Gly Arg Leu
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 Glu Leu Ala Ser Ala Pro Ser Lys Arg Arg Thr Ser Gly Ala Phe Gln
 35 40 45
 Thr Ala Arg Ala Lys Arg Arg Tyr Trp Ile Ile Met Ala Ala Leu Leu
 50 55 60
 Val Thr Ala Leu Ala Phe Thr Trp Gly Leu Ile Trp Tyr Lys Asn Pro
 65 70 75 80
 Met Pro Val Gly His Pro Ala Phe Ala Leu Ile Ala Glu Arg Arg Met
 85 90 95
 Glu Ser Val Phe Val Met Leu Ile Val Ala Val Cys Gln Gly Phe Ala
 100 105 110
 Thr Val Ala Phe Gln Thr Val Thr Asn Asn Arg Ile Ile Thr Pro Ser
 115 120 125
 Ile Met Gly Phe Glu Ser Leu Tyr Thr Leu Ile His Thr Ser Thr Val
 130 135 140
 Phe Phe Phe Gly Ala Thr Ala Leu Leu Ala Thr Arg Asn Leu Glu Met
 145 150 155 160
 Phe Val Gly Gln Leu Val Ile Met Val Leu Leu Thr Leu Val Leu Tyr
 165 170 175

Thr Trp Leu Leu Ser Gly Lys Arg Gly Asp Met His Ala Met Leu Leu
 180 185 190
 Val Gly Ile Ile Ile Gly Gly Gly Leu Gly Ser Ile Ser Thr Phe Met
 195 200 205
 Gln Arg Ile Leu Thr Pro Ser Glu Phe Asp Ile Leu Ser Ala Arg Leu
 210 215 220
 Phe Gly Ser Val Asn Asn Ala Glu Thr Glu Tyr Phe Pro Ile Ala Val
 225 230 235 240
 Pro Leu Val Val Val Ala Ser Val Leu Leu Leu Ser Ser Arg Arg
 245 250 255
 Leu Asn Val Val Gly Leu Gly Lys Asp Ala Ala Thr Asn Leu Gly Ile
 260 265 270
 Asn His Arg Arg Ser Ser Ile Tyr Thr Leu Val Leu Val Ser Val Leu
 275 280 285
 Met Ala Val Ser Thr Ala Leu Val Gly Pro Met Thr Phe Leu Gly Phe
 290 295 300
 Leu Val Ala Thr Leu Ala Tyr Gln Phe Ala Asp Thr Tyr Asp His Arg
 305 310 315 320
 Tyr Ile Leu Pro Met Ser Ala Leu Ile Gly Phe Val Val Leu Ser Gly
 325 330 335
 Ala Tyr Phe Val Met Asn His Val Phe Arg Ala Gln Gly Val Val Ser
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 Arg Lys Gly Arg Leu
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1099)
 <223> RXA00089

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 Met Ala Thr Pro Ala
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 tcg gct ccc act tcc gaa cca cgt ctc aaa cgc acc aga gcc aag ctt 163
 Ser Ala Pro Thr Ser Glu Pro Arg Leu Lys Arg Thr Arg Ala Lys Leu
 10 15 20

ttt gat tgg aag ctt ctc atc ggc atc att ttc gtc gcc ggc ctc gtg	211
Phe Asp Trp Lys Leu Leu Ile Gly Ile Ile Phe Val Ala Gly Leu Val	
25 30 35	
gtg ctt tcc ctc ctc acc ggc caa tac gac att ttc ggt ggc gat gat	259
Val Leu Ser Leu Leu Thr Gly Gln Tyr Asp Ile Phe Gly Gly Asp Asp	
40 45 50	
ggc caa ctg atg ttc gag gca gtt cgc atc ccg cgt acc gtt tcc ctc	307
Gly Gln Leu Met Phe Glu Ala Val Arg Ile Pro Arg Thr Val Ser Leu	
55 60 65	
att ttg tcc ggt gca gca atg gcg atg tgt ggc tta gtc atg cag ctg	355
Ile Leu Ser Gly Ala Ala Met Ala Met Cys Gly Leu Val Met Gln Leu	
70 75 80 85	
ttg acc caa aac aaa ttc gtg gaa ccc agc acc aca gga aca acc gaa	403
Leu Thr Gln Asn Lys Phe Val Glu Pro Ser Thr Thr Gly Thr Thr Glu	
90 95 100	
tgg gca ggt ctt ggc ctc ctc ttc gtg att tac ttc gtg cca gcc gcg	451
Trp Ala Gly Leu Gly Leu Leu Phe Val Ile Tyr Phe Val Pro Ala Ala	
105 110 115	
acc gtt ttg gat cgc atg ctc ggt gcc gtg gtg ttt tcc ttc atc gga	499
Thr Val Leu Asp Arg Met Leu Gly Ala Val Val Phe Ser Phe Ile Gly	
120 125 130	
acc atg gtg ttc ttc ctc ttt cta cgc cga gta aca ctg cgt tcc tca	547
Thr Met Val Phe Phe Leu Phe Leu Arg Arg Val Thr Leu Arg Ser Ser	
135 140 145	
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Leu Ile Val Pro Ile Ile Gly Ile Met Leu Gly Ala Val Val Ser Ser	
150 155 160 165	
atc tcc agc ttc ttc gcc ttg caa ttc gac atg ctc cag caa ttg gga	643
Ile Ser Ser Phe Phe Ala Leu Gln Phe Asp Met Leu Gln Gln Leu Gly	
170 175 180	
aca tgg ttt gcg ggt tcc ttt aat aca gtg ttc cgc gga cag tac gaa	691
Thr Trp Phe Ala Gly Ser Phe Asn Thr Val Phe Arg Gly Gln Tyr Glu	
185 190 195	
gtg ctg tgg atc gtt gtc atc gtc gtt att gca gtg ttc ttc ttc gca	739
Val Leu Trp Ile Val Val Ile Val Val Ile Ala Val Phe Phe Phe Ala	
200 205 210	
gac cgg ctc acc gta gct ggc ctt ggc gag gaa atc gcg aca aac gtg	787
Asp Arg Leu Thr Val Ala Gly Leu Gly Glu Glu Ile Ala Thr Asn Val	
215 220 225	
ggt ctc aat tac aac cgc atg gtc ctt atc gga act ggc ctc atc gcc	835
Gly Leu Asn Tyr Asn Arg Met Val Leu Ile Gly Thr Gly Leu Ile Ala	
230 235 240 245	
atc gca aca ggt gtg gtc acc gtc gtg gtt ggt agc ctg cca ttc ctc	883
Ile Ala Thr Gly Val Val Thr Val Val Val Gly Ser Leu Pro Phe Leu	
250 255 260	

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<213> Corynebacterium glutamicum

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Val Ala Gly Leu Val Val Leu Ser Leu Leu Thr Gly Gln Tyr Asp Ile
      35              40              45
Phe Gly Gly Asp Asp Gly Gln Leu Met Phe Glu Ala Val Arg Ile Pro
    50              55              60
Arg Thr Val Ser Leu Ile Leu Ser Gly Ala Ala Met Ala Met Cys Gly
 65              70              75              80
Leu Val Met Gln Leu Leu Thr Gln Asn Lys Phe Val Glu Pro Ser Thr
          85              90              95
Thr Gly Thr Thr Glu Trp Ala Gly Leu Gly Leu Leu Phe Val Ile Tyr
          100              105              110
Phe Val Pro Ala Ala Thr Val Leu Asp Arg Met Leu Gly Ala Val Val
      115              120              125
Phe Ser Phe Ile Gly Thr Met Val Phe Phe Leu Phe Leu Arg Arg Val
    130              135              140
Thr Leu Arg Ser Ser Leu Ile Val Pro Ile Ile Gly Ile Met Leu Gly
 145              150              155              160
Ala Val Val Ser Ser Ile Ser Ser Phe Phe Ala Leu Gln Phe Asp Met
          165              170              175
Leu Gln Gln Leu Gly Thr Trp Phe Ala Gly Ser Phe Asn Thr Val Phe

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<210> 202
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<212> PRT
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Val Ala Gly Leu Val Val Leu Ser Leu Leu Thr Gly Gln Tyr Asp Ile
      35          40          45
Phe Gly Gly Asp Asp Gly Gln Leu Met Phe Glu Ala Val Arg Ile Pro
  50          55          60
Arg Thr Val Ser Leu Ile Leu Ser Gly Ala Ala Met Ala Met Cys Gly
  65          70          75          80
Leu Val Met Gln Leu Leu Thr Gln Asn Lys Phe Val Glu Pro Ser Thr
          85          90          95
Thr Gly Thr Thr Glu Trp Ala Gly Leu Gly Leu Leu Phe Val Ile Tyr
          100          105          110
Phe Val Pro Ala Ala Thr Val Leu Asp Arg Met Leu Gly Ala Val Val
      115          120          125
Phe Ser Phe Ile Gly Thr Met Val Phe Phe Leu Phe Leu Arg Arg Val
      130          135          140
Thr Leu Arg Ser Ser Leu Ile Val Pro Ile Ile Gly Ile Met Leu Gly
  145          150          155          160
Ala Val Val Ser Ser Ile Ser Ser Phe Phe Ala Leu Gln Phe Asp Met
          165          170          175
Leu Gln Gln Leu Gly Thr Trp Phe Ala Gly Ser Phe Asn Thr Val Phe

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180 185 190

Arg Gly Gln Tyr Glu Val Leu Trp Ile Val Val Ile Val Val Ile Ala
195 200 205

Val Phe Phe Phe Ala Asp Arg Leu Thr Val Ala Gly Leu Gly Glu Glu
210 215 220

Ile Ala Thr Asn Val Gly Leu Asn Tyr Asn Arg Met Val Leu Ile Gly
225 230 235 240

Thr Gly Leu Ile Ala Ile Ala Thr Gly Val Val Thr Val Val Val Gly
245 250 255

Ser Leu Pro Phe Leu Gly Leu Ile Val Pro Asn Val Val Ser Met Phe
260 265 270

Arg Gly Asp Asp Leu Arg Ser Asn Leu Pro Trp Val Cys Leu Thr Gly
275 280 285

Ile Ala Ile Val Thr Ile Cys Asp Leu Ile Ser Arg Thr Ile Ile Ala
290 295 300

Pro Phe Glu Ile Pro Val Ser Val Ile Leu Gly Ile Ile Gly Ala Val
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Val Phe Val Ile Met Ile Val Arg Gln Arg Gly Arg Gly
325 330

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<212> DNA

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<222> (1)..(726)

<223> RXN01285

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aac ggc tgc ggc aaa tcc acc ctg ctc cgc ggt ttc tcc cgc gtg ctc 96
Asn Gly Cys Gly Lys Ser Thr Leu Leu Arg Gly Phe Ser Arg Val Leu
20 25 30

aat ccg cag cac ggc aaa gtg ctt ctc gac ggt cgg caa ctc gat tca 144
Asn Pro Gln His Gly Lys Val Leu Leu Asp Gly Arg Gln Leu Asp Ser
35 40 45

ttc aag cct aaa gag atc gcc cga gaa cta ggc ctg ctg cca cag acc 192
Phe Lys Pro Lys Glu Ile Ala Arg Glu Leu Gly Leu Leu Pro Gln Thr
50 55 60

tcc atc gcc cca gaa ggc atc cgg gtt tac gat ctc atc gcg cgc ggg 240
Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile Ala Arg Gly
65 70 75 80

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cgc gct ccc tac caa agc ctc ata caa caa tgg cgc acc tcc gac gaa 288
 Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr Ser Asp Glu
 85 90 95

gac gcc gtc gcg caa gcg ctc gcc tcc acg aat ctc acc gaa ctt gca 336
 Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr Glu Leu Ala
 100 105 110

gct cgc ctc gtc gat gaa ctc tcc ggt ggc cag cgc caa cga gtg tgg 384
 Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Trp
 115 120 125

gtg gcc atg ttg ctc gcc cag caa aca ccg atc atg ctt ctc gac gag 432
 Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu Leu Asp Glu
 130 135 140

ccc acc acc ttc ctc gac atc gcc cac caa tac gaa ctc ttg gaa ttg 480
 Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu Leu Glu Leu
 145 150 155 160

ctg cgc gca ttc aac gag gcc ggg aaa act gtg gtc act gtg ctt cac 528
 Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr Val Leu His
 165 170 175

gat ctc aac caa gcc gcc cgc tac gcc gac cac ctc atc gtg atg aaa 576
 Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile Val Met Lys
 180 185 190

gat ggg cac gta cat gcc acg ggc aca ccg gag gaa gtc tta act gcc 624
 Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val Leu Thr Ala
 195 200 205

gag atg gtt caa gga gtt ttt ggc ctg ccc tgc atc atc tcc cca gac 672
 Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile Ser Pro Asp
 210 215 220

ccc gtc aca gga acc ccc acc gtc gtt ccc ctc agt cgg tct cgc gca 720
 Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg Ser Arg Ala
 225 230 235 240

gga gct taagtagcta cccctccaac gga 749
 Gly Ala

<210> 204

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

Leu Asn Val Thr Ile Pro Asp Asn Thr Phe Thr Ala Ile Ile Gly Pro
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Asn Gly Cys Gly Lys Ser Thr Leu Leu Arg Gly Phe Ser Arg Val Leu
 20 25 30

Asn Pro Gln His Gly Lys Val Leu Leu Asp Gly Arg Gln Leu Asp Ser
 35 40 45

Phe Lys Pro Lys Glu Ile Ala Arg Glu Leu Gly Leu Leu Pro Gln Thr

50 55 60
 Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile Ala Arg Gly
 65 70 75 80
 Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr Ser Asp Glu
 85 90 95
 Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr Glu Leu Ala
 100 105 110
 Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Trp
 115 120 125
 Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu Leu Asp Glu
 130 135 140
 Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu Leu Glu Leu
 145 150 155 160
 Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr Val Leu His
 165 170 175
 Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile Val Met Lys
 180 185 190
 Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val Leu Thr Ala
 195 200 205
 Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile Ser Pro Asp
 210 215 220
 Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg Ser Arg Ala
 225 230 235 240
 Gly Ala

<210> 205
 <211> 566
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(543)
 <223> FRXA01285

<400> 205
 cca cag acc tcc atc gcc cca gaa ggc atc cgg gtt tac gat ctc atc 48
 Pro Gln Thr Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile
 1 5 10 15
 gcg cgc ggg cgc gct ccc tac caa agc ctc ata caa caa tgg cgc acc 96
 Ala Arg Gly Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr
 20 25 30
 tcc gac gaa gac gcc gtc gcg caa gcg ctc gcc tcc acg aat ctc acc 144
 Ser Asp Glu Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr
 35 40 45

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gaa ctt gca gct cgc ctc gtc gat gaa ctc tcc ggt ggc cag cgc caa 192
Glu Leu Ala Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln
    50                      55                      60

cga gtg tgg gtg gcc atg ttg ctc gcc cag caa aca ccg atc atg ctt 240
Arg Val Trp Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu
    65                      70                      75                      80

ctc gac gag ccc acc acc ttc ctc gac atc gcc cac caa tac gaa ctc 288
Leu Asp Glu Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu
                      85                      90                      95

ttg gaa ttg ctg cgc gca ttc aac gag gcc ggg aaa act gtg gtc act 336
Leu Glu Leu Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr
    100                      105                      110

gtg ctt cac gat ctc aac caa gcc gcc cgc tac gcc gac cac ctc atc 384
Val Leu His Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile
    115                      120                      125

gtg atg aaa gat ggg cac gta cat gcc acg ggc aca ccg gag gaa gtc 432
Val Met Lys Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val
    130                      135                      140

tta act gcc gag atg gtt caa gga gtt ttt ggc ctg ccc tgc atc atc 480
Leu Thr Ala Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile
    145                      150                      155                      160

tcc cca gac ccc gtc aca gga acc ccc acc gtc gtt ccc ctc agt cgg 528
Ser Pro Asp Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg
    165                      170                      175

tct cgc gca gga gct taagtagcta cccctccaac gga 566
Ser Arg Ala Gly Ala
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<210> 206

<211> 181

<212> PRT

<213> Corynebacterium glutamicum

<400> 206

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Pro Gln Thr Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile
    1                      5                      10                      15

Ala Arg Gly Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr
    20                      25                      30

Ser Asp Glu Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr
    35                      40                      45

Glu Leu Ala Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln
    50                      55                      60

Arg Val Trp Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu
    65                      70                      75                      80

Leu Asp Glu Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu
    85                      90                      95

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Leu Glu Leu Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr
 100 105 110
 Val Leu His Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile
 115 120 125
 Val Met Lys Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val
 130 135 140
 Leu Thr Ala Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile
 145 150 155 160
 Ser Pro Asp Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg
 165 170 175
 Ser Arg Ala Gly Ala
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<210> 207
 <211> 936
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(913)
 <223> RXA02728

<400> 207
 atcccatagc ttgccttccg atcggcattt tcacagcgct ggtcggcggc ccaacattct 60
 tcataatggt gcgccgaatg atgaaaaggg cgtgcactaa atg gcc att gtt tcc 115
 Met Ala Ile Val Ser
 1 5
 ctc gac aac gtc acc gta tcc att gaa gga aaa aag ctt ctc gac gcc 163
 Leu Asp Asn Val Thr Val Ser Ile Glu Gly Lys Lys Leu Leu Asp Ala
 10 15 20
 gtc tcc ctc aag gcc tac ccc ggg gaa gtg ttg gga ctc atc ggc cca 211
 Val Ser Leu Lys Ala Tyr Pro Gly Glu Val Leu Gly Leu Ile Gly Pro
 25 30 35
 aac ggt gcc gga aaa tcc act ctg ctg agt gtc ctt tca ggc gat cgg 259
 Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Val Leu Ser Gly Asp Arg
 40 45 50
 ctt ccc gat tca ggc gaa gtc aac gtc ggt ggc tta gat ccc gca aca 307
 Leu Pro Asp Ser Gly Glu Val Asn Val Gly Gly Leu Asp Pro Ala Thr
 55 60 65
 gca gcg gca tcc gat atg gcc agg gtg cga gca gtc atg ctt caa gat 355
 Ala Ala Ala Ser Asp Met Ala Arg Val Arg Ala Val Met Leu Gln Asp
 70 75 80 85
 gtc agc gtg gca ttt tcc ttc ctc gtg tgg gac gtc gta gaa atg ggc 403
 Val Ser Val Ala Phe Ser Phe Leu Val Trp Asp Val Val Glu Met Gly
 90 95 100

agg cgg ccg tgg cag aag gcg tca acc ccc gaa gag gat cat gaa atc 451
 Arg Arg Pro Trp Gln Lys Ala Ser Thr Pro Glu Glu Asp His Glu Ile
 105 110 115

atc gaa gca gcg ctt gcc gcc acc tcg gta tcg cac ctt gcc gaa cgt 499
 Ile Glu Ala Ala Leu Ala Ala Thr Ser Val Ser His Leu Ala Glu Arg
 120 125 130

gaa atc acc aca ctg tca ggc ggc gag cgg gca cgc gtt gcc ttg tcc 547
 Glu Ile Thr Thr Leu Ser Gly Gly Glu Arg Ala Arg Val Ala Leu Ser
 135 140 145

cgt gtc ctt gct cag caa acc ccc att gtg ctg ttg gac gaa cca aca 595
 Arg Val Leu Ala Gln Gln Thr Pro Ile Val Leu Leu Asp Glu Pro Thr
 150 155 160 165

gcc gcg atg gat atc agc cac caa gaa caa act ctg ggc aca gcg cga 643
 Ala Ala Met Asp Ile Ser His Gln Glu Gln Thr Leu Gly Thr Ala Arg
 170 175 180

gca ctg gca gcc gcc ggg gca gca gtg att gtg gtc ctt cat gat ctc 691
 Ala Leu Ala Ala Ala Gly Ala Ala Val Ile Val Val Leu His Asp Leu
 185 190 195

aat gcg gcc gct gca tat tgc gac agc att gtg tgt ctc agt gat ggt 739
 Asn Ala Ala Ala Ala Tyr Cys Asp Ser Ile Val Cys Leu Ser Asp Gly
 200 205 210

cga gtg att gcc tcc ggt tct gtt gat cag gtg tat tcc acg gaa acg 787
 Arg Val Ile Ala Ser Gly Ser Val Asp Gln Val Tyr Ser Thr Glu Thr
 215 220 225

ctg tcc cgt gtt tac ggt tgg cct atc agg gtc gat cat agt gga aaa 835
 Leu Ser Arg Val Tyr Gly Trp Pro Ile Arg Val Asp His Ser Gly Lys
 230 235 240 245

tat gtt cga gtg gag ccg gac cgt tct gag gcg aat tta ccc tcc gta 883
 Tyr Val Arg Val Glu Pro Asp Arg Ser Glu Ala Asn Leu Pro Ser Val
 250 255 260

cta cag gtg aaa aat acg gtt tca cca gct tagatacatg actaactaag 933
 Leu Gln Val Lys Asn Thr Val Ser Pro Ala
 265 270

gtt 936

<210> 208

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

Met Ala Ile Val Ser Leu Asp Asn Val Thr Val Ser Ile Glu Gly Lys
 1 5 10 15

Lys Leu Leu Asp Ala Val Ser Leu Lys Ala Tyr Pro Gly Glu Val Leu
 20 25 30

Gly Leu Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Val
 35 40 45

Leu Ser Gly Asp Arg Leu Pro Asp Ser Gly Glu Val Asn Val Gly Gly
 50 55 60
 Leu Asp Pro Ala Thr Ala Ala Ser Asp Met Ala Arg Val Arg Ala
 65 70 75 80
 Val Met Leu Gln Asp Val Ser Val Ala Phe Ser Phe Leu Val Trp Asp
 85 90 95
 Val Val Glu Met Gly Arg Arg Pro Trp Gln Lys Ala Ser Thr Pro Glu
 100 105 110
 Glu Asp His Glu Ile Ile Glu Ala Ala Leu Ala Ala Thr Ser Val Ser
 115 120 125
 His Leu Ala Glu Arg Glu Ile Thr Thr Leu Ser Gly Gly Glu Arg Ala
 130 135 140
 Arg Val Ala Leu Ser Arg Val Leu Ala Gln Gln Thr Pro Ile Val Leu
 145 150 155 160
 Leu Asp Glu Pro Thr Ala Ala Met Asp Ile Ser His Gln Glu Gln Thr
 165 170 175
 Leu Gly Thr Ala Arg Ala Leu Ala Ala Ala Gly Ala Ala Val Ile Val
 180 185 190
 Val Leu His Asp Leu Asn Ala Ala Ala Tyr Cys Asp Ser Ile Val
 195 200 205
 Cys Leu Ser Asp Gly Arg Val Ile Ala Ser Gly Ser Val Asp Gln Val
 210 215 220
 Tyr Ser Thr Glu Thr Leu Ser Arg Val Tyr Gly Trp Pro Ile Arg Val
 225 230 235 240
 Asp His Ser Gly Lys Tyr Val Arg Val Glu Pro Asp Arg Ser Glu Ala
 245 250 255
 Asn Leu Pro Ser Val Leu Gln Val Lys Asn Thr Val Ser Pro Ala
 260 265 270

<210> 209
 <211> 903
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(880)
 <223> RXN03080

<400> 209
 cttgcaaaca ggcgtggtgg tggcgttcat tggctcacca attttccttt atttactgct 60
 cagcatgcgc aagcgacgcg gattggggct gtaaaaactc atg cct caa tta gtt 115
 Met Pro Gln Leu Val
 1 5

903

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Pro Asn Pro Phe

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<210> 211
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<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(880)  
<223> FRXA02864
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<400> 211																
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cagcatgcgc aagcgacgcg gattggggct gtaaaaaactc atg cct caa tta gtt																115
Met Pro Gln Leu Val																5
1																
gaa att cgt gat ctc aac gtt gaa ttc ccc tct cgc cat gca gtg aaa																163
Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser Arg His Ala Val Lys																20
10 15																
aac gtg tct ttt tct gca cct gct gga aaa gtc acc gca ctg att ggc																211
Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val Thr Ala Leu Ile Gly																35
25 30																
cca aat ggt gct ggt aaa agt act gcc ctt tcg gcg att gca gga ttg																259
Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser Ala Ile Ala Gly Leu																50
40 45																
gtt gaa tcc acc ggc gag gta atg gtt ggt ggg agt ggg gtt gcg tcg																307
Val Glu Ser Thr Gly Glu Val Met Val Gly Gly Ser Gly Val Ala Ser																65
55 60																
aaa agc gct aaa gcc cga gcc cgc ctg ctc tca ctc gtg ccg caa aac																355
Lys Ser Ala Lys Ala Arg Ala Arg Leu Leu Ser Leu Val Pro Gln Asn																85
70 75 80																
acc gag ttg cgc att ggt ttt agt gca cgc gac gtt gtc gcg atg ggc																403
Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp Val Val Ala Met Gly																100
90 95																
cgc tac ccg cat cgt ggc cgc ttc gcc gtg gag acc gac gca gat cga																451
Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu Thr Asp Ala Asp Arg																115
105 110																
cgc gcc acc gat gac gcc ctg cgc gcc atc aac gcg ctc gac atc gcc																499
Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn Ala Leu Asp Ile Ala																130
120 125																
gag cag ccc gtc aac gaa tta tcg ggc ggc cag cag cag ctc atc cac																547
Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln Gln Gln Leu Ile His																145
135 140																
atc ggc cga gcg ctc gcc caa gac acc gcc gtc gtg ctt ctc gac gag																595
Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val Val Leu Leu Asp Glu																165
150 155 160																
ccc gtc tcc gcc ctt gat cta cgg cac caa gtt gaa gtc ctt caa ctc																643

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Pro Val Ser Ala Leu Asp Leu Arg His Gln Val Glu Val Leu Gln Leu
      170                      175                      180

ctg cgc gcc cga gct aat tcc ggc acc acc gtg atc gtc gtc ctt cac    691
Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val Ile Val Val Leu His
      185                      190                      195

gat ctc aac cac gtt gcc cgt tgg tgc gac cat gca gtg ttg atg gcc    739
Asp Leu Asn His Val Ala Arg Trp Cys Asp His Ala Val Leu Met Ala
      200                      205                      210

gac ggc gaa gtt gtc tcc caa ggt gac atc cgc gag gtg ctc gaa cct    787
Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg Glu Val Leu Glu Pro
      215                      220                      225

gcc aca ctg tcc acc gtg tac gga ctg ccc att gcg gtg cgc gat gat    835
Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile Ala Val Arg Asp Asp
      230                      235                      240                      245

ccc gaa acc agc tca ctt cgc gtg atc ccg cat cca aat ccc ttt    880
Pro Glu Thr Ser Ser Leu Arg Val Ile Pro His Pro Asn Pro Phe
      250                      255                      260

tgattgaaag ttgacttaa aaa    903

<210> 212
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 212
Met Pro Gln Leu Val Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser
  1                      5                      10                      15

Arg His Ala Val Lys Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val
      20                      25                      30

Thr Ala Leu Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser
      35                      40                      45

Ala Ile Ala Gly Leu Val Glu Ser Thr Gly Glu Val Met Val Gly Gly
      50                      55                      60

Ser Gly Val Ala Ser Lys Ser Ala Lys Ala Arg Ala Arg Leu Leu Ser
      65                      70                      75                      80

Leu Val Pro Gln Asn Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp
      85                      90                      95

Val Val Ala Met Gly Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu
      100                      105                      110

Thr Asp Ala Asp Arg Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn
      115                      120                      125

Ala Leu Asp Ile Ala Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln
      130                      135                      140

Gln Gln Leu Ile His Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val
      145                      150                      155                      160

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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1126)
<223> RXN00523
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tgtttatattg gattattcgt cgtcagaaaag tcaaagagct atg agc ctt agc cat																	115
Met Ser Leu Ser His																	
1 5																	
caa ctc aag cgc cag cgc gca tgc cgc aac tcc cgc agg tgg ctg att																	163
Gln	Leu	Lys	Arg	Gln	Arg	Ala	Ser	Arg	Asn	Ser	Arg	Arg	Trp	Leu	Ile		
10 15 20																	
gtt gcg gca ttg ggc gtc gtc acg ctt ggt att ttt gct ttt tct ttg																	211
Val	Ala	Ala	Leu	Gly	Val	Val	Thr	Leu	Gly	Ile	Phe	Ala	Phe	Ser	Leu		
25 30 35																	
atg tgg ggc gag gtg ttt tat ggc cct gct cag gtg ctg aaa gtg ttg																	259
Met	Trp	Gly	Glu	Val	Phe	Tyr	Gly	Pro	Ala	Gln	Val	Leu	Lys	Val	Leu		
40 45 50																	
tct gga cag cag gtt ccc ggc gcg agt tat tcc gtt ggc gtg ttg cgt																	307
Ser	Gly	Gln	Gln	Val	Pro	Gly	Ala	Ser	Tyr	Ser	Val	Gly	Val	Leu	Arg		
55 60 65																	
ttg ccg cgc gcg gtg atg ggt ttg act gcg ggt ttg gcg ttt ggc gcg																	355
Leu	Pro	Arg	Ala	Val	Met	Gly	Leu	Thr	Ala	Gly	Leu	Ala	Phe	Gly	Ala		
70 75 80 85																	
gcg ggc gtg att ttt cag acg gtg ttg cgt aat cag ttg gcg tgc ccg																	403

Ala	Gly	Val	Ile	Phe 90	Gln	Thr	Val	Leu	Arg 95	Asn	Gln	Leu	Ala	Ser 100	Pro	
gat Asp	att Ile	atc Ile	ggc Gly 105	att Ile	tct Ser	tct Ser	ggc Gly 110	gcg Ala 110	tcg Ser	gcg Ala	gcg Ala	ggc Gly 115	gta Val 115	att Ile	tgc Cys	451
att Ile	gtg Val	ttt Phe 120	ttc Phe	ggg Gly	atg Met	tcg Ser	cag Gln 125	tct Ser	gca Ala	gtg Val	tcg Ser	gcg Ala 130	att Ile	tct Ser	ttg Leu	499
tgt Cys	gcg Ala 135	tcc Ser	ttg Leu	gct Ala	gtg Val	gcg Ala 140	ttg Leu	ttg Leu	att Ile	tat Tyr	ctg Leu 145	gtg Val	gcg Ala	tat Tyr	cgc Arg	547
ggt Gly 150	ggt Gly	ttt Phe	tcg Ser	gcc Ala	acg Thr 155	cgt Arg	ctg Leu	att Ile	ctt Leu	acc Thr 160	ggc Gly	att Ile	ggt Gly	att Ile	gct Ala 165	595
gcg Ala	atg Met	ctg Leu	aat Asn	tca Ser 170	tta Leu	gtg Val	tcg Ser	tat Tyr	tcg Ser 175	ctg Leu	tcc Ser	aag Lys	gct Ala	gat Asp 180	tct Ser	643
tgg Trp	gat Asp	ctg Leu	ccg Pro	acc Thr	gcg Ala	acg Thr	cgc Arg 190	tgg Trp	ctt Leu	acc Thr	ggc Gly	tcg Ser	ctc Leu 195	aat Asn	ggt Gly	691
gcg Ala	acg Thr	tgg Trp 200	gat Asp	cgt Arg	gcg Ala	atg Met	ccg Pro 205	ctg Leu	att Ile	gtc Val	acc Thr 210	act Thr	gtg Val	gta Val	ctc Leu	739
att Ile	ccg Pro 215	ctg Leu	ctg Leu	gtg Val	gct Ala	aat Asn 220	gcg Ala	cgc Arg	aat Asn	gtg Val	gat Asp 225	ctt Leu	atg Met	cgt Arg	ttg Leu	787
ggc Gly 230	aat Asn	gat Asp	tcc Ser	gcg Ala	gtg Val 235	ggt Gly	ttg Leu	ggc Gly	gtt Val	gct Ala 240	act Thr	aat Asn	cgc Arg	acg Thr 245	cgc Arg	835
gtc Val	att Ile	gcg Ala	att Ile	att Ile 250	gcc Ala	gct Ala	gtt Val	gcg Ala	ctc Leu 255	atc Ile	gcc Ala	gtt Val	gct Ala	acc Thr 260	gct Ala	883
gca Ala	tgc Cys	ggc Gly	ccg Pro 265	atc Ile	gca Ala	ttc Phe	gtg Val 270	gcg Ala	ttt Phe	gtg Val	tct Ser	ggc Gly 275	ccc Pro 275	att Ile	gcc Ala	931
gcg Ala	cgc Arg	att Ile 280	tta Leu	ggc Gly	tcc Ser	ggc Gly	gga Gly 285	tcg Ser	ctc Leu	atc Ile	atc Ile	ccc Pro 290	tcc Ser	gca Ala	ctc Leu	979
atc Ile	ggc Gly 295	ggg Gly	ttg Leu	atc Ile	gtg Val	ctc Leu 300	atc Ile	gcc Ala	gac Asp	cta Leu	att Ile 305	ggc Gly	caa Gln	tac Tyr	ttc Phe	1027
ctc Leu 310	ggc Gly	acc Thr	cgc Arg	tac Tyr	ccc Pro 315	gtc Val	gga Gly	gtt Val	gtc Val	acc Thr 320	ggc Gly	gca Ala	ttc Phe	ggc Gly	gcc Ala 325	1075
cca Pro	ttc Phe	ctt Leu	atc Ile	tat Tyr	tta Leu	ctc Leu	att Ile	cgt Arg	tcc Ser	aac Asn	cgc Arg	gcg Ala	gga Gly	gta Val	acc Thr	1123

330 335 340
 ctg tgaccaccaa ccatcaacta tcc 1149
 Leu

<210> 214
 <211> 342
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 214
 Met Ser Leu Ser His Gln Leu Lys Arg Gln Arg Ala Ser Arg Asn Ser
 1 5 10 15
 Arg Arg Trp Leu Ile Val Ala Ala Leu Gly Val Val Thr Leu Gly Ile
 20 25 30
 Phe Ala Phe Ser Leu Met Trp Gly Glu Val Phe Tyr Gly Pro Ala Gln
 35 40 45
 Val Leu Lys Val Leu Ser Gly Gln Gln Val Pro Gly Ala Ser Tyr Ser
 50 55 60
 Val Gly Val Leu Arg Leu Pro Arg Ala Val Met Gly Leu Thr Ala Gly
 65 70 75 80
 Leu Ala Phe Gly Ala Ala Gly Val Ile Phe Gln Thr Val Leu Arg Asn
 85 90 95
 Gln Leu Ala Ser Pro Asp Ile Ile Gly Ile Ser Ser Gly Ala Ser Ala
 100 105 110
 Ala Gly Val Ile Cys Ile Val Phe Phe Gly Met Ser Gln Ser Ala Val
 115 120 125
 Ser Ala Ile Ser Leu Cys Ala Ser Leu Ala Val Ala Leu Leu Ile Tyr
 130 135 140
 Leu Val Ala Tyr Arg Gly Gly Phe Ser Ala Thr Arg Leu Ile Leu Thr
 145 150 155 160
 Gly Ile Gly Ile Ala Ala Met Leu Asn Ser Leu Val Ser Tyr Ser Leu
 165 170 175
 Ser Lys Ala Asp Ser Trp Asp Leu Pro Thr Ala Thr Arg Trp Leu Thr
 180 185 190
 Gly Ser Leu Asn Gly Ala Thr Trp Asp Arg Ala Met Pro Leu Ile Val
 195 200 205
 Thr Thr Val Val Leu Ile Pro Leu Leu Val Ala Asn Ala Arg Asn Val
 210 215 220
 Asp Leu Met Arg Leu Gly Asn Asp Ser Ala Val Gly Leu Gly Val Ala
 225 230 235 240
 Thr Asn Arg Thr Arg Val Ile Ala Ile Ile Ala Ala Val Ala Leu Ile
 245 250 255

Ala Val Ala Thr Ala Ala Cys Gly Pro Ile Ala Phe Val Ala Phe Val
 260 265 270

Ser Gly Pro Ile Ala Ala Arg Ile Leu Gly Ser Gly Gly Ser Leu Ile
 275 280 285

Ile Pro Ser Ala Leu Ile Gly Gly Leu Ile Val Leu Ile Ala Asp Leu
 290 295 300

Ile Gly Gln Tyr Phe Leu Gly Thr Arg Tyr Pro Val Gly Val Val Thr
 305 310 315 320

Gly Ala Phe Gly Ala Pro Phe Leu Ile Tyr Leu Leu Ile Arg Ser Asn
 325 330 335

Arg Ala Gly Val Thr Leu
 340

<210> 215
 <211> 802
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (30)..(779)
 <223> FRXA00523

<400> 215
 tggcgcggcg ggcgtgaatt ttccagacgggtg ttg cgt aat cag ttg gcg tcg 53
 Val Leu Arg Asn Gln Leu Ala Ser
 1 5

ccg gat att atc ggc att tct tct ggc gcg tcg gcg gcg ggc gta att 101
 Pro Asp Ile Ile Gly Ile Ser Ser Gly Ala Ser Ala Ala Gly Val Ile
 10 15 20

tgc att gtg ttt ttc gga atg tcg cag tct gca gtg tcg gcg att tct 149
 Cys Ile Val Phe Phe Gly Met Ser Gln Ser Ala Val Ser Ala Ile Ser
 25 30 35 40

ttg tgt gcg tcc ttg gct gtg gcg ttg ttg att tat ctg gtg gcg tat 197
 Leu Cys Ala Ser Leu Ala Val Ala Leu Leu Ile Tyr Leu Val Ala Tyr
 45 50 55

cgc ggt ggt ttt tcg gcc acg cgt ctg att ctt acc ggc att ggt att 245
 Arg Gly Gly Phe Ser Ala Thr Arg Leu Ile Leu Thr Gly Ile Gly Ile
 60 65 70

gct gcg atg ctg aat tca tta gtg tcg tat tcg ctg tcc aag gct gat 293
 Ala Ala Met Leu Asn Ser Leu Val Ser Tyr Ser Leu Ser Lys Ala Asp
 75 80 85

tct tgg gat ctg ccg acc gcg acg cgc tgg ctt acc ggc tcg ctc aat 341
 Ser Trp Asp Leu Pro Thr Ala Thr Arg Trp Leu Thr Gly Ser Leu Asn
 90 95 100

ggt gcg acg tgg gat cgt gcg atg ccg ctg att gtc acc act gtg gta 389
 Gly Ala Thr Trp Asp Arg Ala Met Pro Leu Ile Val Thr Thr Val Val
 105 110 115 120

CCG GAT ATT ATC GGC ATT TCT TCT GGC GCG TCG GCG GCG GGC GTA ATT

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ctc att ccg ctg ctg gtg gct aat gcg cgc aat gtg gat ctt atg cgt 437
Leu Ile Pro Leu Leu Val Ala Asn Ala Arg Asn Val Asp Leu Met Arg
      125              130              135

ttg ggc aat gat tcc gcg gtg ggt ttg ggc gtt gct act aat cgc acg 485
Leu Gly Asn Asp Ser Ala Val Gly Leu Gly Val Ala Thr Asn Arg Thr
      140              145              150

cgc gtc att gcg att att gcc gct gtt gcg ctc atc gcc gtt gct acc 533
Arg Val Ile Ala Ile Ile Ala Ala Val Ala Leu Ile Ala Val Ala Thr
      155              160              165

gct gca tgc ggc ccg atc gca ttc gtg gcg ttt gtg tct ggc ccc att 581
Ala Ala Cys Gly Pro Ile Ala Phe Val Ala Phe Val Ser Gly Pro Ile
      170              175              180

gcc gcg cgc att tta ggc tcc ggc gga tcg ctc atc atc ccc tcc gca 629
Ala Ala Arg Ile Leu Gly Ser Gly Gly Ser Leu Ile Ile Pro Ser Ala
      185              190              195              200

ctc atc ggc ggc ttg atc gtg ctc atc gcc gac cta att ggc caa tac 677
Leu Ile Gly Gly Leu Ile Val Leu Ile Ala Asp Leu Ile Gly Gln Tyr
      205              210              215

ttc ctc ggc acc cgc tac ccc gtc gga gtt gtc acc ggc gca ttc ggc 725
Phe Leu Gly Thr Arg Tyr Pro Val Gly Val Val Thr Gly Ala Phe Gly
      220              225              230

gcc cca ttc ctt atc tat tta ctc att cgt tcc aac cgc gcg gga gta 773
Ala Pro Phe Leu Ile Tyr Leu Leu Ile Arg Ser Asn Arg Ala Gly Val
      235              240              245

acc ctg tgaccaccaa ccatcaacta tcc 802
Thr Leu
      250

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<210> 216

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

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Val Leu Arg Asn Gln Leu Ala Ser Pro Asp Ile Ile Gly Ile Ser Ser
  1              5              10              15

Gly Ala Ser Ala Ala Gly Val Ile Cys Ile Val Phe Phe Gly Met Ser
      20              25              30

Gln Ser Ala Val Ser Ala Ile Ser Leu Cys Ala Ser Leu Ala Val Ala
      35              40              45

Leu Leu Ile Tyr Leu Val Ala Tyr Arg Gly Gly Phe Ser Ala Thr Arg
      50              55              60

Leu Ile Leu Thr Gly Ile Gly Ile Ala Ala Met Leu Asn Ser Leu Val
      65              70              75              80

Ser Tyr Ser Leu Ser Lys Ala Asp Ser Trp Asp Leu Pro Thr Ala Thr
      85              90              95

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Arg Trp Leu Thr Gly Ser Leu Asn Gly Ala Thr Trp Asp Arg Ala Met
      100              105              110

Pro Leu Ile Val Thr Thr Val Val Leu Ile Pro Leu Leu Val Ala Asn
      115              120              125

Ala Arg Asn Val Asp Leu Met Arg Leu Gly Asn Asp Ser Ala Val Gly
      130              135              140

Leu Gly Val Ala Thr Asn Arg Thr Arg Val Ile Ala Ile Ile Ala Ala
      145              150              155              160

Val Ala Leu Ile Ala Val Ala Thr Ala Ala Cys Gly Pro Ile Ala Phe
      165              170              175

Val Ala Phe Val Ser Gly Pro Ile Ala Ala Arg Ile Leu Gly Ser Gly
      180              185              190

Gly Ser Leu Ile Ile Pro Ser Ala Leu Ile Gly Gly Leu Ile Val Leu
      195              200              205

Ile Ala Asp Leu Ile Gly Gln Tyr Phe Leu Gly Thr Arg Tyr Pro Val
      210              215              220

Gly Val Val Thr Gly Ala Phe Gly Ala Pro Phe Leu Ile Tyr Leu Leu
      225              230              235              240

Ile Arg Ser Asn Arg Ala Gly Val Thr Leu
      245              250

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<210> 217

<211> 1167

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1144)

<223> RXA01289

<400> 217

ctcacctaag atgttctaag cggttttagtt tcagctagtt ttaaggactt tcgatgtctc 60

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atacttttct ttccccctcg atcttttagga gtcacgcgat atg acg gcg gtg gcg 115
              Met Thr Ala Val Ala
              1              5

```

```

gta gag aag cag aag gag acg tcg ata agc aaa aac ctc ggc agg cgc 163
Val Glu Lys Gln Lys Glu Thr Ser Ile Ser Lys Asn Leu Gly Arg Arg
              10              15              20

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cga gcg ctg ggc att ctc gga atc gtc gtg gca ctg ggt gcg ctt att 211
Arg Ala Leu Gly Ile Leu Gly Ile Val Val Ala Leu Gly Ala Leu Ile
              25              30              35

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gtt tta agt att gct gtg ggt gcg aac cca ctt tct ttt agc tcc gta 259
Val Leu Ser Ile Ala Val Gly Ala Asn Pro Leu Ser Phe Ser Ser Val
              40              45              50

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BGI-131CP
 1167
 DNA
 Corynebacterium glutamicum
 RXA01289

tgg cag ggt ttt acc gca cac gac agc tct gag gcg tcg att atc gtg 307
 Trp Gln Gly Phe Thr Ala His Asp Ser Ser Glu Ala Ser Ile Ile Val
 55 60 65

tgg tca atg cgt att cgg cgc acg ctg gtg ggc atc gtg act ggc gct 355
 Trp Ser Met Arg Ile Pro Arg Thr Leu Val Gly Ile Val Thr Gly Ala
 70 75 80 85

gct ttt ggt gtg gcg ggt gct tta att caa gcg ctg acg cgc aac ccg 403
 Ala Phe Gly Val Ala Gly Ala Leu Ile Gln Ala Leu Thr Arg Asn Pro
 90 95 100

ctt gcc gat ccc gga att ttg gga gtt aac gcg ggt gca ggt ttc gca 451
 Leu Ala Asp Pro Gly Ile Leu Gly Val Asn Ala Gly Ala Gly Phe Ala
 105 110 115

gtg acc gta ggt gtc gga ttt ttc gga ctc agc agc gtg acg ggc tac 499
 Val Thr Val Gly Val Gly Phe Phe Gly Leu Ser Ser Val Thr Gly Tyr
 120 125 130

atc tgg ttc gca ttc ctg ggc gct gcc gcc gct acc ctg ctg gtg tat 547
 Ile Trp Phe Ala Phe Leu Gly Ala Ala Ala Ala Thr Leu Leu Val Tyr
 135 140 145

ttc att ggt gcg agc acc agc ggc agc gtt aat cct gtt gct ctg gtc 595
 Phe Ile Gly Ala Ser Thr Ser Gly Ser Val Asn Pro Val Ala Leu Val
 150 155 160 165

ctc gcc ggc gtt gct ctg gcc gcc gtg ctt ggt ggc gtc acg agc ttc 643
 Leu Ala Gly Val Ala Leu Ala Ala Val Leu Gly Gly Val Thr Ser Phe
 170 175 180

ctc aca ctg att gat cct gag act ttt gaa agc atc cgc aat tgg aat 691
 Leu Thr Leu Ile Asp Pro Glu Thr Phe Glu Ser Ile Arg Asn Trp Asn
 185 190 195

ctt ggt tct gtt gca cgc acc gac ctc agc gac acc atg acc gta ttg 739
 Leu Gly Ser Val Ala Arg Thr Asp Leu Ser Asp Thr Met Thr Val Leu
 200 205 210

cca ttc ctg gca gtc gga ctg gcc atc gcg ctc ctg ctg tcg gga gca 787
 Pro Phe Leu Ala Val Gly Leu Ala Ile Ala Leu Leu Leu Ser Gly Ala
 215 220 225

ctg aac tcc att gcg ctt ggc gat gac ctt gct gca tcc ctg ggc acc 835
 Leu Asn Ser Ile Ala Leu Gly Asp Asp Leu Ala Ala Ser Leu Gly Thr
 230 235 240 245

aaa gtg atg cgc acc cgc gtg ctc ggc atc att tca gtc acc ttg ttg 883
 Lys Val Met Arg Thr Arg Val Leu Gly Ile Ile Ser Val Thr Leu Leu
 250 255 260

gcc ggc ggc gcg acc gcc ctt act ggt ggt atc ggc ttc gta ggc ctt 931
 Ala Gly Gly Ala Thr Ala Leu Thr Gly Gly Ile Gly Phe Val Gly Leu
 265 270 275

atg gtt ccc cac gtt gtg cgc tgg gta gtt ggc ccc gat caa cga tgg 979
 Met Val Pro His Val Val Arg Trp Val Val Gly Pro Asp Gln Arg Trp
 280 285 290

atc atc acc ttc agc gcc ctg tgc gcc cct gtt ctt gta ctc ggc gca 1027

Ile Ile Thr Phe Ser Ala Leu Cys Ala Pro Val Leu Val Leu Gly Ala
 295 300 305

gac att ttg gga cgc atc atc gcc cgc ccc ggc gaa att gaa gta ggc 1075
 Asp Ile Leu Gly Arg Ile Ile Ala Arg Pro Gly Glu Ile Glu Val Gly
 310 315 320 325

att gtt acc gca gtc atc ggc gca cct gtc ctg atc gca cta gtt cga 1123
 Ile Val Thr Ala Val Ile Gly Ala Pro Val Leu Ile Ala Leu Val Arg
 330 335 340

cgg agg aaa gcc agt ggt ctt taatatcaaa tctagaactg atg 1167
 Arg Arg Lys Ala Ser Gly Leu
 345

<210> 218
 <211> 348
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 218
 Met Thr Ala Val Ala Val Glu Lys Gln Lys Glu Thr Ser Ile Ser Lys
 1 5 10 15

Asn Leu Gly Arg Arg Arg Ala Leu Gly Ile Leu Gly Ile Val Val Ala
 20 25 30

Leu Gly Ala Leu Ile Val Leu Ser Ile Ala Val Gly Ala Asn Pro Leu
 35 40 45

Ser Phe Ser Ser Val Trp Gln Gly Phe Thr Ala His Asp Ser Ser Glu
 50 55 60

Ala Ser Ile Ile Val Trp Ser Met Arg Ile Pro Arg Thr Leu Val Gly
 65 70 75 80

Ile Val Thr Gly Ala Ala Phe Gly Val Ala Gly Ala Leu Ile Gln Ala
 85 90 95

Leu Thr Arg Asn Pro Leu Ala Asp Pro Gly Ile Leu Gly Val Asn Ala
 100 105 110

Gly Ala Gly Phe Ala Val Thr Val Gly Val Gly Phe Phe Gly Leu Ser
 115 120 125

Ser Val Thr Gly Tyr Ile Trp Phe Ala Phe Leu Gly Ala Ala Ala Ala
 130 135 140

Thr Leu Leu Val Tyr Phe Ile Gly Ala Ser Thr Ser Gly Ser Val Asn
 145 150 155 160

Pro Val Ala Leu Val Leu Ala Gly Val Ala Leu Ala Ala Val Leu Gly
 165 170 175

Gly Val Thr Ser Phe Leu Thr Leu Ile Asp Pro Glu Thr Phe Glu Ser
 180 185 190

Ile Arg Asn Trp Asn Leu Gly Ser Val Ala Arg Thr Asp Leu Ser Asp
 195 200 205

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Thr Met Thr Val Leu Pro Phe Leu Ala Val Gly Leu Ala Ile Ala Leu
 210                      215                      220

Leu Leu Ser Gly Ala Leu Asn Ser Ile Ala Leu Gly Asp Asp Leu Ala
225                      230                      235                      240

Ala Ser Leu Gly Thr Lys Val Met Arg Thr Arg Val Leu Gly Ile Ile
                245                      250                      255

Ser Val Thr Leu Leu Ala Gly Gly Ala Thr Ala Leu Thr Gly Gly Ile
                260                      265                      270

Gly Phe Val Gly Leu Met Val Pro His Val Val Arg Trp Val Val Gly
                275                      280                      285

Pro Asp Gln Arg Trp Ile Ile Thr Phe Ser Ala Leu Cys Ala Pro Val
 290                      295                      300

Leu Val Leu Gly Ala Asp Ile Leu Gly Arg Ile Ile Ala Arg Pro Gly
305                      310                      315                      320

Glu Ile Glu Val Gly Ile Val Thr Ala Val Ile Gly Ala Pro Val Leu
                325                      330                      335

Ile Ala Leu Val Arg Arg Arg Lys Ala Ser Gly Leu
                340                      345

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<210> 219
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1264)
<223> RXA01290

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<400> 219
ggacgcatca tcgcccgcgc cggcgaaatt gaagtaggca ttgttacgc agtcacgcgc 60

gcacctgtcc tgatcgcaact agttcgacgg aggaaagcca gtg gtc ttt aat atc    115
                    Val Val Phe Asn Ile
                    1                      5

aaa tct aga act gat gaa act cct gtt gct gcg tct gag ccg gtg gaa    163
Lys Ser Arg Thr Asp Glu Thr Pro Val Ala Ala Ser Glu Pro Val Glu
                10                      15                      20

tcc act aga cct gtg tct gaa gct tcg aca agc cct gcg ctt aac ccc    211
Ser Thr Arg Pro Val Ser Glu Ala Ser Thr Ser Pro Ala Leu Asn Pro
                25                      30                      35

ggc tac cac gca gtt tca gtg cag agg cgc cgg ttc tct ttc cgc atc    259
Gly Tyr His Ala Val Ser Val Gln Arg Arg Arg Phe Ser Phe Arg Ile
                40                      45                      50

cca gcc cgc ctc atg gtg gtt agc ctt atc ctt ttc gcc atc gcg cta    307
Pro Ala Arg Leu Met Val Val Ser Leu Ile Leu Phe Ala Ile Ala Leu
                55                      60                      65

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BGI-131CP

tgc agc gcc aca tgg gct atc acg atg ggc gat tac cca ctg tct ttg	355
Cys Ser Ala Thr Trp Ala Ile Thr Met Gly Asp Tyr Pro Leu Ser Leu	
70 75 80 85	
ggg cag gtg att aat gca ctt gct ggc acc ggc gag aaa ttc cag ttg	403
Gly Gln Val Ile Asn Ala Leu Ala Gly Thr Gly Glu Lys Phe Gln Leu	
90 95 100	
ttg gtg gtg cgg gaa tgg cgt cta cct gta gcc att gct gct gtt gtc	451
Leu Val Val Arg Glu Trp Arg Leu Pro Val Ala Ile Ala Ala Val Val	
105 110 115	
ttc ggc gcg ctg ctt ggc ata ggt gga gcg att ttc cag tcg att act	499
Phe Gly Ala Leu Leu Gly Ile Gly Gly Ala Ile Phe Gln Ser Ile Thr	
120 125 130	
cga aac ccg ttg ggt tca cct gac gtg att ggt ttc gat gca ggt tct	547
Arg Asn Pro Leu Gly Ser Pro Asp Val Ile Gly Phe Asp Ala Gly Ser	
135 140 145	
tac acg gcg gtg gtt ctt gtc att ttg gtc ctc ggc aac act cac tac	595
Tyr Thr Ala Val Val Leu Val Ile Leu Val Leu Gly Asn Thr His Tyr	
150 155 160 165	
tgg agc atc gct ttc gct gcc atc gtc ggt ggc att gtt acc gcc ttt	643
Trp Ser Ile Ala Phe Ala Ala Ile Val Gly Gly Ile Val Thr Ala Phe	
170 175 180	
gcc gtg tat gtc ctg gcg tgg cgt aaa ggt gtg caa ggt ttc cgc ttg	691
Ala Val Tyr Val Leu Ala Trp Arg Lys Gly Val Gln Gly Phe Arg Leu	
185 190 195	
atc atc gtg ggc atc ggt gtc tcg gcc atg ctc agt tcc gtt aac gcg	739
Ile Ile Val Gly Ile Gly Val Ser Ala Met Leu Ser Ser Val Asn Ala	
200 205 210	
tat cta atc acc cgc gcc gat gtg gaa gac gcc atg gtt gtg ggc ttc	787
Tyr Leu Ile Thr Arg Ala Asp Val Glu Asp Ala Met Val Val Gly Phe	
215 220 225	
tgg agt gcc ggt tcc atc aac cgc att acc tgg caa tct ctg ctc ccc	835
Trp Ser Ala Gly Ser Ile Asn Arg Ile Thr Trp Gln Ser Leu Leu Pro	
230 235 240 245	
tct ctg gtg atc gct gct gtc atc atc gtg gcc gcc att gtg ctg gca	883
Ser Leu Val Ile Ala Ala Val Ile Ile Val Ala Ala Ile Val Leu Ala	
250 255 260	
agg tca ctg cgt ttc atg gaa atg ggc gat gac gta gcc acc acc ctc	931
Arg Ser Leu Arg Phe Met Glu Met Gly Asp Asp Val Ala Thr Thr Leu	
265 270 275	
ggt gtg aaa aca aac tcc acc cgc ttg gca ctc atc gtt gtc ggc gtt	979
Gly Val Lys Thr Asn Ser Thr Arg Leu Ala Leu Ile Val Val Gly Val	
280 285 290	
gct acc tcc gcg ttg gtt aca gca gct gcc gga ccg atc tcc ttc atc	1027
Ala Thr Ser Ala Leu Val Thr Ala Ala Ala Gly Pro Ile Ser Phe Ile	
295 300 305	
gcg ttg gtt gcc cca cag ctg gca cgt cgc ctc act aaa acc cct ggt	1075


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Ile Val Thr Ala Phe Ala Val Tyr Val Leu Ala Trp Arg Lys Gly Val
      180                      185                      190

Gln Gly Phe Arg Leu Ile Ile Val Gly Ile Gly Val Ser Ala Met Leu
      195                      200                      205

Ser Ser Val Asn Ala Tyr Leu Ile Thr Arg Ala Asp Val Glu Asp Ala
      210                      215                      220

Met Val Val Gly Phe Trp Ser Ala Gly Ser Ile Asn Arg Ile Thr Trp
      225                      230                      235                      240

Gln Ser Leu Leu Pro Ser Leu Val Ile Ala Ala Val Ile Ile Val Ala
      245                      250                      255

Ala Ile Val Leu Ala Arg Ser Leu Arg Phe Met Glu Met Gly Asp Asp
      260                      265                      270

Val Ala Thr Thr Leu Gly Val Lys Thr Asn Ser Thr Arg Leu Ala Leu
      275                      280                      285

Ile Val Val Gly Val Ala Thr Ser Ala Leu Val Thr Ala Ala Ala Gly
      290                      295                      300

Pro Ile Ser Phe Ile Ala Leu Val Ala Pro Gln Leu Ala Arg Arg Leu
      305                      310                      315                      320

Thr Lys Thr Pro Gly Val Ser Leu Val Ala Ala Ala Ala Met Gly Ser
      325                      330                      335

Ala Leu Leu Ser Cys Ala His Leu Leu Ser Leu Ile Ile Ser Ser Phe
      340                      345                      350

Tyr Arg Thr Ile Pro Val Gly Leu Leu Thr Val Ser Ile Gly Gly Cys
      355                      360                      365

Tyr Met Ile Trp Leu Leu Leu Arg Glu Thr Arg Arg Gln Tyr Arg Thr
      370                      375                      380

Gly Thr Ile Arg
      385

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<210> 221
<211> 605
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(582)
<223> RXA01822

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<400> 221
atg gcc aga caa aat agc aat acc ggc ggg ttg cgt ctg gtg ttg gtt      48
Met Ala Arg Gln Asn Ser Asn Thr Gly Gly Leu Arg Leu Val Leu Val
  1                      5                      10                      15

ggt atc gga aca ggt gca ttt ttg ggt gct gct cgt gat ttc ttc atg      96
Gly Ile Gly Thr Gly Ala Phe Leu Gly Ala Ala Arg Asp Phe Phe Met
      20                      25                      30

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gtg cgc gca gat att acg ggt gct tcg acg gta cag ctg tgg tct gcc 144
Val Arg Ala Asp Ile Thr Gly Ala Ser Thr Val Gln Leu Trp Ser Ala
      35              40              45

ggt tcg ttg agc ggg cgc gac tgg aat cat gcc ctg ttg gtg ttg att 192
Gly Ser Leu Ser Gly Arg Asp Trp Asn His Ala Leu Leu Val Leu Ile
      50              55              60

tcg tgt gca gtg att gtg cca gca ctg tgc att att gtc cgc cgt tta 240
Ser Cys Ala Val Ile Val Pro Ala Leu Cys Ile Ile Val Arg Arg Leu
      65              70              75              80

cgc ctg atg gaa atg ggt gat gat gca gct ggg gca ctt gga att tca 288
Arg Leu Met Glu Met Gly Asp Asp Ala Ala Gly Ala Leu Gly Ile Ser
      85              90              95

gtg gag aga aca cgg ttg ata gcc att ttg ttg gct gtg ctg ctg gtg 336
Val Glu Arg Thr Arg Leu Ile Ala Ile Leu Leu Ala Val Leu Leu Val
      100              105              110

ggg atc gcc acc gca gct gca ggt ccc atc gct ttt att gca ctg gca 384
Gly Ile Ala Thr Ala Ala Ala Gly Pro Ile Ala Phe Ile Ala Leu Ala
      115              120              125

gca cct cag att gcc cgg gct ctg gcc cgg gag gat gga gtg ctg gtg 432
Ala Pro Gln Ile Ala Arg Ala Leu Ala Arg Glu Asp Gly Val Leu Val
      130              135              140

gct gcg tcg ata agc att ggc tct ggg ctg tta gtt gcg gcg gat tgc 480
Ala Ala Ser Ile Ser Ile Gly Ser Gly Leu Leu Val Ala Ala Asp Cys
      145              150              155              160

cta gag caa cac gtt gat act gag ctg cac acg ccc gtt ggc ctg gtg 528
Leu Glu Gln His Val Asp Thr Glu Leu His Thr Pro Val Gly Leu Val
      165              170              175

acc agt ttg ctg ggc ggg gtg tat ttg atg tgg ctt ttg agc cga aag 576
Thr Ser Leu Leu Gly Gly Val Tyr Leu Met Trp Leu Leu Ser Arg Lys
      180              185              190

gag gca taaatgctgc aagcgcatga tct 605
Glu Ala

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<210> 222

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

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Met Ala Arg Gln Asn Ser Asn Thr Gly Gly Leu Arg Leu Val Leu Val
  1              5              10              15

Gly Ile Gly Thr Gly Ala Phe Leu Gly Ala Ala Arg Asp Phe Phe Met
      20              25              30

Val Arg Ala Asp Ile Thr Gly Ala Ser Thr Val Gln Leu Trp Ser Ala
      35              40              45

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[illegible]

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<220>  
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<222> (101)..(1096)  
<223> RXN00466
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<400> 223
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gatagggttaa cctgattcga ttagaaaacg gagatttgtc gtg caa tcc cgc ctg 115
Val Gln Ser Arg Leu
1 5

tcc aaa atc ctg cgc agt agc gtc gta ggc gtt gct gtc cta gcc ctg 163
Ser Lys Ile Leu Arg Ser Ser Val Val Gly Val Ala Val Leu Ala Leu
10 15 20

tta gct ggg tgt tct aac aat gca gat gac acc gac gct gat tca aca 211
Leu Ala Gly Cys Ser Asn Asn Ala Asp Asp Thr Asp Ala Asp Ser Thr
25 30 35

tcc acg gga aac tcc gct ttt cct gtt tcg att gaa cac gag ttc gga 259
Ser Thr Gly Asn Ser Ala Phe Pro Val Ser Ile Glu His Glu Phe Gly
40 45 50

acc acc aca atc gat gat gta ccc gaa aga gtt gtc acc ctt ggc gtt 307

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Thr Thr Thr Ile Asp Asp Val Pro Glu Arg Val Val Thr Leu Gly Val
  55                                60                                65

acc gac gcc gat att gtc ctc gca ttg ggg acc gtc cca gta ggc aac 355
Thr Asp Ala Asp Ile Val Leu Ala Leu Gly Thr Val Pro Val Gly Asn
  70                                75                                80                                85

acc gga tac aaa ttc ttc gaa aac gga ttg gga ccg tgg act gat gag 403
Thr Gly Tyr Lys Phe Phe Glu Asn Gly Leu Gly Pro Trp Thr Asp Glu
                                90                                95                                100

tta gtg gaa ggc aaa gaa tta aca ctg ctt gac tct gat tcc aca cca 451
Leu Val Glu Gly Lys Glu Leu Thr Leu Asp Ser Asp Thr Pro
                                105                                110                                115

gat ctt gaa caa gta gca gcc ctg gag cca gac ctg att att gga gtc 499
Asp Leu Glu Gln Val Ala Ala Leu Glu Pro Asp Leu Ile Ile Gly Val
                                120                                125                                130

tct gcg ggg ttt gac gac gtt gta tac gag caa cta tct gat atc gca 547
Ser Ala Gly Phe Asp Asp Val Val Tyr Glu Gln Leu Ser Asp Ile Ala
                                135                                140                                145

ccg gtg gtc gcc cgt cca gcg gga aca gct gca tac gca gta gct cgc 595
Pro Val Val Ala Arg Pro Ala Gly Thr Ala Ala Tyr Ala Val Ala Arg
150                                155                                160                                165

gag gaa gct acc aac ctt gtt gcc cgt gcg atg ggg caa tca gaa aaa 643
Glu Glu Ala Thr Asn Leu Val Ala Arg Ala Met Gly Gln Ser Glu Lys
                                170                                175                                180

gga caa gag ctc aat gag gaa aca gat gct ctg atc caa gct gcg cgt 691
Gly Gln Glu Leu Asn Glu Glu Thr Asp Ala Leu Ile Gln Ala Ala Arg
                                185                                190                                195

gat gaa aat cct tct ttt gac ggt aaa aca gga acc gtc atc ttg cca 739
Asp Glu Asn Pro Ser Phe Asp Gly Lys Thr Gly Thr Val Ile Leu Pro
                                200                                205                                210

tac cag ggt aaa tac ggt gcc tac ctg cca ggc gat gca cgg gga caa 787
Tyr Gln Gly Lys Tyr Gly Ala Tyr Leu Pro Gly Asp Ala Arg Gly Gln
                                215                                220                                225

ttc ctc gat tca ctt ggc att tcg ctg ccg gaa gca gtt ctt tcg cga 835
Phe Leu Asp Ser Leu Gly Ile Ser Leu Pro Glu Ala Val Leu Ser Arg
230                                235                                240                                245

gac acc ggc gac agc ttc ttt gtc gat gtc ccc gct gaa agc gtc aaa 883
Asp Thr Gly Asp Ser Phe Phe Val Asp Val Pro Ala Glu Ser Val Lys
                                250                                255                                260

gac gta gac ggt gat gtt ctc ctc gtg ctt tcc aac gac gaa aat ctg 931
Asp Val Asp Gly Asp Val Leu Leu Val Leu Ser Asn Asp Glu Asn Leu
                                265                                270                                275

gat atc aca gca gag aat cca ctg ttt gaa aca ctc aac gtt gtg caa 979
Asp Ile Thr Ala Glu Asn Pro Leu Phe Glu Thr Leu Asn Val Val Gln
                                280                                285                                290

aaa gac gca gta att gtg gca aca acc gaa gaa cgc ggg gcg att acc 1027
Lys Asp Ala Val Ile Val Ala Thr Thr Glu Glu Arg Gly Ala Ile Thr

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295						300						305							
tac	aac	tca	gtg	ctg	tct	gtt	cct	ttt	gcg	ttg	gaa	cat	ctc	gca	cca				1075
Tyr	Asn	Ser	Val	Leu	Ser	Val	Pro	Phe	Ala	Leu	Glu	His	Leu	Ala	Pro				
310					315					320					325				
cgt	att	gct	gag	gct	ttg	aag	taaaactcaa	ctactcgagc	aca										1119
Arg	Ile	Ala	Glu	Ala	Leu	Lys													
				330															
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<211> 332																			
<212> PRT																			
<213> Corynebacterium glutamicum																			
<400> 224																			
Val	Gln	Ser	Arg	Leu	Ser	Lys	Ile	Leu	Arg	Ser	Ser	Val	Val	Gly	Val				
1				5					10					15					
Ala	Val	Leu	Ala	Leu	Leu	Ala	Gly	Cys	Ser	Asn	Asn	Ala	Asp	Asp	Thr				
			20					25					30						
Asp	Ala	Asp	Ser	Thr	Ser	Thr	Gly	Asn	Ser	Ala	Phe	Pro	Val	Ser	Ile				
		35					40					45							
Glu	His	Glu	Phe	Gly	Thr	Thr	Thr	Ile	Asp	Asp	Val	Pro	Glu	Arg	Val				
	50					55					60								
Val	Thr	Leu	Gly	Val	Thr	Asp	Ala	Asp	Ile	Val	Leu	Ala	Leu	Gly	Thr				
65					70					75					80				
Val	Pro	Val	Gly	Asn	Thr	Gly	Tyr	Lys	Phe	Phe	Glu	Asn	Gly	Leu	Gly				
				85					90					95					
Pro	Trp	Thr	Asp	Glu	Leu	Val	Glu	Gly	Lys	Glu	Leu	Thr	Leu	Leu	Asp				
			100					105					110						
Ser	Asp	Ser	Thr	Pro	Asp	Leu	Glu	Gln	Val	Ala	Ala	Leu	Glu	Pro	Asp				
		115					120					125							
Leu	Ile	Ile	Gly	Val	Ser	Ala	Gly	Phe	Asp	Asp	Val	Val	Tyr	Glu	Gln				
	130					135					140								
Leu	Ser	Asp	Ile	Ala	Pro	Val	Val	Ala	Arg	Pro	Ala	Gly	Thr	Ala	Ala				
145					150					155					160				
Tyr	Ala	Val	Ala	Arg	Glu	Glu	Ala	Thr	Asn	Leu	Val	Ala	Arg	Ala	Met				
				165					170					175					
Gly	Gln	Ser	Glu	Lys	Gly	Gln	Glu	Leu	Asn	Glu	Glu	Thr	Asp	Ala	Leu				
			180				185						190						
Ile	Gln	Ala	Ala	Arg	Asp	Glu	Asn	Pro	Ser	Phe	Asp	Gly	Lys	Thr	Gly				
		195					200					205							
Thr	Val	Ile	Leu	Pro	Tyr	Gln	Gly	Lys	Tyr	Gly	Ala	Tyr	Leu	Pro	Gly				
						215					220								

[illegible]

<400> 225																	
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gatagggttaa				cctgattoga		ttagaaaacg		gagatttgtc		gtg	caa	tcc	cgc	ctg	115		
										Val	Gln	Ser	Arg	Leu	5		
										1							
tcc	aaa	atc	ctg	cgc	agt	agc	gtc	gta	ggc	gtt	gct	gtc	cta	gcc	ctg	163	
Ser	Lys	Ile	Leu	Arg	Ser	Ser	Val	Val	Gly	Val	Ala	Val	Leu	Ala	Leu		
				10				15				20					
tta	gct	ggg	tgt	tot	aac	aat	gca	gat	gac	acc	gac	gct	gat	tca	aca	211	
Leu	Ala	Gly	Cys	Ser	Asn	Asn	Ala	Asp	Asp	Thr	Asp	Ala	Asp	Ser	Thr		
				25				30				35					
tcc	acg	gga	aac	tcc	gct	ttt	cct	gtt	tcg	att	gaa	cac	gag	ttc	gga	259	
Ser	Thr	Gly	Asn	Ser	Ala	Phe	Pro	Val	Ser	Ile	Glu	His	Glu	Phe	Gly		
				40		45				50							
acc	acc	aca	atc	gat	gat	gta	ccc	gaa	aga	gtt	gtc	acc	ctt	ggc	gtt	307	
Thr	Thr	Thr	Ile	Asp	Asp	Val	Pro	Glu	Arg	Val	Val	Thr	Leu	Gly	Val		
				55		60				65							
acc	gac	gcc	gat	att	gtc	ctc	gca	ttg	ggg	acc	gtc	cca	gta	ggc	aac	355	
Thr	Asp	Ala	Asp	Ile	Val	Leu	Ala	Leu	Gly	Thr	Val	Pro	Val	Gly	Asn		
				70		75		80				85					
acc	gga	tac	aaa	ttc	ttc	gaa	aac	gga	ttg	gga	ccg	tggt	act	gat	gag	403	
Thr	Gly	Tyr	Lys	Phe	Phe	Glu	Asn	Gly	Leu	Gly	Pro	Trp	Thr	Asp	Glu		
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<210> 226

<211> 329

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 226

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Val Gln Ser Arg Leu Ser Lys Ile Leu Arg Ser Ser Val Val Gly Val
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Ala Val Leu Ala Leu Leu Ala Gly Cys Ser Asn Asn Ala Asp Asp Thr
      20          25          30

Asp Ala Asp Ser Thr Ser Thr Gly Asn Ser Ala Phe Pro Val Ser Ile
      35          40          45

Glu His Glu Phe Gly Thr Thr Thr Ile Asp Asp Val Pro Glu Arg Val
      50          55          60

Val Thr Leu Gly Val Thr Asp Ala Asp Ile Val Leu Ala Leu Gly Thr
      65          70          75          80

Val Pro Val Gly Asn Thr Gly Tyr Lys Phe Phe Glu Asn Gly Leu Gly
      85          90          95

Pro Trp Thr Asp Glu Leu Val Glu Gly Lys Glu Leu Thr Leu Leu Asp
      100          105          110

Ser Asp Ser Thr Pro Asp Leu Glu Gln Val Ala Ala Leu Glu Pro Asp
      115          120          125

Leu Ile Ile Gly Val Ser Ala Gly Phe Asp Asp Val Val Tyr Glu Gln
      130          135          140

Leu Ser Asp Ile Ala Pro Val Val Ala Arg Pro Ala Gly Thr Ala Ala
      145          150          155          160

Tyr Ala Val Ala Arg Glu Glu Ala Thr Asn Leu Val Ala Arg Ala Met
      165          170          175

Gly Gln Ser Glu Lys Gly Gln Glu Leu Asn Glu Glu Thr Asp Ala Leu
      180          185          190

Ile Gln Ala Ala Arg Asp Glu Asn Pro Ser Phe Asp Gly Lys Thr Gly
      195          200          205

Thr Val Ile Leu Pro Tyr Gln Gly Lys Tyr Gly Ala Tyr Leu Pro Gly
      210          215          220

Asp Ala Arg Gly Gln Phe Leu Asp Ser Leu Gly Ile Ser Leu Pro Glu
      225          230          235          240

Ala Val Leu Ser Arg Asp Thr Gly Asp Ser Phe Phe Val Asp Val Pro
      245          250          255

Ala Glu Ser Val Lys Asp Val Asp Gly Asp Val Leu Leu Val Leu Ser
      260          265          270

Asn Asp Glu Asn Leu Asp Ile Thr Ala Glu Asn Pro Leu Phe Glu Thr
      275          280          285

Leu Asn Val Val Gln Lys Asp Ala Val Ile Val Ala Thr Thr Glu Glu

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ctc aac gtc ccg tagttaactt cgattcagac gct 582
 Leu Asn Val Pro
 150

<210> 228
 <211> 153
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 228
 Met Lys Lys Ser Leu Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser
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 Gly Cys Thr Ser Asp Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val
 20 25 30
 Glu Thr Thr Ser Ile Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe
 35 40 45
 Pro Arg Thr Val Thr Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys
 50 55 60
 Pro Glu Arg Ile Ala Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu
 65 70 75 80
 Pro Ile Thr Gly Ala Asp Arg Val Val Met Thr Ala Glu Met Asp Thr
 85 90 95
 Ala Asp Glu Glu Thr Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val
 100 105 110
 Lys Asn Gly Gly Arg Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro
 115 120 125
 Asp Leu Val Ile Val Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile
 130 135 140
 Asp Ile Leu Glu Gly Leu Asn Val Pro
 145 150

<210> 229
 <211> 1098
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1075)
 <223> FRXA02863

<400> 229
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 atccaaatcc cttttgattg aaagtttgac ttaaaaaccc atg aaa aaa tca ctc 115
 Met Lys Lys Ser Leu
 1 5
 atc gcc att gtt gcc agt gcg ctc gtg tta agc ggc tgc acc tct gat 163

Ile	Ala	Ile	Val	Ala	Ser	Ala	Leu	Val	Leu	Ser	Gly	Cys	Thr	Ser	Asp	
				10					15					20		
tct	tct	gac	tct	tcc	ggc	act	tcc	gga	act	gtg	gaa	acc	act	tcg	att	211
Ser	Ser	Asp	Ser	Ser	Gly	Thr	Ser	Gly	Thr	Val	Glu	Thr	Thr	Ser	Ile	
			25					30					35			
aca	acc	agc	gtt	gcc	gca	gct	gac	ggc	gca	ttc	cca	cgc	acc	gtc	aca	259
Thr	Thr	Ser	Val	Ala	Ala	Ala	Asp	Gly	Ala	Phe	Pro	Arg	Thr	Val	Thr	
			40				45					50				
ctc	gac	gat	tcc	tcc	atc	acc	tta	gaa	tcc	aaa	cca	gag	cgc	atc	gcc	307
Leu	Asp	Asp	Ser	Ser	Ile	Thr	Leu	Glu	Ser	Lys	Pro	Glu	Arg	Ile	Ala	
	55					60					65					
gta	ctc	acc	cca	gag	gca	gca	tcc	ttg	gtt	ctc	ccc	atc	aca	ggc	gcc	355
Val	Leu	Thr	Pro	Glu	Ala	Ala	Ser	Leu	Val	Leu	Pro	Ile	Thr	Gly	Ala	
	70				75					80					85	
gac	cgc	gtc	gtg	atg	acc	gcc	gaa	atg	gac	acc	gct	gac	gaa	gaa	acc	403
Asp	Arg	Val	Val	Met	Thr	Ala	Glu	Met	Asp	Thr	Ala	Asp	Glu	Glu	Thr	
				90					95					100		
gca	gct	ctg	gcc	tcc	caa	gtg	gaa	tac	caa	gtc	aaa	aac	ggc	ggc	agc	451
Ala	Ala	Leu	Ala	Ser	Gln	Val	Glu	Tyr	Gln	Val	Lys	Asn	Gly	Gly	Ser	
			105					110					115			
ctc	gac	ccc	gaa	caa	gtt	gtc	gcc	ggc	gac	cca	gat	ttg	gtg	atc	gtc	499
Leu	Asp	Pro	Glu	Gln	Val	Val	Ala	Gly	Asp	Pro	Asp	Leu	Val	Ile	Val	
		120					125					130				
agt	gcg	cgt	ttc	gat	acc	gaa	caa	ggc	acc	atc	gac	att	ttg	gaa	ggc	547
Ser	Ala	Arg	Phe	Asp	Thr	Glu	Gln	Gly	Thr	Ile	Asp	Ile	Leu	Glu	Gly	
	135					140					145					
ctc	aac	gtc	ccc	gta	gtt	aac	ttc	gat	tca	gac	gct	tgg	gga	gac	atc	595
Leu	Asn	Val	Pro	Val	Val	Asn	Phe	Asp	Ser	Asp	Ala	Trp	Gly	Asp	Ile	
	150				155					160					165	
gac	gcc	atc	acc	aaa	cac	cta	gaa	att	gtg	ggc	gaa	ctc	gtc	ggc	gaa	643
Asp	Ala	Ile	Thr	Lys	His	Leu	Glu	Ile	Val	Gly	Glu	Leu	Val	Gly	Glu	
				170					175					180		
gaa	gac	aaa	gcc	gca	gaa	gca	atc	gca	gaa	atc	gat	gca	aac	cgc	atc	691
Glu	Asp	Lys	Ala	Ala	Glu	Ala	Ile	Ala	Glu	Ile	Asp	Ala	Asn	Arg	Ile	
			185					190					195			
gac	atc	gac	aag	cct	gcc	acc	tcc	ccc	act	gtg	ctc	act	ttg	atg	caa	739
Asp	Ile	Asp	Lys	Pro	Ala	Thr	Ser	Pro	Thr	Val	Leu	Thr	Leu	Met	Gln	
			200				205						210			
cgc	gga	cca	cgc	caa	atg	gtc	atg	cca	gaa	tct	gcc	atg	ctc	aac	ggc	787
Arg	Gly	Pro	Arg	Gln	Met	Val	Met	Pro	Glu	Ser	Ala	Met	Leu	Asn	Gly	
	215					220					225					
ctg	atc	cgc	gaa	gcc	ggc	ggc	act	cca	gtg	gta	gat	tct	ctc	ggc	gcg	835
Leu	Ile	Arg	Glu	Ala	Gly	Gly	Thr	Pro	Val	Val	Asp	Ser	Leu	Gly	Ala	
	230				235					240					245	
gta	ggc	acc	atc	act	gca	gac	cca	gaa	caa	gtt	gtt	gcg	atg	gca	cct	883
Val	Gly	Thr	Ile	Thr	Ala	Asp	Pro	Glu	Gln	Val	Val	Ala	Met	Ala	Pro	

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                250                255                260
gag atc atc atc att cag gac ttc caa ggt aaa ggc cga gag aac ttc 931
Glu Ile Ile Ile Ile Gln Asp Phe Gln Gly Lys Gly Arg Glu Asn Phe
                265                270                275

gct aat ttc ctc tcc aac cca gcg cta gcc aac gtt ccc gcc att gaa 979
Ala Asn Phe Leu Ser Asn Pro Ala Leu Ala Asn Val Pro Ala Ile Glu
                280                285                290

aac gac aag att ttc tac gcc gac act gtc acc act gga gtt act gca 1027
Asn Asp Lys Ile Phe Tyr Ala Asp Thr Val Thr Thr Gly Val Thr Ala
                295                300                305

ggt acc gat atc acc act ggt ctg cag caa gtg gca gaa atg ctg agc 1075
Gly Thr Asp Ile Thr Thr Gly Leu Gln Gln Val Ala Glu Met Leu Ser
310                315                320                325

tagtttttgag atgttgaaac tag 1098

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<210> 230
<211> 325
<212> PRT
<213> Corynebacterium glutamicum

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<400> 230
Met Lys Lys Ser Leu Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser
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Gly Cys Thr Ser Asp Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val
                20                25                30

Glu Thr Thr Ser Ile Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe
                35                40                45

Pro Arg Thr Val Thr Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys
  50                55                60

Pro Glu Arg Ile Ala Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu
  65                70                75                80

Pro Ile Thr Gly Ala Asp Arg Val Val Met Thr Ala Glu Met Asp Thr
                85                90                95

Ala Asp Glu Glu Thr Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val
                100                105                110

Lys Asn Gly Gly Ser Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro
                115                120                125

Asp Leu Val Ile Val Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile
                130                135                140

Asp Ile Leu Glu Gly Leu Asn Val Pro Val Val Asn Phe Asp Ser Asp
145                150                155                160

Ala Trp Gly Asp Ile Asp Ala Ile Thr Lys His Leu Glu Ile Val Gly
                165                170                175

Glu Leu Val Gly Glu Glu Asp Lys Ala Ala Glu Ala Ile Ala Glu Ile

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BGI-131CP

55 60 65

ggt gca ctc aac cca atg aca cgt gag ctc gga cta acc gcg ttc acc 355
 Gly Ala Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr Ala Phe Thr
 70 75 80 85

gag ggt gtt gta act tct tcc ctg ctg ttt ggt gca gca gct ggt gcg 403
 Glu Gly Val Val Thr Ser Ser Leu Leu Phe Gly Ala Ala Ala Gly Ala
 90 95 100

atg ttt ttc ggt cgc att tcc gac aac tgg ggt cgc cgg aaa aca atc 451
 Met Phe Phe Gly Arg Ile Ser Asp Asn Trp Gly Arg Arg Lys Thr Ile
 105 110 115

atc tca ctt gca gta gct ttc ttt gtc ggc acc atg atc tgc gtg ttt 499
 Ile Ser Leu Ala Val Ala Phe Phe Val Gly Thr Met Ile Cys Val Phe
 120 125 130

gct cca tct ttt gca gta atg gtt gtc gga cgt gtg ctt ctt gga ctc 547
 Ala Pro Ser Phe Ala Val Met Val Val Gly Arg Val Leu Leu Gly Leu
 135 140 145

gca gtt ggt ggc gct tcc act gtt gtc cct gtc tac ctg gct gaa ctt 595
 Ala Val Gly Gly Ala Ser Thr Val Val Pro Val Tyr Leu Ala Glu Leu
 150 155 160 165

gct cct ttt gaa atc cgt ggc tca ctg gct ggc cgt aat gag ttg atg 643
 Ala Pro Phe Glu Ile Arg Gly Ser Leu Ala Gly Arg Asn Glu Leu Met
 170 175 180

att gtt gtt ggt cag ctc gca gct ttt gtc atc aat gcg att att gga 691
 Ile Val Val Gly Gln Leu Ala Ala Phe Val Ile Asn Ala Ile Ile Gly
 185 190 195

aat gtt ttt gga cac cac gat ggt gtg tgg cgc tac atg ctg gca att 739
 Asn Val Phe Gly His His Asp Gly Val Trp Arg Tyr Met Leu Ala Ile
 200 205 210

gcc gca atc cca gca att gcc ctc ttc ttt gga atg 775
 Ala Ala Ile Pro Ala Ile Ala Leu Phe Phe Gly Met
 215 220 225

c 776

<210> 232

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Val Phe Arg Asp Pro Ala Pro Pro Ser Lys Gly Thr Thr Asn Leu Gly
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Asp Lys Met Ala Ser Thr Phe Ile Gln Ala Asp Ser Pro Glu Lys Ser
 20 25 30

Lys Lys Leu Pro Pro Leu Thr Glu Gly Pro Tyr Arg Lys Arg Leu Phe
 35 40 45

Tyr Val Ala Leu Val Ala Thr Phe Gly Gly Leu Leu Phe Gly Tyr Asp

50 55 60
 Thr Gly Val Ile Asn Gly Ala Leu Asn Pro Met Thr Arg Glu Leu Gly
 65 70 75 80
 Leu Thr Ala Phe Thr Glu Gly Val Val Thr Ser Ser Leu Leu Phe Gly
 85 90 95
 Ala Ala Ala Gly Ala Met Phe Phe Gly Arg Ile Ser Asp Asn Trp Gly
 100 105 110
 Arg Arg Lys Thr Ile Ile Ser Leu Ala Val Ala Phe Phe Val Gly Thr
 115 120 125
 Met Ile Cys Val Phe Ala Pro Ser Phe Ala Val Met Val Val Gly Arg
 130 135 140
 Val Leu Leu Gly Leu Ala Val Gly Gly Ala Ser Thr Val Val Pro Val
 145 150 155 160
 Tyr Leu Ala Glu Leu Ala Pro Phe Glu Ile Arg Gly Ser Leu Ala Gly
 165 170 175
 Arg Asn Glu Leu Met Ile Val Val Gly Gln Leu Ala Ala Phe Val Ile
 180 185 190
 Asn Ala Ile Ile Gly Asn Val Phe Gly His His Asp Gly Val Trp Arg
 195 200 205
 Tyr Met Leu Ala Ile Ala Ala Ile Pro Ala Ile Ala Leu Phe Phe Gly
 210 215 220
 Met
 225

<210> 233
 <211> 718
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(718)
 <223> FRXA01986

<400> 233
 gccacgatta aagacattgg tgatgtgaat cactgcctac tacatcgtgt ttcgtgaccc 60

tgcacctcca agtaagggca cgacaaactt aggagacaag atg gct agt acc ttc 115
 Met Ala Ser Thr Phe
 1 5

att cag gcc gac agc cct gaa aaa agt aag aag ctg ccc cca ctc aca 163
 Ile Gln Ala Asp Ser Pro Glu Lys Ser Lys Lys Leu Pro Pro Leu Thr
 10 15 20

gaa ggt ccg tat aga aag cgg cta ttc tac gtt gca cta gtt gcg acg 211
 Glu Gly Pro Tyr Arg Lys Arg Leu Phe Tyr Val Ala Leu Val Ala Thr
 25 30 35


```

ttt ggt ggg ctg ctc ttc gga tat gac acc gga gta atc aac ggt gca 259
Phe Gly Gly Leu Leu Phe Gly Tyr Asp Thr Gly Val Ile Asn Gly Ala
      40                      45                      50

ctc aac cca atg aca cgt gag ctc gga cta acc gcg ttc acc gag ggt 307
Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr Ala Phe Thr Glu Gly
      55                      60                      65

gtt gta act tct tcc ctg ctg ttt ggt gca gca gct ggt gcg atg ttt 355
Val Val Thr Ser Ser Leu Leu Phe Gly Ala Ala Ala Gly Ala Met Phe
      70                      75                      80                      85

ttc ggt cgc att tcc gac aac tgg ggt cgc cgg aaa aca atc atc tca 403
Phe Gly Arg Ile Ser Asp Asn Trp Gly Arg Arg Lys Thr Ile Ile Ser
      90                      95                      100

ctt gca gta gct ttc ttt gtc ggc acc atg atc tgc gtg ttt gct cca 451
Leu Ala Val Ala Phe Phe Val Gly Thr Met Ile Cys Val Phe Ala Pro
      105                      110                      115

tct ttt gca gta atg gtt gtc gga cgt gtg ctt ctt gga ctc gca gtt 499
Ser Phe Ala Val Met Val Val Gly Arg Val Leu Leu Gly Leu Ala Val
      120                      125                      130

ggt ggc gct tcc act gtt gtc cct gtc tac ctg gct gaa ctt gct cct 547
Gly Gly Ala Ser Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro
      135                      140                      145

ttt gaa atc cgt ggc tca ctg gct ggc cgt aat gag ttg atg att gtt 595
Phe Glu Ile Arg Gly Ser Leu Ala Gly Arg Asn Glu Leu Met Ile Val
      150                      155                      160                      165

gtt ggt cag ctc gca gct ttt gtc atc aat gcg att att gga aat gtt 643
Val Gly Gln Leu Ala Ala Phe Val Ile Asn Ala Ile Ile Gly Asn Val
      170                      175                      180

ttt gga cac cac gat ggt gtg tgg cgc tac atg ctg gca att gcc gca 691
Phe Gly His His Asp Gly Val Trp Arg Tyr Met Leu Ala Ile Ala Ala
      185                      190                      195

atc cca gca att gcc ctc ttc ttt gga 718
Ile Pro Ala Ile Ala Leu Phe Phe Gly
      200                      205

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<210> 234

<211> 206

<212> PRT

<213> Corynebacterium glutamicum

<400> 234

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Met Ala Ser Thr Phe Ile Gln Ala Asp Ser Pro Glu Lys Ser Lys Lys
  1                      5                      10                      15

Leu Pro Pro Leu Thr Glu Gly Pro Tyr Arg Lys Arg Leu Phe Tyr Val
      20                      25                      30

Ala Leu Val Ala Thr Phe Gly Gly Leu Leu Phe Gly Tyr Asp Thr Gly
      35                      40                      45

Val Ile Asn Gly Ala Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr

```

50 55 60
 Ala Phe Thr Glu Gly Val Val Thr Ser Ser Leu Leu Phe Gly Ala Ala
 65 70 75 80
 Ala Gly Ala Met Phe Phe Gly Arg Ile Ser Asp Asn Trp Gly Arg Arg
 85 90 95
 Lys Thr Ile Ile Ser Leu Ala Val Ala Phe Phe Val Gly Thr Met Ile
 100 105 110
 Cys Val Phe Ala Pro Ser Phe Ala Val Met Val Val Gly Arg Val Leu
 115 120 125
 Leu Gly Leu Ala Val Gly Gly Ala Ser Thr Val Val Pro Val Tyr Leu
 130 135 140
 Ala Glu Leu Ala Pro Phe Glu Ile Arg Gly Ser Leu Ala Gly Arg Asn
 145 150 155 160
 Glu Leu Met Ile Val Val Gly Gln Leu Ala Ala Phe Val Ile Asn Ala
 165 170 175
 Ile Ile Gly Asn Val Phe Gly His His Asp Gly Val Trp Arg Tyr Met
 180 185 190
 Leu Ala Ile Ala Ala Ile Pro Ala Ile Ala Leu Phe Phe Gly
 195 200 205

<210> 235
 <211> 1118
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> {1}..(1095)
 <223> RXN02447

<400> 235
 aca gta gtt ccg gtg tac ctc gct gaa ctc gca cca cta gaa atc cgc 48
 Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro Leu Glu Ile Arg
 1 5 10 15
 ggc tcc ctg acc ggc cga aac gag ctt gct atc gtc acc ggc cag ctg 96
 Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu
 20 25 30
 ctt gcc ttc gtg atc aac gcg ctt atc gcc gtc acc cta cac gga gtt 144
 Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val
 35 40 45
 att gat gga atc tgg cgc atc atg ttc gcc gtc tgt gcc ctc cct gcc 192
 Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala
 50 55 60
 gtc gcc ctc ttc ctc ggc atg ctg cgg atg ccg gaa tca cca cgc tgg 240
 Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp
 65 70 75 80

ctg gtc aac cag ggg cgt tac gac gac gcc cgc cgc gtc atg gag acc 288
 Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr
 85 90 95

gtc cgt acc cct gag cgt gcg aaa gcc gaa atg gat gaa atc atc gcg 336
 Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala
 100 105 110

gtg cac tct gaa aac aat gcg gca ctt cct ggt gtt aag cag tct tcg 384
 Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser
 115 120 125

ggc cag gct tca ggc cag gtt tct agc aag cac acc cac atg tcc atc 432
 Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile
 130 135 140

ggc gaa gtc ctc agc aac aaa tgg ctg gtt cgt ctg ctc atc gcc ggc 480
 Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly
 145 150 155 160

atc ggt gtt gca gtt gcc cag cag ctc acc ggc atc aac gcc atc atg 528
 Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met
 165 170 175

tac tac gga acc cgc gtc ctc gag gaa tcc ggc atg agc gca gaa atg 576
 Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met
 180 185 190

gct gtg gtt gcc aac att gct ttc ggt gcc gtt gcc gtc atc ggt gga 624
 Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly
 195 200 205

ctg atc gca ctg cgc aac atg gac cgc ctg gat cgc cgc acc acc ttc 672
 Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe
 210 215 220

atc atc ggc ctg tca ctg acc acc acc ttc cac ctt ttg atc gca gct 720
 Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu Ile Ala Ala
 225 230 235 240

gcc gcc act ctc ctt cca gaa ggt aac tcc att cga cca ttc gcc atc 768
 Ala Gly Thr Leu Leu Pro Glu Gly Asn Ser Ile Arg Pro Phe Ala Ile
 245 250 255

atg atc ctt gtt gtt ggg ttc gtg ctc tcc atg cag act ttc ctc aac 816
 Met Ile Leu Val Val Gly Phe Val Leu Ser Met Gln Thr Phe Leu Asn
 260 265 270

gtt gca gtg tgg gtg tgg ctg gcg gaa atc ttc cca gtc cga atg aag 864
 Val Ala Val Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys
 275 280 285

ggt atc ggc acc ggt att tcg gta ttc tgc ggt tgg ggc atc aat ggc 912
 Gly Ile Gly Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly
 290 295 300

gtc cta gcg ttg ttc ttc cca gca ctg gtc tcc ggc gtg ggt atc acc 960
 Val Leu Ala Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr
 305 310 315 320

ttc tcc ttc ctt atc ttc gca gtc gtc gga gtc att gcc ctg gcg ttc 1008

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<400> 236
Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro Leu Glu Ile Arg
  1          5          10          15
Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu
          20          25          30
Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val
          35          40          45
Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala
          50          55          60
Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp
          65          70          75          80
Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr
          85          90          95
Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala
          100          105          110
Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser
          115          120          125
Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile
          130          135          140
Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly
          145          150          155          160
Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met
          165          170          175
Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met
          180          185          190
Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly
          195          200          205
Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe
          210          215          220

```

Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu Ile Ala Ala
 225 230 235 240

Ala Gly Thr Leu Leu Pro Glu Gly Asn Ser Ile Arg Pro Phe Ala Ile
 245 250 255

Met Ile Leu Val Val Gly Phe Val Leu Ser Met Gln Thr Phe Leu Asn
 260 265 270

Val Ala Val Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys
 275 280 285

Gly Ile Gly Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly
 290 295 300

Val Leu Ala Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr
 305 310 315 320

Phe Ser Phe Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe
 325 330 335

Val Thr Lys Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu
 340 345 350

Asp His Ala Ala Phe Thr Gly Gln Ile Phe Lys Lys Ala
 355 360 365

<210> 237

<211> 293

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(270)

<223> FRXA02447

<400> 237

tgg	gtg	tgg	ctg	gcg	gaa	atc	ttc	cca	gtc	cga	atg	aag	ggt	atc	ggc	48
Trp	Val	Trp	Leu	Ala	Glu	Ile	Phe	Pro	Val	Arg	Met	Lys	Gly	Ile	Gly	
1				5					10					15		
acc	ggt	att	tcg	gta	ttc	tgc	ggt	tgg	ggc	atc	aat	ggc	gtc	cta	gcg	96
Thr	Gly	Ile	Ser	Val	Phe	Cys	Gly	Trp	Gly	Ile	Asn	Gly	Val	Leu	Ala	
			20					25					30			
ttg	ttc	ttc	cca	gca	ctg	gtc	tcc	ggc	gtg	ggt	atc	acc	ttc	tcc	ttc	144
Leu	Phe	Phe	Pro	Ala	Leu	Val	Ser	Gly	Val	Gly	Ile	Thr	Phe	Ser	Phe	
			35				40					45				
ctt	atc	ttc	gca	gtc	gtc	gga	gtc	att	gcc	ctg	gcg	ttc	gtc	acc	aag	192
Leu	Ile	Phe	Ala	Val	Val	Gly	Val	Ile	Ala	Leu	Ala	Phe	Val	Thr	Lys	
	50					55			60							
ttt	ggt	cct	gaa	acc	cgt	ggc	cgc	tca	ctt	gaa	gaa	ctc	gat	cac	gca	240
Phe	Val	Pro	Glu	Thr	Arg	Gly	Arg	Ser	Leu	Glu	Glu	Leu	Asp	His	Ala	
65					70				75						80	
gca	ttc	acc	ggc	cag	atc	ttc	aag	aag	gct	taa	acccccc	ctc	gat	ctctt		290


```

ctg gtc aac cag ggg cgt tac gac gac gcc cgc cgc gtc atg gag acc 288
Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr
      85                      90                      95

gtc cgt acc cct gag cgt gcg aaa gcc gaa atg gat gaa atc atc gcg 336
Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala
      100                      105                      110

gtg cac tct gaa aac aat gcg gca ctt cct ggt gtt aag cag tct tcg 384
Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser
      115                      120                      125

ggc cag gct tca ggc cag gtt tct agc aag cac acc cac atg tcc atc 432
Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile
      130                      135                      140

ggc gaa gtc ctc agc aac aaa tgg ctg gtt cgt ctg ctc atc gcc ggc 480
Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly
      145                      150                      155                      160

atc ggt gtt gca gtt gcc cag cag ctc acc ggc atc aac gcc atc atg 528
Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met
      165                      170                      175

tac tac gga acc cgc gtc ctc gag gaa tcc ggc atg agc gca gaa atg 576
Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met
      180                      185                      190

gct gtg gtt gcc aac att gct ttc ggt gcc gtt gcc gtc atc ggt gga 624
Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly
      195                      200                      205

ctg atc gca ctg cgc aac atg gac cgc ctg gat cgc cgc acc acc ttc 672
Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe
      210                      215                      220

atc atc ggc ctg tca ctg acc acc acc ttc cac ctt ttg 711
Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu
      225                      230                      235

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<210> 240

<211> 237

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

```

Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro Leu Glu Ile Arg
  1          5          10          15

```

```

Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu
      20          25          30

```

```

Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val
      35          40          45

```

```

Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala
      50          55          60

```

```

Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp

```

[illegible]

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<220>  
<221> CDS  
<222> (3)..(695)  
<223> RXS03220
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<400> 241
ccatg ggc tta agg gaa att ttg tcc agc aag tgg ctt gtg cgc atc ctc 50
  Met Gly Leu Arg Glu Ile Leu Ser Ser Lys Trp Leu Val Arg Ile Leu
    1             5             10             15

ctg gta ggt atc gga ttg ggt gtc gca cag cag ctg acc ggc atc aac 98
Leu Val Gly Ile Gly Leu Gly Val Ala Gln Gln Leu Thr Gly Ile Asn
      20             25             30

tcc atc atg tac tac ggc cag gtt gtt ctc att gag gct ggt ttc tcc 146
Ser Ile Met Tyr Tyr Gly Gln Val Val Leu Ile Glu Ala Gly Phe Ser
      35             40             45

gag aat gca gct ctg atc gcc aac gtg gcg cca gga gtg atc gca gtt 194
Glu Asn Ala Ala Leu Ile Ala Asn Val Ala Pro Gly Val Ile Ala Val
    50             55             60

gtc ggt gca ttc atc gca ctg tgg atg atg gat ggt atc aac cgc cgt 242

```



```

Val Gly Ala Phe Ile Ala Leu Trp Met Met Asp Gly Ile Asn Arg Arg
 65              70              75              80

acc acc ctc att acc ggt tat tct ctc acc acc att agc cac gta ttg   290
Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser His Val Leu
              85              90              95

atc ggt atc gca tcc gta gca ttc cca gtc ggc gat cct ctt cgc ccc   338
Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro Leu Arg Pro
              100              105              110

tac gtt atc ttg act ctg gtt gtg gtc ttc gtg gga tcc atg cag acc   386
Tyr Val Ile Leu Thr Leu Val Val Val Phe Val Gly Ser Met Gln Thr
              115              120              125

ttc ctc aac gta gct acc tgg gtt atg ctc tct gag ctc ttc ccg ctg   434
Phe Leu Asn Val Ala Thr Trp Val Met Leu Ser Glu Leu Phe Pro Leu
              130              135              140

gca atg cgc ggt ttc gca atc ggt atc tca gtg ttc ttc ctc tgg atc   482
Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe Leu Trp Ile
              145              150              155              160

gca aac gcg ttc ctc gga ttg ttc ttc cca acc atc atg gaa gca gta   530
Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met Glu Ala Val
              165              170              175

gga cta acc gga acc ttc ttc atg ttc gcc gga atc ggt gtg gtt gcc   578
Gly Leu Thr Gly Thr Phe Phe Met Phe Ala Gly Ile Gly Val Val Ala
              180              185              190

ttg atc ttc atc tac acc cag gtt cct gaa act cgt gga cgt acc ttg   626
Leu Ile Phe Ile Tyr Thr Gln Val Pro Glu Thr Arg Gly Arg Thr Leu
              195              200              205

gag gag att gat gag gat gtt act tcc ggt gtc att ttc aac aag gac   674
Glu Glu Ile Asp Glu Asp Val Thr Ser Gly Val Ile Phe Asn Lys Asp
              210              215              220

atc cga aaa gga aag gtg cac taaaaaccca gacactgcat agataacacg   725
Ile Arg Lys Gly Lys Val His
225              230

```

<210> 242

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

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Met Gly Leu Arg Glu Ile Leu Ser Ser Lys Trp Leu Val Arg Ile Leu
  1              5              10              15

Leu Val Gly Ile Gly Leu Gly Val Ala Gln Gln Leu Thr Gly Ile Asn
  20              25              30

Ser Ile Met Tyr Tyr Gly Gln Val Val Leu Ile Glu Ala Gly Phe Ser
  35              40              45

Glu Asn Ala Ala Leu Ile Ala Asn Val Ala Pro Gly Val Ile Ala Val
  50              55              60

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BGI-131CP-4226036

Val Gly Ala Phe Ile Ala Leu Trp Met Met Asp Gly Ile Asn Arg Arg
65 70 75 80

Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser His Val Leu
85 90 95

Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro Leu Arg Pro
100 105 110

Tyr Val Ile Leu Thr Leu Val Val Val Phe Val Gly Ser Met Gln Thr
115 120 125

Phe Leu Asn Val Ala Thr Trp Val Met Leu Ser Glu Leu Phe Pro Leu
130 135 140

Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe Leu Trp Ile
145 150 155 160

Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met Glu Ala Val
165 170 175

Gly Leu Thr Gly Thr Phe Phe Met Phe Ala Gly Ile Gly Val Val Ala
180 185 190

Leu Ile Phe Ile Tyr Thr Gln Val Pro Glu Thr Arg Gly Arg Thr Leu
195 200 205

Glu Glu Ile Asp Glu Asp Val Thr Ser Gly Val Ile Phe Asn Lys Asp
210 215 220

Ile Arg Lys Gly Lys Val His
225 230

<210> 243
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> FRXA02762

<400> 243
ttcccgatcg gcgatcctct tcgcccctac gttatcttga ctctggttgt ggtcttcgtg 60

ggatccatgc agaccttcct caacggtagc tacctgggtt atg ctc tct gag ctc 115
Met Leu Ser Glu Leu
1 5

ttc ccg ctg gca atg cgc ggt ttc gca atc ggt atc tca gtg ttc ttc 163
Phe Pro Leu Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe
10 15 20

ctc tgg atc gca aac gcg ttc ctc gga ttg ttc ttc cca acc atc atg 211
Leu Trp Ile Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met
25 30 35

gaa gca gta gga cta acc gga acc ttc ttc atg ttc gcc gga atc ggt 259

```

Glu Ala Val Gly Leu Thr Gly Thr Phe Phe Met Phe Ala Gly Ile Gly
      40                      45                      50

gtg gtt gcc ttg atc ttc atc tac acc cag gtt cct gaa act cgt gga 307
Val Val Ala Leu Ile Phe Ile Tyr Thr Gln Val Pro Glu Thr Arg Gly
      55                      60                      65

cgt acc ttg gag gag att gat gag gat gtt act tcc ggt gtc att ttc 355
Arg Thr Leu Glu Glu Ile Asp Glu Asp Val Thr Ser Gly Val Ile Phe
      70                      75                      80                      85

aac aag gac atc cga aaa gga aag gtg cac taaaaaccca gacactgcat 405
Asn Lys Asp Ile Arg Lys Gly Lys Val His
      90                      95

aga 408

```

```

<210> 244
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 244
Met Leu Ser Glu Leu Phe Pro Leu Ala Met Arg Gly Phe Ala Ile Gly
  1           5           10           15

Ile Ser Val Phe Phe Leu Trp Ile Ala Asn Ala Phe Leu Gly Leu Phe
      20           25           30

Phe Pro Thr Ile Met Glu Ala Val Gly Leu Thr Gly Thr Phe Phe Met
      35           40           45

Phe Ala Gly Ile Gly Val Val Ala Leu Ile Phe Ile Tyr Thr Gln Val
      50           55           60

Pro Glu Thr Arg Gly Arg Thr Leu Glu Glu Ile Asp Glu Asp Val Thr
      65           70           75           80

Ser Gly Val Ile Phe Asn Lys Asp Ile Arg Lys Gly Lys Val His
      85           90           95

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```

<210> 245
<211> 324
<212> DNA
<213> Corynebacterium glutamicum

```

```

<220>
<221> CDS
<222> (101)..(301)
<223> FRXA02761

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<400> 245
cagggttggtc tcattgaggt ggtttctccg agaatgcagc tttgatcgcc aacgtggcgc 60

cagaagtgat cgcagttgtc gggcattcat cgcactgtgg atg atg gat ggt atc 115
              Met Met Asp Gly Ile
              1           5

aac cgc cgt acc acc ctc att acc ggt tat tct ctc acc acc att agc 163

```

```

Asn Arg Arg Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser
                10                15                20
cac gta ttg atc ggt atc gca tcc gta gca ttc cca gtc ggc gat cct 211
His Val Leu Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro
                25                30                35
ctt cgc ccc tac gtt atc ttg act ctg gtt gtg gtc ttc gtg gga tcc 259
Leu Arg Pro Tyr Val Ile Leu Thr Leu Val Val Val Phe Val Gly Ser
                40                45                50
atg cag acc ttc ctc aac ggt agc tac ctg ggt tat gct ctc 301
Met Gln Thr Phe Leu Asn Gly Ser Tyr Leu Gly Tyr Ala Leu
                55                60                65
tgagctcttc ccgctggcaa tgc 324

```

```

<210> 246
<211> 67
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 246
Met Met Asp Gly Ile Asn Arg Arg Thr Thr Leu Ile Thr Gly Tyr Ser
  1                5                10                15
Leu Thr Thr Ile Ser His Val Leu Ile Gly Ile Ala Ser Val Ala Phe
                20                25                30
Pro Val Gly Asp Pro Leu Arg Pro Tyr Val Ile Leu Thr Leu Val Val
                35                40                45
Val Phe Val Gly Ser Met Gln Thr Phe Leu Asn Gly Ser Tyr Leu Gly
                50                55                60
Tyr Ala Leu
  65

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<210> 247
<211> 1242
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1219)
<223> RXA00123

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<400> 247
gaaggatcgt cagaatagct ctcgaatagg ccatttctta cttcatcggc aatactgact 60
tagtagaaat tgctgtccag aactgttgaa ggagttgaaa atg cca aag aat tac 115
                Met Pro Lys Asn Tyr
                1                5
gac atc aac ggg gcg atc cgc aga cgg gat atg ctc aga cgt cgg tac 163
Asp Ile Asn Gly Ala Ile Arg Arg Arg Asp Met Leu Arg Arg Arg Tyr
                10                15                20

```

ctt cct gat tcg gca aat tca act cct gta cct gaa gag gtt tct ccg	211
Leu Pro Asp Ser Ala Asn Ser Thr Pro Val Pro Glu Glu Val Ser Pro	
25 30 35	
ctg acc cgc tat gtc acc gac ggc atc ccg aag cgc cca ccg ctg ggt	259
Leu Thr Arg Tyr Val Thr Asp Gly Ile Pro Lys Arg Pro Pro Leu Gly	
40 45 50	
gcc act gtt gct gac ggt tta aaa ttc gcc gaa ggc gcc tcc aac cgc	307
Ala Thr Val Ala Asp Gly Leu Lys Phe Ala Glu Gly Ala Ser Asn Arg	
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Met Val Met Ser Leu Tyr Pro Ala Pro Ser Lys Pro Ala Ile Glu Glu	
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Leu Ala Glu Ala Trp Asp Leu His Pro Thr Ile Val Glu Asp Leu Leu	
90 95 100	
ctt ggt cag cag cgc cca aaa cta gac cgc tac gaa gac atc att ttt	451
Leu Gly Gln Gln Arg Pro Lys Leu Asp Arg Tyr Glu Asp Ile Ile Phe	
105 110 115	
atc gcg atc cgc tcc gcg cgc tac atc gac tcc cgc gaa gag gtg gac	499
Ile Ala Ile Arg Ser Ala Arg Tyr Ile Asp Ser Arg Glu Glu Val Asp	
120 125 130	
ttc tcc gaa ttc cac atc ctc atg aag cct cag gcc ata gcc att ttg	547
Phe Ser Glu Phe His Ile Leu Met Lys Pro Gln Ala Ile Ala Ile Leu	
135 140 145	
tgc cag gat aac caa tgg att gac ggc acc agc gcc gcc agc ttc agc	595
Cys Gln Asp Asn Gln Trp Ile Asp Gly Thr Ser Ala Ala Ser Phe Ser	
150 155 160 165	
aac ccc gag gag atc gat aag cgc ata aaa aca ttg ctt gcc gac gcc	643
Asn Pro Glu Glu Ile Asp Lys Arg Ile Lys Thr Leu Leu Ala Asp Ala	
170 175 180	
gag tta ctc tcg tcc ggc ccc cgc gcc gcg gcc tat agg ctt ctc gac	691
Glu Leu Leu Ser Ser Gly Pro Arg Ala Ala Ala Tyr Arg Leu Leu Asp	
185 190 195	
gcc atc gtc gac ggc ttc tcc ccc gtt ctt aga ggc atc gcc atc gac	739
Ala Ile Val Asp Gly Phe Ser Pro Val Leu Arg Gly Ile Ala Ile Asp	
200 205 210	
cag gaa cag att gag cgc cag gtg ttc tcc ggc gac gcc gcc gtc gcc	787
Gln Glu Gln Ile Glu Arg Gln Val Phe Ser Gly Asp Ala Ala Val Ala	
215 220 225	
gaa cgt att tac aac ctg tcc caa gaa atc atc gac atg cag cac acc	835
Glu Arg Ile Tyr Asn Leu Ser Gln Glu Ile Ile Asp Met Gln His Thr	
230 235 240 245	
acc agc tca gtt acc gaa gtg gtg caa cgc ctc aac aaa gac ttc atc	883
Thr Ser Ser Val Thr Glu Val Val Gln Arg Leu Asn Lys Asp Phe Ile	
250 255 260	
cga agt ggc atg tcc gaa gaa ctc cgc gcc tac ctc gac gac gtc gcc	931

Arg	Ser	Gly	Met	Ser	Glu	Glu	Leu	Arg	Ala	Tyr	Leu	Asp	Asp	Val	Ala	
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gac	cac	ctc	acc	cgc	gac	aac	acc	cgc	gtc	tcc	gaa	tac	cgc	gaa	tcc	979
Asp	His	Leu	Thr	Arg	Asp	Asn	Thr	Arg	Val	Ser	Glu	Tyr	Arg	Glu	Ser	
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cta	tcc	caa	att	ttg	aac	gtc	aac	gcc	acc	ctt	gta	gcc	caa	cgc	caa	1027
Leu	Ser	Gln	Ile	Leu	Asn	Val	Asn	Ala	Thr	Leu	Val	Ala	Gln	Arg	Gln	
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aac	gaa	gac	atg	aag	aaa	atc	tcc	gga	tgg	gcc	gcc	atc	atc	ttc	gcc	1075
Asn	Glu	Asp	Met	Lys	Lys	Ile	Ser	Gly	Trp	Ala	Ala	Ile	Ile	Phe	Ala	
310					315					320					325	
cca	acc	ctc	gtg	tcc	tcc	atc	tac	ggc	atg	aac	ttc	gac	atc	atg	cca	1123
Pro	Thr	Leu	Val	Ser	Ser	Ile	Tyr	Gly	Met	Asn	Phe	Asp	Ile	Met	Pro	
				330					335					340		
gaa	ctt	cac	tgg	gcg	ttt	ggc	tac	ccg	ttg	gct	ctc	tta	gca	atg	ctc	1171
Glu	Leu	His	Trp	Ala	Phe	Gly	Tyr	Pro	Leu	Ala	Leu	Leu	Ala	Met	Leu	
			345					350					355			
gga	ttc	acc	ctc	ctt	ttg	tac	tgg	atc	ttc	aaa	cgc	agt	aag	tgg	atg	1219
Gly	Phe	Thr	Leu	Leu	Leu	Tyr	Trp	Ile	Phe	Lys	Arg	Ser	Lys	Trp	Met	
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Glu	Glu	Val	Ser	Pro	Leu	Thr	Arg	Tyr	Val	Thr	Asp	Gly	Ile	Pro	Lys	
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Arg	Pro	Pro	Leu	Gly	Ala	Thr	Val	Ala	Asp	Gly	Leu	Lys	Phe	Ala	Glu	
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Gly	Ala	Ser	Asn	Arg	Met	Val	Met	Ser	Leu	Tyr	Pro	Ala	Pro	Ser	Lys	
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Pro	Ala	Ile	Glu	Glu	Leu	Ala	Glu	Ala	Trp	Asp	Leu	His	Pro	Thr	Ile	
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Val	Glu	Asp	Leu	Leu	Leu	Gly	Gln	Gln	Arg	Pro	Lys	Leu	Asp	Arg	Tyr	
			100				105						110			
Glu	Asp	Ile	Ile	Phe	Ile	Ala	Ile	Arg	Ser	Ala	Arg	Tyr	Ile	Asp	Ser	
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130 135 140
 Ala Ile Ala Ile Leu Cys Gln Asp Asn Gln Trp Ile Asp Gly Thr Ser
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 Ala Ala Ser Phe Ser Asn Pro Glu Glu Ile Asp Lys Arg Ile Lys Thr
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 Leu Leu Ala Asp Ala Glu Leu Leu Ser Ser Gly Pro Arg Ala Ala Ala
 180 185 190
 Tyr Arg Leu Leu Asp Ala Ile Val Asp Gly Phe Ser Pro Val Leu Arg
 195 200 205
 Gly Ile Ala Ile Asp Gln Glu Gln Ile Glu Arg Gln Val Phe Ser Gly
 210 215 220
 Asp Ala Ala Val Ala Glu Arg Ile Tyr Asn Leu Ser Gln Glu Ile Ile
 225 230 235 240
 Asp Met Gln His Thr Thr Ser Ser Val Thr Glu Val Val Gln Arg Leu
 245 250 255
 Asn Lys Asp Phe Ile Arg Ser Gly Met Ser Glu Glu Leu Arg Ala Tyr
 260 265 270
 Leu Asp Asp Val Ala Asp His Leu Thr Arg Asp Asn Thr Arg Val Ser
 275 280 285
 Glu Tyr Arg Glu Ser Leu Ser Gln Ile Leu Asn Val Asn Ala Thr Leu
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 Val Ala Gln Arg Gln Asn Glu Asp Met Lys Lys Ile Ser Gly Trp Ala
 305 310 315 320
 Ala Ile Ile Phe Ala Pro Thr Leu Val Ser Ser Ile Tyr Gly Met Asn
 325 330 335
 Phe Asp Ile Met Pro Glu Leu His Trp Ala Phe Gly Tyr Pro Leu Ala
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 Arg Ser Lys Trp Met
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<212> DNA

<213> Corynebacterium glutamicum

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<223> RXA02441

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								Met	Ala	Glu	Leu	Ser					
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gtc	cgg	aat	ctc	aca	tgc	aca	tac	ggc	aat	cac	atc	gcg	ctc	aac	aac		163
Val	Arg	Asn	Leu	Thr	Cys	Thr	Tyr	Gly	Asn	His	Ile	Ala	Leu	Asn	Asn		
				10					15					20			
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Ile	Thr	Ala	Arg	Phe	Pro	Thr	Gly	Lys	Ile	Thr	Ala	Leu	Ile	Gly	Ser		
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Asn	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Glu	Thr	Leu	Ala	Gly	Met	Leu		
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gca	ccc	cgc	agc	gga	agc	att	aac	aac	ctt	gtg	cca	gaa	atc	gcg	ttc		307
Ala	Pro	Arg	Ser	Gly	Ser	Ile	Asn	Asn	Leu	Val	Pro	Glu	Ile	Ala	Phe		
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Val	Pro	Gln	Arg	Ser	His	Val	Ser	His	Asn	Leu	Pro	Ile	Thr	Ile	Arg		
	70				75				80						85		
caa	aca	gtc	agc	atg	ggg	cga	tgg	tca	gcc	aag	aaa	aac	tgg	caa	cga		403
Gln	Thr	Val	Ser	Met	Gly	Arg	Trp	Ser	Ala	Lys	Lys	Asn	Trp	Gln	Arg		
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Leu	Thr	Ala	Ala	Asp	Cys	Asn	Ile	Val	Asp	Ser	Cys	Leu	Asp	Arg	Leu		
			105					110					115				
gaa	atc	tcc	ggc	ctc	gcc	gac	cgc	ccc	ctc	ggc	gaa	gta	tca	ggc	ggg		499
Glu	Ile	Ser	Gly	Leu	Ala	Asp	Arg	Pro	Leu	Gly	Glu	Val	Ser	Gly	Gly		
		120					125					130					
cag	cgc	caa	cgc	gcc	ctc	ata	gcg	caa	ggt	tta	gcg	caa	cag	gcg	ccc		547
Gln	Arg	Gln	Arg	Ala	Leu	Ile	Ala	Gln	Gly	Leu	Ala	Gln	Gln	Ala	Pro		
	135					140					145						
tta	ttg	ctt	ctc	gac	gaa	ccc	ctc	gcc	gcc	gtg	gac	tcc	cac	gcg	gca		595
Leu	Leu	Leu	Leu	Asp	Glu	Pro	Leu	Ala	Ala	Val	Asp	Ser	His	Ala	Ala		
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agt	ctt	atc	gaa	gat	gtc	att	aac	caa	caa	cgc	aac	caa	gga	acc	aca		643
Ser	Leu	Ile	Glu	Asp	Val	Ile	Asn	Gln	Gln	Arg	Asn	Gln	Gly	Thr	Thr		
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Ile	Ile																

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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Leu Ala Gly Met Leu Ala Pro Arg Ser Gly Ser Ile Asn Asn Leu Val
 50 55 60
 Pro Glu Ile Ala Phe Val Pro Gln Arg Ser His Val Ser His Asn Leu
 65 70 75 80
 Pro Ile Thr Ile Arg Gln Thr Val Ser Met Gly Arg Trp Ser Ala Lys
 85 90 95
 Lys Asn Trp Gln Arg Leu Thr Ala Ala Asp Cys Asn Ile Val Asp Ser
 100 105 110
 Cys Leu Asp Arg Leu Glu Ile Ser Gly Leu Ala Asp Arg Pro Leu Gly
 115 120 125
 Glu Val Ser Gly Gly Gln Arg Gln Arg Ala Leu Ile Ala Gln Gly Leu
 130 135 140
 Ala Gln Gln Ala Pro Leu Leu Leu Leu Asp Glu Pro Leu Ala Ala Val
 145 150 155 160
 Asp Ser His Ala Ala Ser Leu Ile Glu Asp Val Ile Asn Gln Gln Arg
 165 170 175
 Asn Gln Gly Thr Thr Ile Ile Leu Ala Thr His Asp Leu Asp Gln Ala
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 His Gln Ala Asp Gln Ile Ile Ala Leu Glu Lys Gly Ile Ile Lys Pro
 195 200 205
 Gln Arg Lys Ala Thr Glu Ser Ile Lys Lys Arg
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 <212> DNA
 <213> Corynebacterium glutamicum

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 210                               215                220

Ile Ser Leu Ile Met Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile
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Tyr Leu Gly Leu Leu Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala
                245                               250                255

Thr Ile Thr Leu Leu Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr
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Lys Ser Ala Ile Ser Arg Leu Asn Phe Thr Ala
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                               Met Lys Phe Phe Thr
                               1                    5

gac gcc ctc ata gtg cct ttt gac gtt tca ttc atc tcc cgc gcc ctg    163
Asp Ala Leu Ile Val Pro Phe Asp Val Ser Phe Ile Ser Arg Ala Leu
                10                15                20

gtc gcc gga tgc ctg gcc gca att tta tgc tca ctc att gga acg tgg    211
Val Ala Gly Cys Leu Ala Ala Ile Leu Cys Ser Leu Ile Gly Thr Trp
                25                30                35

gtt att ttg cgc agg cta acc ttt ttc ggc gac gct atg tcg cac ggc    259
Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp Ala Met Ser His Gly
                40                45                50

ttg ctc ccc gga gta gcc acg gca tca cta ttg ggc gga aat ctc atg    307
Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu Gly Gly Asn Leu Met
                55                60                65

ttc ggc gca gca atc agc gca tta atc atg tca gcc gga gtg gtg tgg    355
Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser Ala Gly Val Val Trp
                70                75                80                85

acc agc aga aaa tcc agc ctc tcc caa gac gtc agc att ggc ctg caa    403
Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val Ser Ile Gly Leu Gln
                90                95                100

ttt att acc atg ctt tcc ctc ggc gtg gtt att gtg tcc cac tcc gat    451
Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile Val Ser His Ser Asp
                105                110                115

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BGI-131CP

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gtg cga ccc tcg gat ata ttc atc atc gcc att gca aca gtg ttg ggt 547
 Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile Ala Thr Val Leu Gly
 135 140 145

gga ttg act att ttt ctc ttc cac cga cag ttc act gca ctc gct ttc 595
 Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe Thr Ala Leu Ala Phe
 150 155 160 165

gac gag cgt aaa gct cac acc tta gga ctc aat ccc cgc ttt gca cac 643
 Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn Pro Arg Phe Ala His
 170 175 180

cta ctc atg ctg gca ctg atc gca tta gct acg gtg gtg tcg ttt cag 691
 Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr Val Val Ser Phe Gln
 185 190 195

gtg gtg gga acg ctt tta gtg ttt gga ctt ctc att ggt ccg ccc gcc 739
 Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu Ile Gly Pro Pro Ala
 200 205 210

acg gct gca ctt tta gtg caa gac aaa gca agt att tca ctg atc atg 787
 Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser Ile Ser Leu Ile Met
 215 220 225

atc gtc gcg tcg ctt ctt gga tgc gcg gaa att tac ctc ggg ctt tta 835
 Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile Tyr Leu Gly Leu Leu
 230 235 240 245

atc agc tgg cac gca agc act gcc gcg gga gcc act atc act ttg tta 883
 Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala Thr Ile Thr Leu Leu
 250 255 260

agt gct gcg ata ttt ttt gcc acc tta ttg aca aag agt gcc att agt 931
 Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr Lys Ser Ala Ile Ser
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 Arg Leu Asn Phe Thr Ala
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<211> 283

<212> PRT

<213> Corynebacterium glutamicum

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Leu Ile Gly Thr Trp Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp
 35 40 45

Ala Met Ser His Gly Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu
50 55 60

Gly Gly Asn Leu Met Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser
65 70 75 80

Ala Gly Val Val Trp Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val
85 90 95

Ser Ile Gly Leu Gln Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile
100 105 110

Val Ser His Ser Asp Ser His Ala Val Asp Leu Thr Ser Phe Leu Phe
115 120 125

Gly Asp Ile Leu Gly Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile
130 135 140

Ala Thr Val Leu Gly Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe
145 150 155 160

Thr Ala Leu Ala Phe Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn
165 170 175

Pro Arg Phe Ala His Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr
180 185 190

Val Val Ser Phe Gln Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu
195 200 205

Ile Gly Pro Pro Ala Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser
210 215 220

Ile Ser Leu Ile Met Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile
225 230 235 240

Tyr Leu Gly Leu Leu Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala
245 250 255

Thr Ile Thr Leu Leu Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr
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Lys Ser Ala Ile Ser Arg Leu Asn Phe Thr Ala
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<211> 1431

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1408)

<223> RXA01756

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Met Lys Glu Leu Glu

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ctg ggc gag gcg agg gac gtc gct gca acg ttg gaa gcg atg ccg atc			163
Leu Gly Glu Ala Arg Asp Val Ala Ala Thr Leu Glu Ala Met Pro Ile			
	10	20	
cag gag gtt att gat cag gtt gag cga act tct ata act aaa ggt gcg			211
Gln Glu Val Ile Asp Gln Val Glu Arg Thr Ser Ile Thr Lys Gly Ala			
	25	35	
gta ctg ctg cgt ctg ctc agt aaa gat cga tcg ttg ttg gtc ttc gat			259
Val Leu Leu Arg Leu Leu Ser Lys Asp Arg Ser Leu Leu Val Phe Asp			
	40	50	
gct ctt ggt ccg cga ctc cag gct gat ctc att ggt gct ttt cag gat			307
Ala Leu Gly Pro Arg Leu Gln Ala Asp Leu Ile Gly Ala Phe Gln Asp			
	55	65	
gcg gaa gtg ctg gat tat ttc gct gac ctt gac cct gat gac cgc gtt			355
Ala Glu Val Leu Asp Tyr Phe Ala Asp Leu Asp Pro Asp Asp Arg Val			
	70	80	85
tca ctg ctt gat gag ctg ccg gcg tcg atc gct gac gag ttg ctt cgc			403
Ser Leu Leu Asp Glu Leu Pro Ala Ser Ile Ala Asp Glu Leu Leu Arg			
	90	95	100
agt ctc gat ccg cag gaa aag cag gtc acg gag ctg gtc ttg ggt tac			451
Ser Leu Asp Pro Gln Glu Lys Gln Val Thr Glu Leu Val Leu Gly Tyr			
	105	110	115
gca aag ggg tcg gtt gga cgt tgg atg tcg ccc cag gtt tta ttg ctt			499
Ala Lys Gly Ser Val Gly Arg Trp Met Ser Pro Gln Val Leu Leu Leu			
	120	125	130
ttc gac gac atg tcc gtc gcc gaa gtc tta gat ttt gtg cgc aat cat			547
Phe Asp Asp Met Ser Val Ala Glu Val Leu Asp Phe Val Arg Asn His			
	135	140	145
gct gct gag gct gag acg att tat gcc tta cct att gtg aac cgt gct			595
Ala Ala Glu Ala Glu Thr Ile Tyr Ala Leu Pro Ile Val Asn Arg Ala			
	150	155	160
cgc caa gtg atg ggc gtg gtg tcg ttg cga aag ctg ttc atc gca gat			643
Arg Gln Val Met Gly Val Val Ser Leu Arg Lys Leu Phe Ile Ala Asp			
	170	175	180
ccc act cta aaa gtc tcg gaa atc atg gtg cgt cct gtt tcg gtg ttg			691
Pro Thr Leu Lys Val Ser Glu Ile Met Val Arg Pro Val Ser Val Leu			
	185	190	195
gcg tcc gcg gat att gaa gaa acc gcc cgc tgg ttc cta cag ttg gac			739
Ala Ser Ala Asp Ile Glu Glu Thr Ala Arg Trp Phe Leu Gln Leu Asp			
	200	205	210
ctc gtt gcg atg ccc gtt gtg gat gaa tcg aac atg ctc tta gga gtg			787
Leu Val Ala Met Pro Val Val Asp Glu Ser Asn Met Leu Leu Gly Val			
	215	220	225
ctg acc ttc gat gat gcg caa gac atc gtg gag caa gcc gac tct gag			835
Leu Thr Phe Asp Asp Ala Gln Asp Ile Val Glu Gln Ala Asp Ser Glu			
	230	235	240
			245

gac tcc gct cgc agt ggt ggt tcg gaa cct ctc cag cag ccg tat cta 883
 Asp Ser Ala Arg Ser Gly Gly Ser Glu Pro Leu Gln Gln Pro Tyr Leu
 250 255 260

tcc acg ccg att cgg aaa ctg gtg aag tcc cgc atc gta tgg ctt ctg 931
 Ser Thr Pro Ile Arg Lys Leu Val Lys Ser Arg Ile Val Trp Leu Leu
 265 270 275

gtt ttg gca gtg tca gca att ttg acg gtt caa gtt ctt gat att ttc 979
 Val Leu Ala Val Ser Ala Ile Leu Thr Val Gln Val Leu Asp Ile Phe
 280 285 290

gaa gcc acc ttg gtt gaa gcc gtg gta ctg gca ttg ttc att cct ttg 1027
 Glu Ala Thr Leu Val Glu Ala Val Val Leu Ala Leu Phe Ile Pro Leu
 295 300 305

ctc act ggt act ggc gga aac acc gga aac caa gct gca aca acc gtg 1075
 Leu Thr Gly Thr Gly Gly Asn Thr Gly Asn Gln Ala Ala Thr Thr Val
 310 315 320 325

acc cgt gcg ctc gca ttg ggt gac gtc cga aaa tca gat gtc ttc cgc 1123
 Thr Arg Ala Leu Ala Leu Gly Asp Val Arg Lys Ser Asp Val Phe Arg
 330 335 340

gtc ttg ggc aga gaa atc cga gtc ggc ctc atg ctc ggg gca ttg ttg 1171
 Val Leu Gly Arg Glu Ile Arg Val Gly Leu Met Leu Gly Ala Leu Leu
 345 350 355

ggt gcc gtt gga ttt gtg atc gca tcg ctt gtt tac ggc atg ccc gta 1219
 Gly Ala Val Gly Phe Val Ile Ala Ser Leu Val Tyr Gly Met Pro Val
 360 365 370

ggc act gtc atc ggt ctg aca ttg ttg gcg gtg tgc acg atg gcc gca 1267
 Gly Thr Val Ile Gly Leu Thr Leu Leu Ala Val Cys Thr Met Ala Ala
 375 380 385

tca gtt ggc gga gta atg cca att att gcc aag gcg atc gga gcg gac 1315
 Ser Val Gly Gly Val Met Pro Ile Ile Ala Lys Ala Ile Gly Ala Asp
 390 395 400 405

cca gcg gtg ttc tct aat cct ttt att tca acc ttc tgt gat gca aca 1363
 Pro Ala Val Phe Ser Asn Pro Phe Ile Ser Thr Phe Cys Asp Ala Thr
 410 415 420

ggt ttg atc atc tac ttt gca att gcc aag ttg gtg ctc gga atc 1408
 Gly Leu Ile Ile Tyr Phe Ala Ile Ala Lys Leu Val Leu Gly Ile
 425 430 435

taaaagattt ttgcttttcg acg 1431

<210> 256
 <211> 436
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 256
 Met Lys Glu Leu Glu Leu Gly Glu Ala Arg Asp Val Ala Ala Thr Leu
 1 5 10 15


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Glu Ala Met Pro Ile Gln Glu Val Ile Asp Gln Val Glu Arg Thr Ser
      20                      25                      30

Ile Thr Lys Gly Ala Val Leu Leu Arg Leu Leu Ser Lys Asp Arg Ser
      35                      40                      45

Leu Leu Val Phe Asp Ala Leu Gly Pro Arg Leu Gln Ala Asp Leu Ile
      50                      55                      60

Gly Ala Phe Gln Asp Ala Glu Val Leu Asp Tyr Phe Ala Asp Leu Asp
      65                      70                      75                      80

Pro Asp Asp Arg Val Ser Leu Leu Asp Glu Leu Pro Ala Ser Ile Ala
      85                      90                      95

Asp Glu Leu Leu Arg Ser Leu Asp Pro Gln Glu Lys Gln Val Thr Glu
      100                     105                     110

Leu Val Leu Gly Tyr Ala Lys Gly Ser Val Gly Arg Trp Met Ser Pro
      115                     120                     125

Gln Val Leu Leu Leu Phe Asp Asp Met Ser Val Ala Glu Val Leu Asp
      130                     135                     140

Phe Val Arg Asn His Ala Ala Glu Ala Glu Thr Ile Tyr Ala Leu Pro
      145                     150                     155                     160

Ile Val Asn Arg Ala Arg Gln Val Met Gly Val Val Ser Leu Arg Lys
      165                     170                     175

Leu Phe Ile Ala Asp Pro Thr Leu Lys Val Ser Glu Ile Met Val Arg
      180                     185                     190

Pro Val Ser Val Leu Ala Ser Ala Asp Ile Glu Glu Thr Ala Arg Trp
      195                     200                     205

Phe Leu Gln Leu Asp Leu Val Ala Met Pro Val Val Asp Glu Ser Asn
      210                     215                     220

Met Leu Leu Gly Val Leu Thr Phe Asp Asp Ala Gln Asp Ile Val Glu
      225                     230                     235                     240

Gln Ala Asp Ser Glu Asp Ser Ala Arg Ser Gly Gly Ser Glu Pro Leu
      245                     250                     255

Gln Gln Pro Tyr Leu Ser Thr Pro Ile Arg Lys Leu Val Lys Ser Arg
      260                     265                     270

Ile Val Trp Leu Leu Val Leu Ala Val Ser Ala Ile Leu Thr Val Gln
      275                     280                     285

Val Leu Asp Ile Phe Glu Ala Thr Leu Val Glu Ala Val Val Leu Ala
      290                     295                     300

Leu Phe Ile Pro Leu Leu Thr Gly Thr Gly Gly Asn Thr Gly Asn Gln
      305                     310                     315                     320

Ala Ala Thr Thr Val Thr Arg Ala Leu Ala Leu Gly Asp Val Arg Lys
      325                     330                     335

Ser Asp Val Phe Arg Val Leu Gly Arg Glu Ile Arg Val Gly Leu Met

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340 345 350
 Leu Gly Ala Leu Leu Gly Ala Val Gly Phe Val Ile Ala Ser Leu Val
 355 360 365
 Tyr Gly Met Pro Val Gly Thr Val Ile Gly Leu Thr Leu Leu Ala Val
 370 375 380
 Cys Thr Met Ala Ala Ser Val Gly Gly Val Met Pro Ile Ile Ala Lys
 385 390 395 400
 Ala Ile Gly Ala Asp Pro Ala Val Phe Ser Asn Pro Phe Ile Ser Thr
 405 410 415
 Phe Cys Asp Ala Thr Gly Leu Ile Ile Tyr Phe Ala Ile Ala Lys Leu
 420 425 430
 Val Leu Gly Ile
 435

<210> 257
 <211> 1142
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1119)
 <223> RXA02068

<400> 257
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 Ile Phe Val Pro Met Leu Arg Ile Ala Ala Ile Glu Pro Lys Asp Ile
 1 5 10 15
 act ttg gtt acc ggt tct gta tca ctt cga acc ttt cgc gtg cgc acc 96
 Thr Leu Val Thr Gly Ser Val Ser Leu Arg Thr Phe Arg Val Arg Thr
 20 25 30
 ggt gaa ttg cag gtc atg ggc gat att gtg ggt gca aaa gta cat acc 144
 Gly Glu Leu Gln Val Met Gly Asp Ile Val Gly Ala Lys Val His Thr
 35 40 45
 gat gat cca gag ctg caa caa ttc cac ggt cgc gcg gta gaa atc gcc 192
 Asp Asp Pro Glu Leu Gln Gln Phe His Gly Arg Ala Val Glu Ile Ala
 50 55 60
 gat gtg gag ctg gag tta tcg cgc act cgc gat tgg atc atc acg cgc 240
 Asp Val Glu Leu Glu Leu Ser Arg Thr Arg Asp Trp Ile Ile Thr Arg
 65 70 75 80
 gtg gcg gtg ctg ggt gag cgc cct aaa ttt ggc cgg cgc cca gtg ctg 288
 Val Ala Val Leu Gly Glu Arg Pro Lys Phe Gly Arg Arg Pro Val Leu
 85 90 95
 cac aca gtg ccg tgg agt cat atc cac ggc atc acc gca ggt ggt gtc 336
 His Thr Val Pro Trp Ser His Ile His Gly Ile Thr Ala Gly Gly Val
 100 105 110
 ggc gag tcc aat cac acc gcc gaa ctc atc gca ggg ttt gag gat atg 384

Gly	Glu	Ser	Asn	His	Thr	Ala	Glu	Leu	Ile	Ala	Gly	Phe	Glu	Asp	Met		
		115					120					125					
agg	cct	gcg	gac	gtc	gca	aag	cag	ctt	tat	cag	ctg	cct	acg	gct	cag	432	
Arg	Pro	Ala	Asp	Val	Ala	Lys	Gln	Leu	Tyr	Gln	Leu	Pro	Thr	Ala	Gln		
		130				135					140						
cgt	acc	gaa	gtg	acg	gaa	gag	ctt	gac	gac	gaa	aag	ctg	gcg	gat	atc	480	
Arg	Thr	Glu	Val	Thr	Glu	Glu	Leu	Asp	Asp	Glu	Lys	Leu	Ala	Asp	Ile		
		145			150					155					160		
ctg	cag	gaa	ttg	tcc	gag	gac	cgc	caa	gcc	gag	ttg	att	gaa	gaa	tta	528	
Leu	Gln	Glu	Leu	Ser	Glu	Asp	Arg	Gln	Ala	Glu	Leu	Ile	Glu	Glu	Leu		
				165				170							175		
gac	atc	gaa	cgt	gcc	gcg	gac	att	ctg	gag	gaa	atg	gat	cca	gat	gat	576	
Asp	Ile	Glu	Arg	Ala	Ala	Asp	Ile	Leu	Glu	Glu	Met	Asp	Pro	Asp	Asp		
			180					185					190				
gct	gca	gac	ttg	ttg	ggt	gag	ctg	cct	gat	gac	aaa	gct	gat	gtg	ttg	624	
Ala	Ala	Asp	Leu	Leu	Gly	Glu	Leu	Pro	Asp	Asp	Lys	Ala	Asp	Val	Leu		
		195					200					205					
ttg	gat	ctg	atg	gac	cct	gag	gaa	tct	gcg	ccg	gtg	cgt	cgt	ttg	atg	672	
Leu	Asp	Leu	Met	Asp	Pro	Glu	Glu	Ser	Ala	Pro	Val	Arg	Arg	Leu	Met		
		210				215					220						
gat	ttc	tcc	ccg	gac	acc	gtt	ggt	gcg	ctg	atg	act	cct	gag	cca	tta	720	
Asp	Phe	Ser	Pro	Asp	Thr	Val	Gly	Ala	Leu	Met	Thr	Pro	Glu	Pro	Leu		
		225			230				235						240		
att	atg	gat	cct	tcc	acc	aca	gtc	gct	gaa	gcg	ttg	gcg	atg	gcc	aga	768	
Ile	Met	Asp	Pro	Ser	Thr	Thr	Val	Ala	Glu	Ala	Leu	Ala	Met	Ala	Arg		
				245					250						255		
aac	ccc	gac	ctt	cct	act	tct	ttg	gca	tgc	ttg	atc	ttt	gtg	gtg	cgc	816	
Asn	Pro	Asp	Leu	Pro	Thr	Ser	Leu	Ala	Ser	Leu	Ile	Phe	Val	Val	Arg		
			260					265					270				
cca	ccc	acg	gcc	acg	cct	act	gga	aaa	tac	ctc	ggc	tgc	gtg	cat	ctg	864	
Pro	Pro	Thr	Ala	Thr	Pro	Thr	Gly	Lys	Tyr	Leu	Gly	Cys	Val	His	Leu		
		275					280					285					
cag	aaa	ctg	ctt	cgg	gag	cct	cca	tca	agt	ttg	att	ggt	ggc	atc	ctc	912	
Gln	Lys	Leu	Leu	Arg	Glu	Pro	Pro	Ser	Ser	Leu	Ile	Gly	Gly	Ile	Leu		
		290				295					300						
gac	ccc	gat	ctg	cca	ccg	ctc	tac	gct	gat	gat	tct	caa	gaa	acc	gca	960	
Asp	Pro	Asp	Leu	Pro	Pro	Leu	Tyr	Ala	Asp	Asp	Ser	Gln	Glu	Thr	Ala		
		305			310					315					320		
gct	cga	ttc	ttt	gcc	acc	tac	aac	ttg	gtg	tgc	ggc	ccc	gtc	ttg	gat	1008	
Ala	Arg	Phe	Phe	Ala	Thr	Tyr	Asn	Leu	Val	Cys	Gly	Pro	Val	Leu	Asp		
				325				330							335		
gaa	aac	cgc	cat	ctg	ctt	ggt	gcc	gta	gct	gtc	gat	gac	ttg	ctc	gac	1056	
Glu	Asn	Arg	His	Leu	Leu	Gly	Ala	Val	Ala	Val	Asp	Asp	Leu	Leu	Asp		
			340				345						350				
cac	atg	ctg	cca	gaa	gac	tgg	cgc	gac	gcc	gga	atc	cga	cca	gga	aag	1104	
His	Met	Leu	Pro	Glu	Asp	Trp	Arg	Asp	Ala	Gly	Ile	Arg	Pro	Gly	Lys		

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<400> 258
Ile Phe Val Pro Met Leu Arg Ile Ala Ala Ile Glu Pro Lys Asp Ile
  1           5           10           15
Thr Leu Val Thr Gly Ser Val Ser Leu Arg Thr Phe Arg Val Arg Thr
      20           25           30
Gly Glu Leu Gln Val Met Gly Asp Ile Val Gly Ala Lys Val His Thr
      35           40
Asp Asp Pro Glu Leu Gln Gln Phe His Gly Arg Ala Val Glu Ile Ala
      50           55           60
Asp Val Glu Leu Glu Leu Ser Arg Thr Arg Asp Trp Ile Ile Thr Arg
      65           70           75           80
Val Ala Val Leu Gly Glu Arg Pro Lys Phe Gly Arg Arg Pro Val Leu
      85           90           95
His Thr Val Pro Trp Ser His Ile His Gly Ile Thr Ala Gly Gly Val
      100           105           110
Gly Glu Ser Asn His Thr Ala Glu Leu Ile Ala Gly Phe Glu Asp Met
      115           120           125
Arg Pro Ala Asp Val Ala Lys Gln Leu Tyr Gln Leu Pro Thr Ala Gln
      130           135           140
Arg Thr Glu Val Thr Glu Glu Leu Asp Asp Glu Lys Leu Ala Asp Ile
      145           150           155           160
Leu Gln Glu Leu Ser Glu Asp Arg Gln Ala Glu Leu Ile Glu Glu Leu
      165           170           175
Asp Ile Glu Arg Ala Ala Asp Ile Leu Glu Glu Met Asp Pro Asp Asp
      180           185           190
Ala Ala Asp Leu Leu Gly Glu Leu Pro Asp Asp Lys Ala Asp Val Leu
      195           200           205
Leu Asp Leu Met Asp Pro Glu Glu Ser Ala Pro Val Arg Arg Leu Met
      210           215           220
Asp Phe Ser Pro Asp Thr Val Gly Ala Leu Met Thr Pro Glu Pro Leu
      225           230           235           240
Ile Met Asp Pro Ser Thr Thr Val Ala Glu Ala Leu Ala Met Ala Arg
      245           250           255

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Asn Pro Asp Leu Pro Thr Ser Leu Ala Ser Leu Ile Phe Val Val Arg
 260 265 270
 Pro Pro Thr Ala Thr Pro Thr Gly Lys Tyr Leu Gly Cys Val His Leu
 275 280 285
 Gln Lys Leu Leu Arg Glu Pro Pro Ser Ser Leu Ile Gly Gly Ile Leu
 290 295 300
 Asp Pro Asp Leu Pro Pro Leu Tyr Ala Asp Asp Ser Gln Glu Thr Ala
 305 310 315 320
 Ala Arg Phe Phe Ala Thr Tyr Asn Leu Val Cys Gly Pro Val Leu Asp
 325 330 335
 Glu Asn Arg His Leu Leu Gly Ala Val Ala Val Asp Asp Leu Leu Asp
 340 345 350
 His Met Leu Pro Glu Asp Trp Arg Asp Ala Gly Ile Arg Pro Gly Lys
 355 360 365
 Glu His Thr His Gly
 370

<210> 259

<211> 538

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(538)

<223> RXA00665

<400> 259

accaaacact tctgtgcgtg acaacgcgcca ccttatactc ccacaagcaa cacagaacac 60

 tcgggatctc aaagtttcga gaaacacaga aagggcagca atg agc agc tca aca 115
 Met Ser Ser Ser Thr
 1 5

 ctt ctc ctg gct tca gga caa gtc acg gca tta gcc gct gac tac acg 163
 Leu Leu Leu Ala Ser Gly Gln Val Thr Ala Leu Ala Ala Asp Tyr Thr
 10 15 20

 ctc agc cac acc ccc tca gat ggc atc ctg gta gtc ctt ggc ttc gcc 211
 Leu Ser His Thr Pro Ser Asp Gly Ile Leu Val Val Leu Gly Phe Ala
 25 30 35

 atg atc ctc acc ttc atg acc ctg atc atg ctg ggt cga ctc acc cca 259
 Met Ile Leu Thr Phe Met Thr Leu Ile Met Leu Gly Arg Leu Thr Pro
 40 45 50

 atg gtg gcc atg ctg ttg gtc ccc acc atc ttc ggt ctc atc gcc ggc 307
 Met Val Ala Met Leu Leu Val Pro Thr Ile Phe Gly Leu Ile Ala Gly
 55 60 65

 gca gga ctc ggc ctt ggt gac atg gcg ctt gac gcc atc aag gac atg 355
 Ala Gly Leu Gly Leu Gly Asp Met Ala Leu Asp Ala Ile Lys Asp Met
 70 75 80 85

 GCGGATCTC AAAGTTTCGA GAAACACAGA AAGGGCAGCA ATG AGC AGC TCA ACA 115
 Met Ser Ser Ser Thr
 1 5

gcg cct acc gcg gca ctc ctg atg ttc gcg att atg ttc ttc gga atc 403
 Ala Pro Thr Ala Ala Leu Leu Met Phe Ala Ile Met Phe Phe Gly Ile
 90 95 100

atg atc gac gtc gga ctc ttc gac ccc ctg atc cgc gtg atc acc cgc 451
 Met Ile Asp Val Gly Leu Phe Asp Pro Leu Ile Arg Val Ile Thr Arg
 105 110 115

gtt ctt cac gat gac ccc gca aag gtc gtc atc ggc acc gca gta ctt 499
 Val Leu His Asp Asp Pro Ala Lys Val Val Ile Gly Thr Ala Val Leu
 120 125 130

gca ggt gtt gtc tcc ctc gac ggc gac ggc tcc acc acc 538
 Ala Gly Val Val Ser Leu Asp Gly Asp Gly Ser Thr Thr
 135 140 145

<210> 260

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

Met Ser Ser Ser Thr Leu Leu Leu Ala Ser Gly Gln Val Thr Ala Leu
 1 5 10 15

Ala Ala Asp Tyr Thr Leu Ser His Thr Pro Ser Asp Gly Ile Leu Val
 20 25 30

Val Leu Gly Phe Ala Met Ile Leu Thr Phe Met Thr Leu Ile Met Leu
 35 40 45

Gly Arg Leu Thr Pro Met Val Ala Met Leu Leu Val Pro Thr Ile Phe
 50 55 60

Gly Leu Ile Ala Gly Ala Gly Leu Gly Leu Gly Asp Met Ala Leu Asp
 65 70 75 80

Ala Ile Lys Asp Met Ala Pro Thr Ala Ala Leu Leu Met Phe Ala Ile
 85 90 95

Met Phe Phe Gly Ile Met Ile Asp Val Gly Leu Phe Asp Pro Leu Ile
 100 105 110

Arg Val Ile Thr Arg Val Leu His Asp Asp Pro Ala Lys Val Val Ile
 115 120 125

Gly Thr Ala Val Leu Ala Gly Val Val Ser Leu Asp Gly Asp Gly Ser
 130 135 140

Thr Thr
 145

<210> 261

<211> 281

<212> DNA

<213> Corynebacterium glutamicum

<220>

CCDS: C131CP.1

<221> CDS
 <222> (1)..(258)
 <223> RXA02808

<400> 261

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ttt tac ttc ggc atc ctc cca gtc ctt gca gaa agt gct tcc cac ttc   48
Phe Tyr Phe Gly Ile Leu Pro Val Leu Ala Glu Ser Ala Ser His Phe
  1             5             10             15

ggc atc gag cct gtg gaa atg gcc cgc gca tcc atc act ggc cag ccc   96
Gly Ile Glu Pro Val Glu Met Ala Arg Ala Ser Ile Thr Gly Gln Pro
             20             25             30

gtt cac atg caa agc ccg ctg gtc cca gcg atc ctc ctg ctg gtt tcc  144
Val His Met Gln Ser Pro Leu Val Pro Ala Ile Leu Leu Leu Val Ser
             35             40             45

ctc gcc aac gtc aac ctt ggc gac cac cac aag aag gtt ctg tgg cgc  192
Leu Ala Asn Val Asn Leu Gly Asp His His Lys Lys Val Leu Trp Arg
             50             55             60

gcc tgc atc gtg tcc atc gcg atg ctc gcc gta gcc ctc ttc atc ggc  240
Ala Cys Ile Val Ser Ile Ala Met Leu Ala Val Ala Leu Phe Ile Gly
             65             70             75             80

gtc gtg cca ctc agc gca taaaatagct tttcgacgcc aaa                281
Val Val Pro Leu Ser Ala
             85

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<210> 262
 <211> 86
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 262

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Phe Tyr Phe Gly Ile Leu Pro Val Leu Ala Glu Ser Ala Ser His Phe
  1             5             10             15

Gly Ile Glu Pro Val Glu Met Ala Arg Ala Ser Ile Thr Gly Gln Pro
             20             25             30

Val His Met Gln Ser Pro Leu Val Pro Ala Ile Leu Leu Leu Val Ser
             35             40             45

Leu Ala Asn Val Asn Leu Gly Asp His His Lys Lys Val Leu Trp Arg
             50             55             60

Ala Cys Ile Val Ser Ile Ala Met Leu Ala Val Ala Leu Phe Ile Gly
             65             70             75             80

Val Val Pro Leu Ser Ala
             85

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<210> 263
 <211> 960
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

BGI-131CP: RXA02808

[illegible]

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<210> 264
<211> 279
<212> PRT
<213> Corynebacterium glutamicum

<400> 264
Met Val Leu Ala Gln Thr Lys Lys Ala Arg Arg Ser Glu Asn His Ile
  1          5          10
Leu Pro Gly Trp Leu Leu Ile Pro Ala Thr Leu Ala Met Leu Leu Ile
          20          25          30
Ile Gly Pro Ile Phe Ala Leu Leu Leu Gln Ile Pro Trp Asp Arg Ser
          35          40          45
Trp Glu Leu Leu Thr Ala Pro Glu Ser Leu Gly Thr Ala Arg Leu Ser
          50          55          60
Ile Gly Thr Ala Leu Phe Ser Thr Ala Leu Cys Ala Ile Val Gly Phe
          65          70          75          80
Pro Leu Ala Leu Ala Leu His Leu Tyr Glu Arg Ser His Pro Arg Val
          85          90          95
Thr Ser Val Leu Thr Val Leu Val Tyr Ala Pro Leu Val Leu Ser Pro
          100          105          110
Val Val Ser Gly Leu Ala Leu Thr Phe Leu Trp Gly Arg Arg Gly Phe
          115          120          125
Leu Gly Ser Trp Leu Asp Gln Val Gly Leu Pro Ile Ala Phe Thr Thr
          130          135          140
Thr Ala Val Val Phe Ala Gln Val Phe Val Ala Leu Pro Phe Phe Ile
          145          150          155          160
Ser Thr Val Thr Thr Ala Leu Arg Gly Ile Pro Lys Gln Phe Glu Glu
          165          170          175

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Phe Ser Lys Val Arg Lys Val
275

gcg cct ttg gtg ttg tcg ccg gtg gtg tct ggt ttg gcg ctg act ttt 403

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Ala Pro Leu Val Leu Ser Pro Val Val Ser Gly Leu Ala Leu Thr Phe
          90                      95                      100

ctg tgg ggc agg cgt ggt ttt tta ggt tct tgg ctt gat cag gtt gga 451
Leu Trp Gly Arg Arg Gly Phe Leu Gly Ser Trp Leu Asp Gln Val Gly
          105                      110                      115

ttg ccg att gca ttt acc acc acg gct gtg gtg ttt gcc cag gtg ttt 499
Leu Pro Ile Ala Phe Thr Thr Thr Ala Val Val Phe Ala Gln Val Phe
          120                      125                      130

gta gcg ttg cca ttt ttc att tcc act gtg act act gca ctg cgt ggc 547
Val Ala Leu Pro Phe Phe Ile Ser Thr Val Thr Thr Ala Leu Arg Gly
          135                      140                      145

att cca aaa cag ttt gag gaa atc gca gct act gaa ggc gca acc cgc 595
Ile Pro Lys Gln Phe Glu Glu Ile Ala Ala Thr Glu Gly Ala Thr Arg
          150                      155                      160

tgg gag atc atg cac aag atg atc att ccg ctg gcg atg cct gga att 643
Trp Glu Ile Met His Lys Met Ile Ile Pro Leu Ala Met Pro Gly Ile
          170                      175                      180

ttc acc ggt atg att ttg gga ttc gcc agg gcc ttg ggc gag tat ggt 691
Phe Thr Gly Met Ile Leu Gly Phe Ala Arg Ala Leu Gly Glu Tyr Gly
          185                      190                      195

gcg aca ctg act ttt gct gga aat att gca ggt gtt acc cgc acc att 739
Ala Thr Leu Thr Phe Ala Gly Asn Ile Ala Gly Val Thr Arg Thr Ile
          200                      205                      210

ccg ttg cat att gag ctt ggt ttg agt tcc aat gac atg gat aaa gcc 787
Pro Leu His Ile Glu Leu Gly Leu Ser Ser Asn Asp Met Asp Lys Ala
          215                      220                      225

ttg gga gcg gtg att atg ctt ttg gct gtc tat gtc ctc atc att gga 835
Leu Gly Ala Val Ile Met Leu Leu Ala Val Tyr Val Leu Ile Ile Gly
          230                      235                      240

gcc atc gga gcg tta cga ttg ttt tcc aag gtg aga aag gtt 877
Ala Ile Gly Ala Leu Arg Leu Phe Ser Lys Val Arg Lys Val
          250                      255

taattgatgt ctcgttcgcc gga 900

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<210> 266

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

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Leu Leu Ile Pro Ala Thr Leu Ala Met Leu Leu Ile Ile Gly Pro Ile
  1                      5                      10                      15

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Phe Ala Leu Leu Leu Gln Ile Pro Trp Asp Arg Ser Trp Glu Leu Leu
  20                      25                      30

```

```

Thr Ala Pro Glu Ser Leu Gly Thr Ala Arg Leu Ser Ile Gly Thr Ala
  35                      40                      45

```

Leu Phe Ser Thr Ala Leu Cys Ala Ile Val Gly Phe Pro Leu Ala Leu
 50 55 60
 Ala Leu His Leu Tyr Glu Arg Ser His Pro Arg Val Thr Ser Val Leu
 65 70 75 80
 Thr Val Leu Val Tyr Ala Pro Leu Val Leu Ser Pro Val Val Ser Gly
 85 90 95
 Leu Ala Leu Thr Phe Leu Trp Gly Arg Arg Gly Phe Leu Gly Ser Trp
 100 105 110
 Leu Asp Gln Val Gly Leu Pro Ile Ala Phe Thr Thr Thr Ala Val Val
 115 120 125
 Phe Ala Gln Val Phe Val Ala Leu Pro Phe Phe Ile Ser Thr Val Thr
 130 135 140
 Thr Ala Leu Arg Gly Ile Pro Lys Gln Phe Glu Glu Ile Ala Ala Thr
 145 150 155 160
 Glu Gly Ala Thr Arg Trp Glu Ile Met His Lys Met Ile Ile Pro Leu
 165 170 175
 Ala Met Pro Gly Ile Phe Thr Gly Met Ile Leu Gly Phe Ala Arg Ala
 180 185 190
 Leu Gly Glu Tyr Gly Ala Thr Leu Thr Phe Ala Gly Asn Ile Ala Gly
 195 200 205
 Val Thr Arg Thr Ile Pro Leu His Ile Glu Leu Gly Leu Ser Ser Asn
 210 215 220
 Asp Met Asp Lys Ala Leu Gly Ala Val Ile Met Leu Leu Ala Val Tyr
 225 230 235 240
 Val Leu Ile Ile Gly Ala Ile Gly Ala Leu Arg Leu Phe Ser Lys Val
 245 250 255
 Arg Lys Val

<210> 267
 <211> 852
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(829)
 <223> RXN02614

<400> 267
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 acaccttccg ctaccgaaac gcataagaaa gttgctcgcc atg act gcc aca ttg 115
 Met Thr Ala Thr Leu
 1 5
 tca ctc aaa ccc gca gcc act gtc cgt gga ttg cgc aaa tca tac gga 163

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Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu Arg Lys Ser Tyr Gly
                10                15                20

act aaa gaa gtc ctc caa gga atc gac ctc acc atc aac tgc ggc gaa 211
Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr Ile Asn Cys Gly Glu
                25                30                35

gta acc gcg ctg atc gga cgc tca ggt tca gga aaa tcc acc atc ctg 259
Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly Lys Ser Thr Ile Leu
                40                45                50

cgc gtg ttg gcg ggc cta tct aaa gag cat tcc ggc tct gta gaa att 307
Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser Gly Ser Val Glu Ile
                55                60                65

tcc gga aac ccg gcc gtt gcc ttc caa gag cct cgc ctg ttg ccg tgg 355
Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro Arg Leu Leu Pro Trp
                70                75                80                85

aaa acg gtg ctc gat aat gtg acc ttt ggc ctc aac cgc act gat att 403
Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu Asn Arg Thr Asp Ile
                90                95                100

tcc tgg tca gaa gca caa gaa cgc gcc tcg gca ctg ctt gca gaa gtc 451
Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala Leu Leu Ala Glu Val
                105                110                115

aaa ctt ccc gac tcc gac gcc gcc tgg ccc ctc acg ctc tcc ggc ggc 499
Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu Thr Leu Ser Gly Gly
                120                125                130

caa gcc cag cgc gtc tcc ctt gcg cga gcg ctc atc tcc gag cca gag 547
Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu Ile Ser Glu Pro Glu
                135                140                145

ctt ttg ctt ctc gac gaa ccc ttc ggc gcc ctc gat gct ctg aca aga 595
Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu Thr Arg
                150                155                160                165

ctg aca gcc caa gac ctg ctg ctc aaa acc gtg aac acc cga aac ttg 643
Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val Asn Thr Arg Asn Leu
                170                175                180

gga gtt ctg ctg gtc acc cat gat gtt tcc gag gcc atc gcc ctg gcc 691
Gly Val Leu Leu Val Thr His Asp Val Ser Glu Ala Ile Ala Leu Ala
                185                190                195

gac cac gtc ctt ctt ctt gac gac gcc gcc atc aca cac agt ttg act 739
Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile Thr His Ser Leu Thr
                200                205                210

gta gat atc ccc ggc gat cgc cgc acc cac ccc tcc ttt gcc tcc tac 787
Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro Ser Phe Ala Ser Tyr
                215                220                225

acc gct caa ctc ctt gag tgg ctc gaa atc acc aca cct gcc 829
Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr Thr Pro Ala
                230                235                240

tagaaagaaa tcatgaaatt taa 852

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<210> 268
 <211> 243
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 268

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Met Thr Ala Thr Leu Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu
  1          5          10          15

Arg Lys Ser Tyr Gly Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr
          20          25          30

Ile Asn Cys Gly Glu Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly
          35          40          45

Lys Ser Thr Ile Leu Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser
          50          55          60

Gly Ser Val Glu Ile Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro
          65          70          75          80

Arg Leu Leu Pro Trp Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu
          85          90          95

Asn Arg Thr Asp Ile Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala
          100          105          110

Leu Leu Ala Glu Val Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu
          115          120          125

Thr Leu Ser Gly Gly Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu
          130          135          140

Ile Ser Glu Pro Glu Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu
          145          150          155          160

Asp Ala Leu Thr Arg Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val
          165          170          175

Asn Thr Arg Asn Leu Gly Val Leu Leu Val Thr His Asp Val Ser Glu
          180          185          190

Ala Ile Ala Leu Ala Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile
          195          200          205

Thr His Ser Leu Thr Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro
          210          215          220

Ser Phe Ala Ser Tyr Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr
          225          230          235          240

Thr Pro Ala
  
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<210> 269
 <211> 852
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(829)

<223> FRXA02614

<400> 269

tcattgtata cgccaccctc ggtctgctgt ctgaagcgct gatcagagct tgggaacgtc 60

acaccttccg	ctaccgaaac	gcataagaaa	gttgctcgcc	atg	act	gcc	aca	ttg	115
				Met	Thr	Ala	Thr	Leu	
				1				5	

tca	ctc	aaa	ccc	gca	gcc	act	gtc	cgt	gga	ttg	cgc	aaa	tca	tac	gga	163
Ser	Leu	Lys	Pro	Ala	Ala	Thr	Val	Arg	Gly	Leu	Arg	Lys	Ser	Tyr	Gly	
			10					15						20		

act	aaa	gaa	gtc	ctc	caa	gga	atc	gac	ctc	acc	atc	aac	tgc	ggc	gaa	211
Thr	Lys	Glu	Val	Leu	Gln	Gly	Ile	Asp	Leu	Thr	Ile	Asn	Cys	Gly	Glu	
			25					30					35			

gta	acc	gcg	ctg	atc	gga	cgc	tca	ggc	tca	gga	aaa	tcc	acc	atc	ctg	259
Val	Thr	Ala	Leu	Ile	Gly	Arg	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Ile	Leu	
		40				45						50				

cgc	gtg	ttg	gcg	ggc	cta	tct	aaa	gag	cat	tcc	ggc	tct	gta	gaa	att	307
Arg	Val	Leu	Ala	Gly	Leu	Ser	Lys	Glu	His	Ser	Gly	Ser	Val	Glu	Ile	
	55					60					65					

tcc	gga	aac	ccg	gcc	gtt	gcc	ttc	caa	gag	cct	cgc	ctg	ttg	ccg	tgg	355
Ser	Gly	Asn	Pro	Ala	Val	Ala	Phe	Gln	Glu	Pro	Arg	Leu	Leu	Pro	Trp	
	70				75					80					85	

aaa	acg	gtg	ctc	gat	aat	gtg	acc	ttt	ggc	ctc	aac	cgc	act	gat	att	403
Lys	Thr	Val	Leu	Asp	Asn	Val	Thr	Phe	Gly	Leu	Asn	Arg	Thr	Asp	Ile	
				90					95					100		

tcc	tgg	tca	gaa	gca	caa	gaa	cgc	gcc	tgc	gca	ctg	ctt	gca	gaa	gtc	451
Ser	Trp	Ser	Glu	Ala	Gln	Glu	Arg	Ala	Ser	Ala	Leu	Leu	Ala	Glu	Val	
			105					110					115			

aaa	ctt	ccc	gac	tcc	gac	gcc	gcc	tgg	ccc	ctc	acg	ctc	tcc	ggc	ggc	499
Lys	Leu	Pro	Asp	Ser	Asp	Ala	Ala	Trp	Pro	Leu	Thr	Leu	Ser	Gly	Gly	
		120					125					130				

caa	gcc	cag	cgc	gtc	tcc	ctt	gcg	cga	gcg	ctc	atc	tcc	gag	cca	gag	547
Gln	Ala	Gln	Arg	Val	Ser	Leu	Ala	Arg	Ala	Leu	Ile	Ser	Glu	Pro	Glu	
	135					140					145					

ctt	ttg	ctt	ctc	gac	gaa	ccc	ttc	ggc	gcc	ctc	gat	gct	ctg	aca	aga	595
Leu	Leu	Leu	Leu	Asp	Glu	Pro	Phe	Gly	Ala	Leu	Asp	Ala	Leu	Thr	Arg	
	150				155					160					165	

ctg	aca	gcc	caa	gac	ctg	ctg	ctc	aaa	acc	gtg	aac	acc	cga	aac	ttg	643
Leu	Thr	Ala	Gln	Asp	Leu	Leu	Leu	Lys	Thr	Val	Asn	Thr	Arg	Asn	Leu	
				170				175						180		

gga	gtt	ctg	ctg	gtc	acc	cat	gat	gtt	tcc	gag	gcc	atc	gcc	ctg	gcc	691
Gly	Val	Leu	Leu	Val	Thr	His	Asp	Val	Ser	Glu	Ala	Ile	Ala	Leu	Ala	
		185						190					195			

gac	cac	gtc	ctt	ctt	ctt	gac	gac	ggc	gcc	atc	aca	cac	agt	ttg	act	739
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115
163
211
259
307
355
403
451
499
547
595
643
691
739

Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile Thr His Ser Leu Thr
 200 205 210

gta gat atc ccc ggc gat cgc cgc acc cac ccc tcc ttt gcc tcc tac 787
 Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro Ser Phe Ala Ser Tyr
 215 220 225

acc gct caa ctc ctt gag tgg ctc gaa atc acc aca cct gcc 829
 Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr Thr Pro Ala
 230 235 240

tagaaagaaa tcatgaaatt taa 852

<210> 270
 <211> 243
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 270
 Met Thr Ala Thr Leu Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu
 1 5 10 15

Arg Lys Ser Tyr Gly Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr
 20 25 30

Ile Asn Cys Gly Glu Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly
 35 40 45

Lys Ser Thr Ile Leu Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser
 50 55 60

Gly Ser Val Glu Ile Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro
 65 70 75 80

Arg Leu Leu Pro Trp Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu
 85 90 95

Asn Arg Thr Asp Ile Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala
 100 105 110

Leu Leu Ala Glu Val Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu
 115 120 125

Thr Leu Ser Gly Gly Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu
 130 135 140

Ile Ser Glu Pro Glu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu
 145 150 155 160

Asp Ala Leu Thr Arg Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val
 165 170 175

Asn Thr Arg Asn Leu Gly Val Leu Leu Val Thr His Asp Val Ser Glu
 180 185 190

Ala Ile Ala Leu Ala Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile
 195 200 205

Thr His Ser Leu Thr Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro
 210 215 220

Ser Phe Ala Ser Tyr Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr
 225 230 235 240

Thr Pro Ala

<210> 271
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(598)
 <223> RXN01142

<400> 271
 ctccccatcc accggcacag tcagcgcagg caacgaagaa attaaaggac caggacctga 60
 ccgaggcatg gttttccaag accacgcctt cctgccctga ttg acc gca cgc ggc 115
 Leu Thr Ala Arg Gly
 1 5
 aac atc gac ttc ggg ctc cgc tcc gcg cgc ccc tcc ttg agc aaa acc 163
 Asn Ile Asp Phe Gly Leu Arg Ser Ala Arg Pro Ser Leu Ser Lys Thr
 10 15 20
 gaa cgc gcc gac atc acc cgc acc cac ctc gaa caa gta ggc ctc acc 211
 Glu Arg Ala Asp Ile Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr
 25 30 35
 gac gcc gcc gaa cgg cgc ccc gcc cgc ctc tcc ggc ggc atg caa cag 259
 Asp Ala Ala Glu Arg Arg Pro Ala Arg Leu Ser Gly Gly Met Gln Gln
 40 45 50
 cga gtc ggc atc gca cgc gcc ttc gcc atc gac cca cca atc atg ctt 307
 Arg Val Gly Ile Ala Arg Ala Phe Ala Ile Asp Pro Pro Ile Met Leu
 55 60 65
 ctc gac gaa ccc ttc ggc gcc ctc gac gcc ctc acc cgc cgc gaa ctc 355
 Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu
 70 75 80 85
 cag ctc caa cta ctc aac att tgg gaa gcc tcc cgc cgc acc gtc gtc 403
 Gln Leu Gln Leu Leu Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val
 90 95 100
 atg gtc acc cac gac gtc gac gag gcc atc ctg ctc tcc gac cga gtt 451
 Met Val Thr His Asp Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val
 105 110 115
 ctc gtg atg tcc aag agc ccc gaa gcc acc atc atc acc gat att cca 499
 Leu Val Met Ser Lys Ser Pro Glu Ala Thr Ile Ile Thr Asp Ile Pro
 120 125 130
 gtg aat ctt ccc cgc ccc aga cac gag ctg agt gaa gac gct tct gtt 547
 Val Asn Leu Pro Arg Pro Arg His Glu Leu Ser Glu Asp Ala Ser Val
 135 140 145

gaa gcc gag acc aca gcc ctg cgt aag cgg atg ctg cat ctg ctg gag 595
 Glu Ala Glu Thr Thr Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu
 150 155 160 165

cac tagtttctaa cacgtctttt aaa 621
 His

<210> 272

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Leu Thr Ala Arg Gly Asn Ile Asp Phe Gly Leu Arg Ser Ala Arg Pro
 1 5 10 15

Ser Leu Ser Lys Thr Glu Arg Ala Asp Ile Thr Arg Thr His Leu Glu
 20 25 30

Gln Val Gly Leu Thr Asp Ala Ala Glu Arg Arg Pro Ala Arg Leu Ser
 35 40 45

Gly Gly Met Gln Gln Arg Val Gly Ile Ala Arg Ala Phe Ala Ile Asp
 50 55 60

Pro Pro Ile Met Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu
 65 70 75 80

Thr Arg Arg Glu Leu Gln Leu Gln Leu Leu Asn Ile Trp Glu Ala Ser
 85 90 95

Arg Arg Thr Val Val Met Val Thr His Asp Val Asp Glu Ala Ile Leu
 100 105 110

Leu Ser Asp Arg Val Leu Val Met Ser Lys Ser Pro Glu Ala Thr Ile
 115 120 125

Ile Thr Asp Ile Pro Val Asn Leu Pro Arg Pro Arg His Glu Leu Ser
 130 135 140

Glu Asp Ala Ser Val Glu Ala Glu Thr Thr Ala Leu Arg Lys Arg Met
 145 150 155 160

Leu His Leu Leu Glu His
 165

<210> 273

<211> 443

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(420)

<223> FRXA01142

<400> 273

acc cgc acc cac ctc gaa caa gta ggc ctc acc gac gcc gcc gaa cgg 48

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Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr Asp Ala Ala Glu Arg
 1           5           10           15

cgc ccc gcc cgc ctc tcc ggc ggc atg caa cag cga gtc ggc atc gca 96
Arg Pro Ala Arg Leu Ser Gly Gly Met Gln Gln Arg Val Gly Ile Ala
          20           25           30

cgc gcc ttc gcc atc gac cca cca atc atg ctt ctc gac gaa ccc ttc 144
Arg Ala Phe Ala Ile Asp Pro Pro Ile Met Leu Leu Asp Glu Pro Phe
          35           40           45

gga gcc ctc gac gcc ctc acc cgc cgc gaa ctc cag ctc caa cta ctc 192
Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu Gln Leu Leu
          50           55           60

aac att tgg gaa gcc tcc cgc cgc acc gtc gtc atg gtc acc cac gac 240
Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val Met Val Thr His Asp
          65           70           75           80

gtc gac gag gcc atc ctg ctc tcc gac cga gtt ctc gtg atg tcc aag 288
Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val Leu Val Met Ser Lys
          85           90           95

agc ccc gaa gcc acc atc atc acc gat att cca gtg aat ctt ccc cgc 336
Ser Pro Glu Ala Thr Ile Ile Thr Asp Ile Pro Val Asn Leu Pro Arg
          100          105          110

ccc aga cac gag ctg agt gaa gac gct tct gtt gaa gcc gag acc aca 384
Pro Arg His Glu Leu Ser Glu Asp Ala Ser Val Glu Ala Glu Thr Thr
          115          120          125

gcc ctg cgt aag cgg atg ctg cat ctg ctg gag cac tagttttctaa 430
Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu His
          130          135          140

cacgtctttt aaa 443

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<210> 274

<211> 140

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

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Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr Asp Ala Ala Glu Arg
 1           5           10           15

Arg Pro Ala Arg Leu Ser Gly Gly Met Gln Gln Arg Val Gly Ile Ala
          20           25           30

Arg Ala Phe Ala Ile Asp Pro Pro Ile Met Leu Leu Asp Glu Pro Phe
          35           40           45

Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu Gln Leu Gln Leu Leu
          50           55           60

Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val Met Val Thr His Asp
          65           70           75           80

Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val Leu Val Met Ser Lys
          85           90           95

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Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu His
130 135 140

<213> *Corynebacterium glutamicum*

<223> RXN01141

aaagaacact cggtatggca cctgatttaa ggatgctgca atcgtgacac atatacctctt 60

gcc gga gcg gcc cgc tac gtg acg tcg aca agc aat aat gaa cct gcg 163
Ala Gly Ala Ala Arg Tyr Val Thr Ser Thr Ser Asn Asn Glu Pro Ala
10 15 20

gat aac act ccc ctg acc att ggc tac gtg cct att gcg ggc tcg gcg 211
Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro Ile Ala Gly Ser Ala
25 30 35

cgc att gct atc gca gat gcg cta ggg ctg ttt aag aaa cac ggc gtg 259
Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe Lys Lys His Gly Val
40 45 50

aat gtc acg ttg aag aag tac tca ggc tgg tcc gac ctg tgg acc gcc 307
Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser Asp Leu Trp Thr Ala
55 60 65

tat	gca	aca	gag	cag	ctt	gat	gtt	gog	cac	atg	ctg	tcg	ccg	atg	act	355
Tyr	Ala	Thr	Glu	Gln	Leu	Asp	Val	Ala	His	Met	Leu	Ser	Pro	Met	Thr	
70					75					80					85	

gtg gcg att aat gct gga gtg acc aac gcg tcg cgc ccg acg gag ctg 403
Val Ala Ile Asn Ala Gly Val Thr Asn Ala Ser Arg Pro Thr Glu Leu
90 95 100

tcg ttt acc cag aac acc aat ggg caa gca att acc ttg gcg tca aag 451
Ser Phe Thr Gln Asn Thr Asn Gly Gln Ala Ile Thr Leu Ala Ser Lys
105 110 115

cac tat ggt tcc gtc aat tca gcg gcg gat ctt aaa ggc atg gtg ctg 499
 His Tyr Gly Ser Val Asn Ser Ala Ala Asp Leu Lys Gly Met Val Leu
 120 125 130

gga att cct ttt gaa tat tca gtc cat gcg ctg ctc ctg cgc gat tat 547

[illegible]

Gly Ile Pro Phe Glu Tyr Ser Val His Ala Leu Leu Leu Arg Asp Tyr
 135 140 145
 ctc gtc tca aac gca gtt gat ccc atc gcc gat ctt gag ctt cgc ctg 595
 Leu Val Ser Asn Ala Val Asp Pro Ile Ala Asp Leu Glu Leu Arg Leu
 150 155 160 165
 ctc cga cct gcc gat atg gtc gca caa ttg aca gtt gag ggc atc gat 643
 Leu Arg Pro Ala Asp Met Val Ala Gln Leu Thr Val Glu Gly Ile Asp
 170 175 180
 gga ttc att ggg cct ggg ccg ttt aat gaa cgc gcc atc agc aat ggc 691
 Gly Phe Ile Gly Pro Gly Pro Phe Asn Glu Arg Ala Ile Ser Asn Gly
 185 190 195
 tcc ggc cgg att tgg ctg ctg acc aaa caa ctg tgg gac aaa cat cca 739
 Ser Gly Arg Ile Trp Leu Leu Thr Lys Gln Leu Trp Asp Lys His Pro
 200 205 210
 tgc tgc gcc gtg gcg atg gcc aaa gag tgg aaa gct gaa cac ccc acg 787
 Cys Cys Ala Val Ala Met Ala Lys Glu Trp Lys Ala Glu His Pro Thr
 215 220 225
 gcg gct cag ggt gtg ctt aat gcg ctg gag gaa gcc tcc gca att ttg 835
 Ala Ala Gln Gly Val Leu Asn Ala Leu Glu Glu Ala Ser Ala Ile Leu
 230 235 240 245
 agc aat ccg gca caa ttt gat tcc tcg gca cgc acg ctg tcg cag gaa 883
 Ser Asn Pro Ala Gln Phe Asp Ser Ser Ala Arg Thr Leu Ser Gln Glu
 250 255 260
 aaa tac ctc aac cag cct gcc acg ttg ctg gat gga ccg tcg 925
 Lys Tyr Leu Asn Gln Pro Ala Thr Leu Leu Asp Gly Pro Ser
 265 270 275
 taatcatcgg catcacccggc tta 948

<210> 276

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

Leu Ser Thr Ala Leu Ala Gly Ala Ala Arg Tyr Val Thr Ser Thr Ser
 1 5 10 15
 Asn Asn Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro
 20 25 30
 Ile Ala Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe
 35 40 45
 Lys Lys His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser
 50 55 60
 Asp Leu Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met
 65 70 75 80
 Leu Ser Pro Met Thr Val Ala Ile Asn Ala Gly Val Thr Asn Ala Ser
 85 90 95

Arg Pro Thr Glu Leu Ser Phe Thr Gln Asn Thr Asn Gly Gln Ala Ile
 100 105 110
 Thr Leu Ala Ser Lys His Tyr Gly Ser Val Asn Ser Ala Ala Asp Leu
 115 120 125
 Lys Gly Met Val Leu Gly Ile Pro Phe Glu Tyr Ser Val His Ala Leu
 130 135 140
 Leu Leu Arg Asp Tyr Leu Val Ser Asn Ala Val Asp Pro Ile Ala Asp
 145 150 155 160
 Leu Glu Leu Arg Leu Leu Arg Pro Ala Asp Met Val Ala Gln Leu Thr
 165 170 175
 Val Glu Gly Ile Asp Gly Phe Ile Gly Pro Gly Pro Phe Asn Glu Arg
 180 185 190
 Ala Ile Ser Asn Gly Ser Gly Arg Ile Trp Leu Leu Thr Lys Gln Leu
 195 200 205
 Trp Asp Lys His Pro Cys Cys Ala Val Ala Met Ala Lys Glu Trp Lys
 210 215 220
 Ala Glu His Pro Thr Ala Ala Gln Gly Val Leu Asn Ala Leu Glu Glu
 225 230 235 240
 Ala Ser Ala Ile Leu Ser Asn Pro Ala Gln Phe Asp Ser Ser Ala Arg
 245 250 255
 Thr Leu Ser Gln Glu Lys Tyr Leu Asn Gln Pro Ala Thr Leu Leu Asp
 260 265 270
 Gly Pro Ser
 275

<210> 277
 <211> 424
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(424)
 <223> FRXA01135

<400> 277
 catttactaa tctcacaaga catgcgcttaa tgaatacaga cttagcctatt caaattcaaa 60
 gaacactcgg tatggcacct gatttaagga tgctgcaatc gtg aca cat atc ctc 115
 Val Thr His Ile Leu
 1 5
 ttc gac agc agg cgt ttt ctg caa ctg ggc gct ttt gcg tcc ttg agc 163
 Phe Asp Ser Arg Arg Phe Leu Gln Leu Gly Ala Phe Ala Ser Leu Ser
 10 15 20
 acc gca ttg gcc gga gcg gcc cgc tac gtg acg tcg aca agc aat aat 211
 Thr Ala Leu Ala Gly Ala Ala Arg Tyr Val Thr Ser Thr Ser Asn Asn

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                25                30                35
gaa cct gcg gat aac act ccc ctg acc att ggc tac gtg cct att gcg 259
Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro Ile Ala
      40                45                50

ggc tcg gcg ccg att gct atc gca gat gcg cta ggg ctg ttt aag aaa 307
Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe Lys Lys
      55                60                65

cac ggc gtg aat gtc acg ttg aag aag tac tca ggc tgg tcc gac ctg 355
His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser Asp Leu
      70                75                80

tgg acc gcc tat gca aca gag cag ctt gat gtt gcg cac atg ctg tcg 403
Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met Leu Ser
                90                95                100

ccg atg act gtg gcg att aat 424
Pro Met Thr Val Ala Ile Asn
                105

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<210> 278
<211> 108
<212> PRT
<213> Corynebacterium glutamicum

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<400> 278
Val Thr His Ile Leu Phe Asp Ser Arg Arg Phe Leu Gln Leu Gly Ala
  1                5                10                15

Phe Ala Ser Leu Ser Thr Ala Leu Ala Gly Ala Ala Arg Tyr Val Thr
                20                25                30

Ser Thr Ser Asn Asn Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly
                35                40                45

Tyr Val Pro Ile Ala Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu
                50                55                60

Gly Leu Phe Lys Lys His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser
                65                70                75                80

Gly Trp Ser Asp Leu Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val
                85                90                95

Ala His Met Leu Ser Pro Met Thr Val Ala Ile Asn
                100                105

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<210> 279
<211> 485
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(462)
<223> FRXA01141

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BGI-131CP-367

<400> 279

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gtc aat tca gcg gcg gat ctt aaa ggc atg gtg ctg gga att cct ttt 48
Val Asn Ser Ala Ala Asp Leu Lys Gly Met Val Leu Gly Ile Pro Phe
  1             5             10             15

gaa tat tca gtc cat gcg ctg ctc ctg cgc gat tat ctc gtc tca aac 96
Glu Tyr Ser Val His Ala Leu Leu Leu Arg Asp Tyr Leu Val Ser Asn
          20             25             30

gca gtt gat ccc atc gcc gat ctt gag ctt cgc ctg ctc cga cct gcc 144
Ala Val Asp Pro Ile Ala Asp Leu Glu Leu Arg Leu Leu Arg Pro Ala
          35             40             45

gat atg gtc gca caa ttg aca gtt gag ggc atc gat gga ttc att ggg 192
Asp Met Val Ala Gln Leu Thr Val Glu Gly Ile Asp Gly Phe Ile Gly
          50             55             60

cct ggg ccg ttt aat gaa cgc gcc atc agc aat ggc tcc ggc ccg att 240
Pro Gly Pro Phe Asn Glu Arg Ala Ile Ser Asn Gly Ser Gly Arg Ile
          65             70             75             80

tgg ctg ctg acc aaa caa ctg tgg gac aaa cat cca tgc tgc gcc gtg 288
Trp Leu Leu Thr Lys Gln Leu Trp Asp Lys His Pro Cys Cys Ala Val
          85             90             95

gcg atg gcc aaa gag tgg aaa gct gaa cac ccc acg gcg gct cag ggt 336
Ala Met Ala Lys Glu Trp Lys Ala Glu His Pro Thr Ala Ala Gln Gly
          100            105            110

gtg ctt aat gcg ctg gag gaa gcc tcc gca att ttg agc aat ccg gca 384
Val Leu Asn Ala Leu Glu Glu Ala Ser Ala Ile Leu Ser Asn Pro Ala
          115            120            125

caa ttt gat tcc tcg gca cgc acg ctg tcg cag gaa aaa tac ctc aac 432
Gln Phe Asp Ser Ser Ala Arg Thr Leu Ser Gln Glu Lys Tyr Leu Asn
          130            135            140

cag cct gcc acg ttg ctg gat gga ccg tcg taatcatcgg catcaccggc 482
Gln Pro Ala Thr Leu Leu Asp Gly Pro Ser
          145            150

tta 485

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<210> 280

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 280

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Val Asn Ser Ala Ala Asp Leu Lys Gly Met Val Leu Gly Ile Pro Phe
  1             5             10             15

Glu Tyr Ser Val His Ala Leu Leu Leu Arg Asp Tyr Leu Val Ser Asn
          20             25             30

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Trp Leu Leu Thr Lys Gln Leu Trp Asp Lys His Pro Cys Cys Ala Val
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Val Leu Asn Ala Leu Glu Glu Ala Ser Ala Ile Leu Ser Asn Pro Ala
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 Ile Val Ala Leu Leu Ala Trp Phe Ile Ile Ser Ala Leu Asn Asn Glu
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 Ala Tyr Gly Trp Asp Thr Tyr Arg Ser Tyr Leu Phe Asp Thr Arg Ile
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gcc acc gcg gca ctt cac acc att gcg ctg acc ttg ctg tcc atg atc 259
 Ala Thr Ala Ala Leu His Thr Ile Ala Leu Thr Leu Leu Ser Met Ile
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 Leu Gly Val Val Leu Gly Ala Ile Leu Ala Val Met Arg Met Ser Gly
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 Asn Pro Val Met Gln Gly Val Ala Trp Leu Tyr Leu Trp Ile Phe Arg
 70 75 80 85

ggc acc cca att tat gtg cag ttg gtg ttc tgg ggc ctg ctg ggt tcc 403
 Gly Thr Pro Ile Tyr Val Gln Leu Val Phe Trp Gly Leu Leu Gly Ser
 90 95 100

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 Glu Ala Ala Tyr Met Ala Glu Ile Val Arg Ser Gly Ile Gln Ala Val
 135 140 145

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 Pro Glu Gly Gln Met Glu Ala Ser Lys Ala Leu Gly Met Asn Trp Ser
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 215 220 225

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 Ser Trp Tyr Leu Val Ile Thr Ser Ile Leu Met Val Gly Gln Tyr Tyr
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Phe Asp Thr Arg Ile Ala Thr Ala Ala Leu His Thr Ile Ala Leu Thr
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Leu Leu Ser Met Ile Leu Gly Val Val Leu Gly Ala Ile Leu Ala Val

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                                         Met Ala Pro Ile Leu
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Val Phe Ala Thr Val Leu Val Ala Asp Ala Ile Val Phe Glu Ala Ser

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Asn	Ile	Leu	Ala	Asp	Gly	Lys	Ala	Leu	Leu	Leu	Ser	Gly	Ala	Trp	Trp														
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Pro	Thr	Phe	Phe	Pro	Gly	Leu	Met	Ile	Leu	Leu	Thr	Val	Leu	Cys	Leu														
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Lys	Pro	Val	Ser	Ala	Ser	Ala	Lys	Lys	Ala	Leu	Lys	Lys	Glu	Glu	Ser														
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Gly	Glu	Lys	Glu	Gly	Ser	Gly	Ile	Val	Leu	Gly	His	Thr	Thr	Arg	Glu														
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Glu	Ala	Asn	Ala	Ser	Leu	Leu	Ala	Ser	Leu	Ala	Ala	Leu	Ser	Thr	Ser														
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Glu	Asn	Asn	Ser	Asn	Asn	Arg	Leu	Ile	Phe	Asp	Gly	Asn	Pro	Thr	Pro														
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Asp	Ile	Asn	Ile	Val	Asp	Gly	Val	Asn	Phe	Thr	Val	Ala	Pro	Gly	Gln														
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tcc	tca	ctc	aac	cca	tcc	atg	ctg	atc	agc	gcc	caa	atg	aag	cag	ctg														883
Ser	Ser	Leu	Asn	Pro	Ser	Met	Leu	Ile	Ser	Ala	Gln	Met	Lys	Gln	Leu														
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BGI-131CP - 426.036

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 Thr Arg Arg Gly Gly Lys Arg Ser Ala Glu Glu Leu Leu Glu Leu Val
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 Gly Leu Asp Pro Lys Arg Thr Leu Gln Ser Tyr Pro His Glu Leu Ser
 280 285 290

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 Gly Thr Thr Arg Glu Ile Leu Ile Asp Pro Arg His Glu Tyr Thr Arg
 375 380 385

ggt ttg ctc gga tcc gtg ctc tcc atc gaa gct ggt gtg gac cgc ctc 1315
 Gly Leu Leu Gly Ser Val Leu Ser Ile Glu Ala Gly Val Asp Arg Leu
 390 395 400 405

tac cag gtc cca ggc act gtt cca tca cca aag gaa ttc gtg gca ggc 1363
 Tyr Gln Val Pro Gly Thr Val Pro Ser Pro Lys Glu Phe Val Ala Gly
 410 415 420

gac cgc ttt gca cca cga tca gaa ttc cca gaa ctt ggc ctt gac caa 1411
 Asp Arg Phe Ala Pro Arg Ser Glu Phe Pro Glu Leu Gly Leu Asp Gln
 425 430 435

aag cca gta ctt cgc ccc atc acg ggc aca gag cat gca tac gca gca 1459
 Lys Pro Val Leu Arg Pro Ile Thr Gly Thr Glu His Ala Tyr Ala Ala
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Ala Ser Pro Lys Pro Lys Pro Val Ser Ala Ser Ala Lys Lys Ala Leu
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Lys Lys Glu Glu Ser Gly Glu Lys Glu Gly Ser Gly Ile Val Leu Gly
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His Thr Thr Arg Glu Glu Ala Asn Ala Ser Leu Leu Ala Ser Leu Ala
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Gly Asn Pro Thr Pro Leu Leu Glu Val Arg Asp Leu Lys Ile Ser Phe
          145          150          155          160

Pro Asn Ala His Gly Asp Ile Asn Ile Val Asp Gly Val Asn Phe Thr
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Lys Ser Ile Thr Ala Met Ser Ile Met Gly Leu Leu Pro Pro Thr Ala
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Lys Ile Glu Gly Glu Ile Leu Phe Asp Gly Lys Asn Leu Leu Asp Leu
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Lys Pro Asp Glu Leu Asn Ala Leu Arg Gly His Glu Ile Ala Met Ile
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Tyr Gln Asp Ala Leu Ser Ser Leu Asn Pro Ser Met Leu Ile Ser Ala
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Gln Met Lys Gln Leu Thr Arg Arg Gly Gly Lys Arg Ser Ala Glu Glu
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Leu Leu Glu Leu Val Gly Leu Asp Pro Lys Arg Thr Leu Gln Ser Tyr
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Pro His Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Leu Ile Ala Met
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Ala Leu Thr Arg Asn Pro Arg Leu Leu Ile Ala Asp Glu Pro Thr Thr
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Ala Leu Val Ala Arg Leu Val His Lys Leu Thr Val Met Tyr Ala Gly
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Gln Val Val Glu Gln Gly Thr Thr Arg Glu Ile Leu Ile Asp Pro Arg
370 375 380

His Glu Tyr Thr Arg Gly Leu Leu Gly Ser Val Leu Ser Ile Glu Ala
385 390 395 400

Gly Val Asp Arg Leu Tyr Gln Val Pro Gly Thr Val Pro Ser Pro Lys
405 410 415

Glu Phe Val Ala Gly Asp Arg Phe Ala Pro Arg Ser Glu Phe Pro Glu
420 425 430

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His Ala Tyr Ala Ala Thr Asp Glu Leu Leu Ala Ala Lys Gly Glu Gln
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Val Gly Glu Ser Gly
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Cys Gly Lys Ser Thr Leu Ala Arg Val Met Val Gly Leu Gln Pro Val
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acc tcc ggc gaa gtg ctg ttc aaa ggc aag ccc atg aag cct cgt ggt 211
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Ala Gln Arg Lys Glu Leu Gly Ser Ser Val Ser Val Val Phe Gln Asp
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CCDS:TXC00950

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Trp Val Ser Glu Leu Ile Ser Met Val Gly Leu Pro Gln Ser Ala Leu
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Glu Val Leu Pro Arg Gln Val Ser Gly Gly Gln Arg Gln Arg Val Ala
                      105                      110                      115

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Ile Ala Arg Ala Leu Ala Leu Lys Pro Asp Ile Ile Val Ala Asp Glu
                      120                      125                      130

cca acc tcc gcg ctg gat gta tcc gtt cgt gcg cag gtc ctc aac ctt 547
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ctg ctg gat ctg aaa act gaa ctc ggc ctg gga ttg gta ttc atc tcc 595
Leu Leu Asp Leu Lys Thr Glu Leu Gly Leu Gly Leu Val Phe Ile Ser
150                      155                      160                      165

cac gac atc aac act gtt cgc tac gtt tct gat cgc atc gca gtc atg 643
His Asp Ile Asn Thr Val Arg Tyr Val Ser Asp Arg Ile Ala Val Met
                      170                      175                      180

ctg gct gga gaa atc att gag gaa aac acc acc tca gag atc ttc aac 691
Leu Ala Gly Glu Ile Ile Glu Glu Asn Thr Thr Ser Glu Ile Phe Asn
                      185                      190                      195

aat gcg cag cag gac tac acc cgc act ctg ctc gaa gcg aca cca tcg 739
Asn Ala Gln Gln Asp Tyr Thr Arg Thr Leu Leu Glu Ala Thr Pro Ser
                      200                      205                      210

ctg ctg aac aaa act cgt ttg tagtctccaa ccctttattc cct 783
Leu Leu Asn Lys Thr Arg Leu
215                      220

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<210> 286

<211> 220

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

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Gly Leu Gln Pro Val Thr Ser Gly Glu Val Leu Phe Lys Gly Lys Pro
                20                      25                      30

Met Lys Pro Arg Gly Ala Gln Arg Lys Glu Leu Gly Ser Ser Val Ser
                35                      40                      45

Val Val Phe Gln Asp Pro Ala Thr Ser Leu Asn Pro Arg Met Thr Val
  50                      55                      60

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Arg Glu Gln Leu Leu Asp Pro Leu Arg Val His Lys Val Gly Asp Glu
65 70 75 80

Ala Ser Arg Asn Gln Trp Val Ser Glu Leu Ile Ser Met Val Gly Leu
85 90 95

Pro Gln Ser Ala Leu Glu Val Leu Pro Arg Gln Val Ser Gly Gly Gln
100 105 110

Arg Gln Arg Val Ala Ile Ala Arg Ala Leu Ala Leu Lys Pro Asp Ile
115 120 125

Ile Val Ala Asp Glu Pro Thr Ser Ala Leu Asp Val Ser Val Arg Ala
130 135 140

Gln Val Leu Asn Leu Leu Leu Asp Leu Lys Thr Glu Leu Gly Leu Gly
145 150 155 160

Leu Val Phe Ile Ser His Asp Ile Asn Thr Val Arg Tyr Val Ser Asp
165 170 175

Arg Ile Ala Val Met Leu Ala Gly Glu Ile Ile Glu Glu Asn Thr Thr
180 185 190

Ser Glu Ile Phe Asn Asn Ala Gln Gln Asp Tyr Thr Arg Thr Leu Leu
195 200 205

Glu Ala Thr Pro Ser Leu Leu Asn Lys Thr Arg Leu
210 215 220

<210> 287

<211> 1155

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1132)

<223> RXA00760

<400> 287

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gtggacttga tctacgccgt tctcgatccg aggatccgct atg cct aat aat gaa 115
Met Pro Asn Asn Glu
1 5

ttc cac aca aac cac tcg ttg ggc caa gat gat caa acc cca gat cag 163
Phe His Thr Asn His Ser Leu Gly Gln Asp Asp Gln Thr Pro Asp Gln
10 15 20

gct cat ttc ttc cca caa gga cga ggc gag gct cta gtt cga cca ggt 211
Ala His Phe Phe Pro Gln Gly Arg Gly Glu Ala Leu Val Arg Pro Gly
25 30 35

caa gag cac ttc atc gca gcc act gat gaa acc gga ctt ggt gcc gtc 259
Gln Glu His Phe Ile Ala Ala Thr Asp Glu Thr Gly Leu Gly Ala Val
40 45 50

gat gct gtt gct gat gac tct gca cca acc tcc atg tgg ggc gaa gcg 307
Asp Ala Val Ala Asp Asp Ser Ala Pro Thr Ser Met Trp Gly Glu Ala
55 60 65

tgg cga gac ctt cgt cgt cga cca ctg ttc tgg gtc tct gcg gtg ttg 355
Trp Arg Asp Leu Arg Arg Arg Pro Leu Phe Trp Val Ser Ala Val Leu
70 75 80 85

att att ttg gcg ctt ctc ctg gcc gca gtt ccg cag ctg ttt acc tca 403
Ile Ile Leu Ala Leu Leu Leu Ala Ala Val Pro Gln Leu Phe Thr Ser
90 95 100

acg gat ccc cag ttc tgt gtg ctg gca aac tct ctt gat ggt cca cag 451
Thr Asp Pro Gln Phe Cys Val Leu Ala Asn Ser Leu Asp Gly Pro Gln
105 110 115

tct gga cat ccc ttc gga ttc gac cgt caa ggt tgc gat att ttt gct 499
Ser Gly His Pro Phe Gly Phe Asp Arg Gln Gly Cys Asp Ile Phe Ala
120 125 130

cgt acc gtc tac ggt gct cgt gcc tcg gtc gcc gtc ggt gtg ttg acc 547
Arg Thr Val Tyr Gly Ala Arg Ala Ser Val Ala Val Gly Val Leu Thr
135 140 145

acg tta ctg gtc gcc ctc atc ggt act gta ttt ggt gct ttg gct ggc 595
Thr Leu Leu Val Ala Leu Ile Gly Thr Val Phe Gly Ala Leu Ala Gly
150 155 160 165

ttc ttt ggt ggc atc atg gat acc atc ctc tcc cgc atc acc gac atg 643
Phe Phe Gly Gly Ile Met Asp Thr Ile Leu Ser Arg Ile Thr Asp Met
170 175 180

ttc ttc gcc att cca ctg gtt ctg gca gcc atc gtt gtg atg cag atg 691
Phe Phe Ala Ile Pro Leu Val Leu Ala Ala Ile Val Val Met Gln Met
185 190 195

ttc aag gaa cac cgc acc atc gtc acc gtg gtt ttg gtg ctt ggg ctt 739
Phe Lys Glu His Arg Thr Ile Val Thr Val Val Leu Val Leu Gly Leu
200 205 210

ttc ggc tgg acc aac att gcg cgt att acc cgt gga gcg gtg atg acc 787
Phe Gly Trp Thr Asn Ile Ala Arg Ile Thr Arg Gly Ala Val Met Thr
215 220 225

gca aag aat gaa gag tat gtc acc tcc gca cgt gcg ctt ggt gca tca 835
Ala Lys Asn Glu Glu Tyr Val Thr Ser Ala Arg Ala Leu Gly Ala Ser
230 235 240 245

aaa gcc aag ata ctg ctg tct cac atc atg cca aac gcc gca gca ccc 883
Lys Ala Lys Ile Leu Leu Ser His Ile Met Pro Asn Ala Ala Ala Pro
250 255 260

atc att gtg tat gca act gtg gca ctg gga aca ttc atc gtg gca gag 931
Ile Ile Val Tyr Ala Thr Val Ala Leu Gly Thr Phe Ile Val Ala Glu
265 270 275

gcg acg ctc tcc ttc ctg ggc att ggc ctt cca cca tca att gtc tcc 979
Ala Thr Leu Ser Phe Leu Gly Ile Gly Leu Pro Pro Ser Ile Val Ser
280 285 290

tgg ggt gct gat atc gcg aag gca caa acc tcc ctt cgt acc caa ccc 1027

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<210> 288
<211> 344
<212> PRT
<213> Corynebacterium glutamicum

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          20          25          30
Leu Val Arg Pro Gly Gln Glu His Phe Ile Ala Ala Thr Asp Glu Thr
          35          40          45
Gly Leu Gly Ala Val Asp Ala Val Ala Asp Asp Ser Ala Pro Thr Ser
          50          55          60
Met Trp Gly Glu Ala Trp Arg Asp Leu Arg Arg Arg Pro Leu Phe Trp
 65          70          75          80
Val Ser Ala Val Leu Ile Ile Leu Ala Leu Leu Leu Ala Ala Val Pro
          85          90          95
Gln Leu Phe Thr Ser Thr Asp Pro Gln Phe Cys Val Leu Ala Asn Ser
          100          105          110
Leu Asp Gly Pro Gln Ser Gly His Pro Phe Gly Phe Asp Arg Gln Gly
          115          120          125
Cys Asp Ile Phe Ala Arg Thr Val Tyr Gly Ala Arg Ala Ser Val Ala
          130          135          140
Val Gly Val Leu Thr Thr Leu Leu Val Ala Leu Ile Gly Thr Val Phe
145          150          155          160
Gly Ala Leu Ala Gly Phe Phe Gly Gly Ile Met Asp Thr Ile Leu Ser
          165          170          175
Arg Ile Thr Asp Met Phe Phe Ala Ile Pro Leu Val Leu Ala Ala Ile
          180          185          190
Val Val Met Gln Met Phe Lys Glu His Arg Thr Ile Val Thr Val Val
          195          200          205

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Variable	Unit	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																																																																																																																																																						
Population	millions	10.0	10.1	10.2	10.3	10.4	10.5	10.6	10.7	10.8	10.9	11.0	11.1	11.2	11.3	11.4	11.5	11.6	11.7	11.8	11.9	12.0	12.1	12.2	12.3	12.4	12.5	12.6	12.7	12.8	12.9	13.0	13.1	13.2	13.3	13.4	13.5	13.6	13.7	13.8	13.9	14.0	14.1	14.2	14.3	14.4	14.5	14.6	14.7	14.8	14.9	15.0	15.1	15.2	15.3	15.4	15.5	15.6	15.7	15.8	15.9	16.0	16.1	16.2	16.3	16.4	16.5	16.6	16.7	16.8	16.9	17.0	17.1	17.2	17.3	17.4	17.5	17.6	17.7	17.8	17.9	18.0	18.1	18.2	18.3	18.4	18.5	18.6	18.7	18.8	18.9	19.0	19.1	19.2	19.3	19.4	19.5	19.6	19.7	19.8	19.9	20.0	20.1	20.2	20.3	20.4	20.5	20.6	20.7	20.8	20.9	21.0	21.1	21.2	21.3	21.4	21.5	21.6	21.7	21.8	21.9	22.0	22.1	22.2	22.3	22.4	22.5	22.6	22.7	22.8	22.9	23.0	23.1	23.2	23.3	23.4	23.5	23.6	23.7	23.8	23.9	24.0	24.1	24.2	24.3	24.4	24.5	24.6	24.7	24.8	24.9	25.0	25.1	25.2	25.3	25.4	25.5	25.6	25.7	25.8	25.9	26.0	26.1	26.2	26.3	26.4	26.5	26.6	26.7	26.8	26.9	27.0	27.1	27.2	27.3	27.4	27.5	27.6	27.7	27.8	27.9	28.0	28.1	28.2	28.3	28.4	28.5	28.6	28.7	28.8	28.9	29.0	29.1	29.2	29.3	29.4	29.5	29.6	29.7	29.8	29.9	30.0	30.1	30.2	30.3	30.4	30.5	30.6	30.7	30.8	30.9	31.0	31.1	31.2	31.3	31.4	31.5	31.6	31.7	31.8	31.9	32.0	32.1	32.2	32.3	32.4	32.5	32.6	32.7	32.8	32.9	33.0	33.1	33.2	33.3	33.4	33.5	33.6	33.7	33.8	33.9	34.0	34.1	34.2	34.3	34.4	34.5	34.6	34.7	34.8	34.9	35.0	35.1	35.2	35.3	35.4	35.5	35.6	35.7	35.8	35.9	36.0	36.1	36.2	36.3	36.4	36.5	36.6	36.7	36.8	36.9	37.0	37.1	37.2	37.3	37.4	37.5	37.6	37.7	37.8	37.9	38.0	38.1	38.2	38.3	38.4	38.5	38.6	38.7	38.8	38.9	39.0	39.1	39.2

Leu Val Leu Gly Leu Phe Gly Trp Thr Asn Ile Ala Arg Ile Thr Arg
 210 215 220
 Gly Ala Val Met Thr Ala Lys Asn Glu Glu Tyr Val Thr Ser Ala Arg
 225 230 235 240
 Ala Leu Gly Ala Ser Lys Ala Lys Ile Leu Leu Ser His Ile Met Pro
 245 250 255
 Asn Ala Ala Ala Pro Ile Ile Val Tyr Ala Thr Val Ala Leu Gly Thr
 260 265 270
 Phe Ile Val Ala Glu Ala Thr Leu Ser Phe Leu Gly Ile Gly Leu Pro
 275 280 285
 Pro Ser Ile Val Ser Trp Gly Ala Asp Ile Ala Lys Ala Gln Thr Ser
 290 295 300
 Leu Arg Thr Gln Pro Met Val Leu Phe Tyr Pro Ala Met Ala Leu Ala
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 Leu Thr Val Leu Ser Phe Ile Met Met Gly Asp Val Val Arg Asp Ala
 325 330 335
 Leu Asp Pro Lys Ser Arg Lys Arg
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 <211> 1632
 <212> DNA
 <213> Corynebacterium glutamicum
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 <222> (101)..(1609)
 <223> RXA02035

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 Met Lys Ile Thr Arg
 1 5
 gga ctc ctg cca tca ttg ctg ttg gca agc aca atc gtg gtg tcg tca 163
 Gly Leu Leu Pro Ser Leu Leu Leu Ala Ser Thr Ile Val Val Ser Ser
 10 15 20
 tgc tct gct gga tcg act gcg tat cag cag ccc cct gct gtt gat caa 211
 Cys Ser Ala Gly Ser Thr Ala Tyr Gln Gln Pro Pro Ala Val Asp Gln
 25 30 35
 tca tcc att gtc att gct acc acg gct gct gcg gcg tca ctt gat ttc 259
 Ser Ser Ile Val Ile Ala Thr Thr Ala Ala Ala Ala Ser Leu Asp Phe
 40 45 50
 acc aat gct gcg ggc gct gct att ccg cag gcg atg atg tcc aat att 307
 Thr Asn Ala Ala Gly Ala Ala Ile Pro Gln Ala Met Met Ser Asn Ile
 55 60 65

BGI-131CP

tac gag ggg ctt gtg cgc atc gat gcg gag ggt gag att cag ccg ctg 355
 Tyr Glu Gly Leu Val Arg Ile Asp Ala Glu Gly Glu Ile Gln Pro Leu
 70 75 80 85

ctt gcc acg tcg tgg gat att tca gac gat cgc acc gag tac att ttc 403
 Leu Ala Thr Ser Trp Asp Ile Ser Asp Asp Arg Thr Glu Tyr Ile Phe
 90 95 100

cat ttg cgg gag ggt gtg ctg ttt tcc aac ggc gat ccc ttc aat gct 451
 His Leu Arg Glu Gly Val Leu Phe Ser Asn Gly Asp Pro Phe Asn Ala
 105 110 115

gat tct gcg aag ttt tcc att gat cgg gta aaa act gac tgg acc aat 499
 Asp Ser Ala Lys Phe Ser Ile Asp Arg Val Lys Thr Asp Trp Thr Asn
 120 125 130

ggt ttg aaa agt ggc atg gat gtg gtg gag tcc acc gag gtg att gac 547
 Gly Leu Lys Ser Gly Met Asp Val Val Glu Ser Thr Glu Val Ile Asp
 135 140 145

gat cac acg ctg aaa gtt tcg ctg gtc agg ccg tcc aac caa tgg ttg 595
 Asp His Thr Leu Lys Val Ser Leu Val Arg Pro Ser Asn Gln Trp Leu
 150 155 160 165

tgg agc atg ggt acc gcg atc ggt gcc atg atg acg gag ggg ggc gtc 643
 Trp Ser Met Gly Thr Ala Ile Gly Ala Met Met Thr Glu Gly Gly Val
 170 175 180

gat aag ctg gca act gat ccc gtt ggc acc ggc ccg tac acg gtg acg 691
 Asp Lys Leu Ala Thr Asp Pro Val Gly Thr Gly Pro Tyr Thr Val Thr
 185 190 195

cac tgg gcg ccg ggc cgc gca att ggg ttc ggc gcg ccg gcc gat tat 739
 His Trp Ala Pro Gly Arg Ala Ile Gly Phe Gly Ala Arg Ala Asp Tyr
 200 205 210

tgg ggg cag aag ccg ctt aac gac gcc gca acc atc cgc tac ttc agc 787
 Trp Gly Gln Lys Pro Leu Asn Asp Ala Ala Thr Ile Arg Tyr Phe Ser
 215 220 225

gat gcg acg gcc tcg acc aat gcg ctg caa agc ggt gac gtg gac gtg 835
 Asp Ala Thr Ala Ser Thr Asn Ala Leu Gln Ser Gly Asp Val Asp Val
 230 235 240 245

att tgg gcg atg caa gcg ccc gaa cag ctg gct acg ctg cag gaa tac 883
 Ile Trp Ala Met Gln Ala Pro Glu Gln Leu Ala Thr Leu Gln Glu Tyr
 250 255 260

acc gtg gaa gtg ggc aca acc aat ggt gag atg ttg ctg tcg atg aat 931
 Thr Val Glu Val Gly Thr Thr Asn Gly Glu Met Leu Leu Ser Met Asn
 265 270 275

aat cag cgt gca cct ttt gat gat gtg cgt gtg cgc cag gcg gtg atg 979
 Asn Gln Arg Ala Pro Phe Asp Asp Val Arg Val Arg Gln Ala Val Met
 280 285 290

ttt gcg att gat cgc caa gcc gtc att gat acc gcg ttg gaa ggt tac 1027
 Phe Ala Ile Asp Arg Gln Ala Val Ile Asp Thr Ala Leu Glu Gly Tyr
 295 300 305

ggc acc gac act ggt ggc gtg cct gtt ccg ccg act gat ccg tgg tac 1075

<400> 290
Met Lys Ile Thr Arg Gly Leu Leu Pro Ser Leu Leu Leu Ala Ser Thr
1 5 10 15

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Pro Ala Val Asp Gln Ser Ser Ile Val Ile Ala Thr Thr Ala Ala Ala
      35                      40                      45

Ala Ser Leu Asp Phe Thr Asn Ala Ala Gly Ala Ala Ile Pro Gln Ala
      50                      55                      60

Met Met Ser Asn Ile Tyr Glu Gly Leu Val Arg Ile Asp Ala Glu Gly
      65                      70                      75                      80

Glu Ile Gln Pro Leu Leu Ala Thr Ser Trp Asp Ile Ser Asp Asp Arg
      85                      90                      95

Thr Glu Tyr Ile Phe His Leu Arg Glu Gly Val Leu Phe Ser Asn Gly
      100                     105                     110

Asp Pro Phe Asn Ala Asp Ser Ala Lys Phe Ser Ile Asp Arg Val Lys
      115                     120                     125

Thr Asp Trp Thr Asn Gly Leu Lys Ser Gly Met Asp Val Val Glu Ser
      130                     135                     140

Thr Glu Val Ile Asp Asp His Thr Leu Lys Val Ser Leu Val Arg Pro
      145                     150                     155                     160

Ser Asn Gln Trp Leu Trp Ser Met Gly Thr Ala Ile Gly Ala Met Met
      165                     170                     175

Thr Glu Gly Gly Val Asp Lys Leu Ala Thr Asp Pro Val Gly Thr Gly
      180                     185                     190

Pro Tyr Thr Val Thr His Trp Ala Pro Gly Arg Ala Ile Gly Phe Gly
      195                     200                     205

Ala Arg Ala Asp Tyr Trp Gly Gln Lys Pro Leu Asn Asp Ala Ala Thr
      210                     215                     220

Ile Arg Tyr Phe Ser Asp Ala Thr Ala Ser Thr Asn Ala Leu Gln Ser
      225                     230                     235                     240

Gly Asp Val Asp Val Ile Trp Ala Met Gln Ala Pro Glu Gln Leu Ala
      245                     250                     255

Thr Leu Gln Glu Tyr Thr Val Glu Val Gly Thr Thr Asn Gly Glu Met
      260                     265                     270

Leu Leu Ser Met Asn Asn Gln Arg Ala Pro Phe Asp Asp Val Arg Val
      275                     280                     285

Arg Gln Ala Val Met Phe Ala Ile Asp Arg Gln Ala Val Ile Asp Thr
      290                     295                     300

Ala Leu Glu Gly Tyr Gly Thr Asp Thr Gly Gly Val Pro Val Pro Pro
      305                     310                     315                     320

Thr Asp Pro Trp Tyr Glu Lys Ser Thr Met Tyr Pro Tyr Asp Pro Asp
      325                     330                     335

Arg Ala Arg Ala Leu Leu Glu Glu Ala Gly Ala Glu Gly Thr Arg Ile

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340 345 350
 Thr Met Ser Ile Pro Ser Leu Pro Tyr Ala Gln Ala Ala Ser Glu Ile
 355 360 365
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 370 375 380
 Thr Glu Phe Pro Ala Val Trp Leu Ala Gln Val Met Gly Gln Lys Asp
 385 390 395 400
 Tyr Asp Met Ser Leu Ile Ala His Val Glu Pro Arg Asp Ile Pro Thr
 405 410 415
 Leu Phe Ser Pro Asn Tyr Tyr Leu Gly Phe Asp Asp Thr Glu Thr Gln
 420 425 430
 Ala Leu Leu Ala Glu Ala Asp Ser Ser Ala Asn Glu Val Glu Leu Met
 435 440 445
 Gln Gln Ala Val Asp Arg Ile Met Glu Gln Ala Val Ala Asp Asn Leu
 450 455 460
 Met Asn Val Ala Asn Ile Val Val Met Ser Pro Glu Ile Thr Gly Ile
 465 470 475 480
 Asp Pro Asn Val Val Ser Gly Ala Leu Glu Leu Ser Leu Ile Gly Arg
 485 490 495
 Lys Glu Ser Gly Val Ala Gln
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<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXN01002

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caactaattt ccctgtttcc aataactcaag gtgtgcgcat atg aat tct gat gct 115
 Met Asn Ser Asp Ala
 1 5

tcg gct acc acc aac tcc tgg gct atc aac ttc gac cat gtg tcg gtg 163
 Ser Ala Thr Thr Asn Ser Trp Ala Ile Asn Phe Asp His Val Ser Val
 10 15 20

acg tat ccc aat ggg acg aaa gcc ctc gat gat gtt tcc ctc acc atc 211
 Thr Tyr Pro Asn Gly Thr Lys Ala Leu Asp Asp Val Ser Leu Thr Ile
 25 30 35

aat ccc ggt gag atg gtt gcc atc gtg ggt ctg tca gga tcg ggt aaa 259
 Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu Ser Gly Ser Gly Lys
 40 45 50


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tcc acg ctg att cgc acg atc aac ggt ctt gtc cgc gct acg gaa ggc 307
Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val Arg Ala Thr Glu Gly
    55                      60                      65

acc gtg acg gtg ggg ccg cat cag atc aac acc ttg aag ggg aaa gca 355
Thr Val Thr Val Gly Pro His Gln Ile Asn Thr Leu Lys Gly Lys Ala
    70                      75                      80                      85

ctg cgt gat gcc cgt ggg cag atc ggc atg att ttc cag ggg ttc aac 403
Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile Phe Gln Gly Phe Asn
                      90                      95                      100

ctg tcg gaa cgc agc agt gtg ttc cag aat gtt ttg gtg ggc cgc ttc 451
Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val Leu Val Gly Arg Phe
                      105                      110                      115

gcg cac aca gcg tgg tgg cgt aac ctc ctc ggg ttt ccc acg gag cac 499
Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly Phe Pro Thr Glu His
                      120                      125                      130

gac aag cag att gct ttt cac gcg ttg gag tcc gtg ggc att ttg cac 547
Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val Gly Ile Leu His
                      135                      140                      145

aaa gtg tgg acc cga gct ggt gct ttg tcg ggt gga cag aaa cag cgc 595
Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly Gln Lys Gln Arg
                      150                      155                      160                      165

gtt gct att gcg cgc gcc tta tcg caa gat ccg tct gtc atg ctg gca 643
Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser Val Met Leu Ala
                      170                      175                      180

gat gag cct gtg gca agc ctt gat ccg cca acc gcg cat tcc gtg atg 691
Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala His Ser Val Met
                      185                      190                      195

cgc gat cta gaa aac atc aac aac gtg gaa ggc ctc acc gtg ttg gtg 739
Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu Thr Val Leu Val
                      200                      205                      210

aac ttg cac ttg att gat ttg gct cgt caa tac acc aca agg ctt gtg 787
Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr Thr Arg Leu Val
                      215                      220                      225

ggt ttg cgt gcc ggc aag ctg gtc tat gac ggt cct atc tct gag gcc 835
Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro Ile Ser Glu Ala
                      230                      235                      240                      245

acc gat aaa gac ttt gaa gct atc tat ggt cgc ccc atc cag gct aaa 883
Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro Ile Gln Ala Lys
                      250                      255                      260

gac ctg cta ggt gat cgc gca tgaccacgcc ttcttctaca ctt 927
Asp Leu Leu Gly Asp Arg Ala
                      265

<210> 292
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<213> Corynebacterium glutamicum

<400> 292

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          20          25          30

Val Ser Leu Thr Ile Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu
          35          40          45

Ser Gly Ser Gly Lys Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val
          50          55          60

Arg Ala Thr Glu Gly Thr Val Thr Val Gly Pro His Gln Ile Asn Thr
          65          70          75          80

Leu Lys Gly Lys Ala Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile
          85          90          95

Phe Gln Gly Phe Asn Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val
          100          105          110

Leu Val Gly Arg Phe Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly
          115          120          125

Phe Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser
          130          135          140

Val Gly Ile Leu His Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly
          145          150          155          160

Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro
          165          170          175

Ser Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr
          180          185          190

Ala His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly
          195          200          205

Leu Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr
          210          215          220

Thr Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly
          225          230          235          240

Pro Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg
          245          250          255

Pro Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala
          260          265

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<210> 293

<211> 440

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (1)..(417)
 <223> FRXA01002

<400> 293

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ccc acg gag cac gac aag cag att gct ttt cac gcg ttg gag tcc gtg   48
Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val
   1                               10                               15

ggc att ttg gac aaa gtg tgg acc cga gct ggt gct ttg tcg ggt gga   96
Gly Ile Leu Asp Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly
                20                25                30

cag aaa cag cgc gtt gct att gcg cgc gcc tta tcg caa gat ccg tct   144
Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser
                35                40                45

gtc atg ctg gca gat gag cct gtg gca agc ctt gat ccg cca acc gcg   192
Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala
   50                55                60

cat tcc gtg atg cgc gat cta gaa aac atc aac aac gtg gaa ggc ctc   240
His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu
   65                70                75                80

acc gtg ttg gtg aac ttg cac ttg att gat ttg gct cgt caa tac acc   288
Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr
                85                90                95

aca agg ctt gtg ggt ttg cgt gcc ggc aag ctg gtc tat gac ggt cct   336
Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro
                100                105                110

atc tct gag gcc acc gat aaa gac ttt gaa gct atc tat ggt cgc ccc   384
Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro
                115                120                125

atc cag gct aaa gac ctg cta ggt gat cgc gca tgaccacgcc ttctttctaca 437
Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala
                130                135

ctt                                                                    440

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<210> 294
 <211> 139
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 294

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Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val
   1                               10                               15

Gly Ile Leu Asp Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly
   20                25                30

Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser
   35                40                45

Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala
   50                55                60

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His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu
 65 70 75 80
 Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr
 85 90 95
 Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro
 100 105 110
 Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro
 115 120 125
 Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala
 130 135

<210> 295

<211> 969

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(946)

<223> RXN01000

<400> 295

ctttctatgc ctacgcggat gtttccgtga tcattctgga aatcctcatc gtggtgattg 60

tcattgaagt aatctccaac gcacttcgaa agaggctggt atg agc acc tta acc 115
 Met Ser Thr Leu Thr
 1 5

tct cac cgc aca gta ccg gcc ccc agc tct ccc ccg gcg cgc ccc aac 163
 Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro Pro Ala Arg Pro Asn
 10 15 20

aaa ctg gcg cgc aat atc gtt gca att gtc gct gcg ctg att gtc ctt 211
 Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala Ala Leu Ile Val Leu
 25 30 35

ata gct acc ggc acg ctc aag atc gag tgg aat gag ctt ccg cag atg 259
 Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn Glu Leu Pro Gln Met
 40 45 50

ccc gcg cag gtg tgg cat tac tta gag ctg atg ttt agc gat ccc gat 307
 Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met Phe Ser Asp Pro Asp
 55 60 65

tgg tcg aag ttt ggc cgc gcc gtc cag gaa atg tgg cgt tcc atc gcc 355
 Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met Trp Arg Ser Ile Ala
 70 75 80 85

atg gcg tgg ttg ggt gcc att tta tgc gtg gtg gtc tct gtc cct ctg 403
 Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val Val Ser Val Pro Leu
 90 95 100

gga atg ttg gct gcc cgc ggg gtg gga cct tat tgg ctg cgt acc gtt 451
 Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val
 105 110 115

BGI-131CP
 - 388 -
 <210> 295
 <211> 969
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(946)
 <223> RXN01000
 <400> 295
 ctttctatgc ctacgcggat gtttccgtga tcattctgga aatcctcatc gtggtgattg 60
 tcattgaagt aatctccaac gcacttcgaa agaggctggt atg agc acc tta acc 115
 Met Ser Thr Leu Thr
 1 5
 tct cac cgc aca gta ccg gcc ccc agc tct ccc ccg gcg cgc ccc aac 163
 Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro Pro Ala Arg Pro Asn
 10 15 20
 aaa ctg gcg cgc aat atc gtt gca att gtc gct gcg ctg att gtc ctt 211
 Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala Ala Leu Ile Val Leu
 25 30 35
 ata gct acc ggc acg ctc aag atc gag tgg aat gag ctt ccg cag atg 259
 Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn Glu Leu Pro Gln Met
 40 45 50
 ccc gcg cag gtg tgg cat tac tta gag ctg atg ttt agc gat ccc gat 307
 Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met Phe Ser Asp Pro Asp
 55 60 65
 tgg tcg aag ttt ggc cgc gcc gtc cag gaa atg tgg cgt tcc atc gcc 355
 Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met Trp Arg Ser Ile Ala
 70 75 80 85
 atg gcg tgg ttg ggt gcc att tta tgc gtg gtg gtc tct gtc cct ctg 403
 Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val Val Ser Val Pro Leu
 90 95 100
 gga atg ttg gct gcc cgc ggg gtg gga cct tat tgg ctg cgt acc gtt 451
 Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val
 105 110 115

tta cgg ttc gtg ttc gcg gtg att cgt gcg ttc ccc gaa gtg gtt atc 499
 Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile
 120 125 130

gca att att ttg cta act gtc acc ggc cta act cct ttt act ggt gcg 547
 Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala
 135 140 145

ctc gca ttg ggt atc tcc ggt att gga caa cag gca aag tgg acc tat 595
 Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr
 150 155 160 165

gaa gcc att gag tcc act ccc acc ggc cgg tca gag gca gtg cgt gca 643
 Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala
 170 175 180

gcg ggt gga act acg cgg gag gtt ctg cgg tgg gcg ttg tgg cca cag 691
 Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln
 185 190 195

gtt gcg cca tcc att gca tct ttt gcc ctg tac cgc ttt gag atc aac 739
 Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn
 200 205 210

atc cgt acc tct gcg gta ttg ggc atc gtt ggt gca ggt ggt atc ggt 787
 Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly
 215 220 225

agt atg ctt gcc aat tac acc aac tac agg cag tgg gac acc gtg ggc 835
 Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly
 230 235 240 245

atg ctg ctc atc gtc gtg gtt gtc gca acg atg atc gtc gat ctc atc 883
 Met Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile
 250 255 260

tcc ggc acc atc cgc cgc cgc atc atg aag ggg gct agt gac cgt gtc 931
 Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val
 265 270 275

gtg gca cca agc aac tgacgctcca ccaagcatcc gca 969
 Val Ala Pro Ser Asn
 280

<210> 296

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

Met Ser Thr Leu Thr Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro
1 5 10 15

Pro Ala Arg Pro Asn Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala
20 25 30

Ala Leu Ile Val Leu Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn
35 40 45

```

Glu Leu Pro Gln Met Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met
 50                               55                               60

Phe Ser Asp Pro Asp Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met
 65                               70                               75                               80

Trp Arg Ser Ile Ala Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val
                               85                               90                               95

Val Ser Val Pro Leu Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr
          100                               105                               110

Trp Leu Arg Thr Val Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe
          115                               120                               125

Pro Glu Val Val Ile Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr
          130                               135                               140

Pro Phe Thr Gly Ala Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln
          145                               150                               155                               160

Ala Lys Trp Thr Tyr Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser
          165                               170                               175

Glu Ala Val Arg Ala Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp
          180                               185                               190

Ala Leu Trp Pro Gln Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr
          195                               200                               205

Arg Phe Glu Ile Asn Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly
          210                               215                               220

Ala Gly Gly Ile Gly Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln
          225                               230                               235                               240

Trp Asp Thr Val Gly Met Leu Leu Ile Val Val Val Val Ala Thr Met
          245                               250                               255

Ile Val Asp Leu Ile Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly
          260                               265                               270

Ala Ser Asp Arg Val Val Ala Pro Ser Asn
          275                               280

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<210> 297

<211> 563

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(540)

<223> FRXA01000

<400> 297

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atg ttg gct gcc cgc ggg gtg gga cct tat tgg ctg cgt acc gtt tta
Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val Leu
  1                               5                               10                               15

```

48

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cgg ttc gtg ttc gcg gtg att cgt gcg ttc ccc gaa gtg gtt atc gca 96
Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile Ala
      20                25                30

att att ttg cta act gtc acc ggc cta act cct ttt act ggt gcg ctc 144
Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala Leu
      35                40                45

gca ttg ggt atc tcc ggt att gga caa cag gca aag tgg acc tat gaa 192
Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr Glu
      50                55                60

gcc att gag tcc act ccc acc ggc ccg tca gag gca gtg cgt gca gcg 240
Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala Ala
      65                70                75                80

ggg gga act acg ccg gag gtt ctg ccg tgg gcg ttg tgg cca cag gtt 288
Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln Val
      85                90                95

gcg cca tcc att gca tct ttt gcc ctg tac cgc ttt gag atc aac atc 336
Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn Ile
      100                105                110

cgt acc tct gcg gta ttg ggc atc gtt ggt gca ggt ggt atc ggt agt 384
Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Ser
      115                120                125

atg ctt gcc aat tac acc aac tac agg cag tgg gac acc gtg ggc atg 432
Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly Met
      130                135                140

ctg ctc atc gtc gtg gtt gtc gca acg atg atc gtc gat ctc atc tcc 480
Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile Ser
      145                150                155                160

ggc acc atc cgc cgc cgc atc atg aag ggg gct agt gac cgt gtc gtg 528
Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val Val
      165                170                175

gca cca agc aac tgacgctcca ccaagcatcc gca 563
Ala Pro Ser Asn
      180

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<210> 298

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

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Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val Leu
  1                5                10                15

Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile Ala
      20                25                30

Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala Leu
      35                40                45

Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr Glu

```

50 55 60
 Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala Ala
 65 70 75 80
 Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln Val
 85 90 95
 Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn Ile
 100 105 110
 Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Ser
 115 120 125
 Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly Met
 130 135 140
 Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile Ser
 145 150 155 160
 Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val Val
 165 170 175
 Ala Pro Ser Asn
 180

<210> 299

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXA01003

<400> 299

agctggtcta tgacggtcct atctctgagg ccaccgataa agactttgaa gctatctatg 60

gtgcgccccat ccaggctaaa gacctgctag gtgatcgcgc atg acc acg cct tct 115
 Met Thr Thr Pro Ser
 1 5

tct aca ctt atc cca caa aag cct cgg gct ggg gta aag acc tat ctc 163
 Ser Thr Leu Ile Pro Gln Lys Pro Arg Ala Gly Val Lys Thr Tyr Leu
 10 15 20

atc atc ggc gcc atc gtt gtc ttc acc gtg gca aca gca acc cca gcg 211
 Ile Ile Gly Ala Ile Val Val Phe Thr Val Ala Thr Ala Thr Pro Ala
 25 30 35

cta ggt ggc att gag ctt gat ttc gct tcc att gct gcg aat tgg cgc 259
 Leu Gly Gly Ile Glu Leu Asp Phe Ala Ser Ile Ala Ala Asn Trp Arg
 40 45 50

aat ggt gcc aac aaa ctc ctg caa atg ctg cag ccc aac ttt gcg ttc 307
 Asn Gly Ala Asn Lys Leu Leu Gln Met Leu Gln Pro Asn Phe Ala Phe
 55 60 65

ttg cct cgt acg tgg ctt ccc atg ttg gaa acc ctg cag atg gcg ctt 355


```

Leu Pro Arg Thr Trp Leu Pro Met Leu Glu Thr Leu Gln Met Ala Leu
 70              75              80              85

gtt gga gct gtc ttg tct gct gcc gta tgc gtg cct ttg acg ttg tgg 403
Val Gly Ala Val Leu Ser Ala Ala Val Ser Val Pro Leu Thr Leu Trp
              90              95              100

gca gcg cag gca acc aac acc agt gcg att ggt cgt ggc att gtc cgc 451
Ala Ala Gln Ala Thr Asn Thr Ser Ala Ile Gly Arg Gly Ile Val Arg
              105              110              115

acc atc att aac gtg gtg cgc tct gtc ccc gac ttg gtg tat gcc acc 499
Thr Ile Ile Asn Val Val Arg Ser Val Pro Asp Leu Val Tyr Ala Thr
              120              125              130

atc ttg gtc gcc atg gtt ggt gtc ggc gca tta cct ggc att ttg acg 547
Ile Leu Val Ala Met Val Gly Val Gly Ala Leu Pro Gly Ile Leu Thr
              135              140              145

ctg ttt ctg ttc aac ctg ggc atc gtg gtc aag ctt gtc tct gag gcc 595
Leu Phe Leu Phe Asn Leu Gly Ile Val Val Lys Leu Val Ser Glu Ala
150              155              160              165

att gat tcc act gag cat ccc tat atg gaa gca gga cgc gca gca ggt 643
Ile Asp Ser Thr Glu His Pro Tyr Met Glu Ala Gly Arg Ala Ala Gly
              170              175              180

gga tca cag ttc caa atc aac cga gtc tcc gcg ctt cct gaa gtc atg 691
Gly Ser Gln Phe Gln Ile Asn Arg Val Ser Ala Leu Pro Glu Val Met
              185              190              195

ccg ctc ttt gcc aac caa tgg ctc tac acc cta gag ctg aat gta cgc 739
Pro Leu Phe Ala Asn Gln Trp Leu Tyr Thr Leu Glu Leu Asn Val Arg
              200              205              210

atc tcc gcc atc ctt ggc atc gtg ggc gca ggt ggc atc ggc agg ctg 787
Ile Ser Ala Ile Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Arg Leu
              215              220              225

ctt gat gaa cgc cga gct ttc tat gcc tac gcg gat gtt tcc gtg atc 835
Leu Asp Glu Arg Arg Ala Phe Tyr Ala Tyr Ala Asp Val Ser Val Ile
230              235              240              245

att ctg gaa atc ctc atc gtg gtg att gtc att gaa gta atc tcc aac 883
Ile Leu Glu Ile Leu Ile Val Val Ile Val Ile Glu Val Ile Ser Asn
              250              255              260

gca ctt cga aag agg ctg gta tgagcacctt aacctctcac cgc 927
Ala Leu Arg Lys Arg Leu Val
              265

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<210> 300

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

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Met Thr Thr Pro Ser Ser Thr Leu Ile Pro Gln Lys Pro Arg Ala Gly
 1              5              10              15

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Val Lys Thr Tyr Leu Ile Ile Gly Ala Ile Val Val Phe Thr Val Ala
 20 25 30
 Thr Ala Thr Pro Ala Leu Gly Gly Ile Glu Leu Asp Phe Ala Ser Ile
 35 40 45
 Ala Ala Asn Trp Arg Asn Gly Ala Asn Lys Leu Leu Gln Met Leu Gln
 50 55 60
 Pro Asn Phe Ala Phe Leu Pro Arg Thr Trp Leu Pro Met Leu Glu Thr
 65 70 75 80
 Leu Gln Met Ala Leu Val Gly Ala Val Leu Ser Ala Ala Val Ser Val
 85 90 95
 Pro Leu Thr Leu Trp Ala Ala Gln Ala Thr Asn Thr Ser Ala Ile Gly
 100 105 110
 Arg Gly Ile Val Arg Thr Ile Ile Asn Val Val Arg Ser Val Pro Asp
 115 120 125
 Leu Val Tyr Ala Thr Ile Leu Val Ala Met Val Gly Val Gly Ala Leu
 130 135 140
 Pro Gly Ile Leu Thr Leu Phe Leu Phe Asn Leu Gly Ile Val Val Lys
 145 150 155 160
 Leu Val Ser Glu Ala Ile Asp Ser Thr Glu His Pro Tyr Met Glu Ala
 165 170 175
 Gly Arg Ala Ala Gly Gly Ser Gln Phe Gln Ile Asn Arg Val Ser Ala
 180 185 190
 Leu Pro Glu Val Met Pro Leu Phe Ala Asn Gln Trp Leu Tyr Thr Leu
 195 200 205
 Glu Leu Asn Val Arg Ile Ser Ala Ile Leu Gly Ile Val Gly Ala Gly
 210 215 220
 Gly Ile Gly Arg Leu Leu Asp Glu Arg Arg Ala Phe Tyr Ala Tyr Ala
 225 230 235 240
 Asp Val Ser Val Ile Ile Leu Glu Ile Leu Ile Val Val Ile Val Ile
 245 250 255
 Glu Val Ile Ser Asn Ala Leu Arg Lys Arg Leu Val
 260 265

<210> 301

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(594)

<223> RXN00193

<400> 301

aaa gct ttc tnc caa cgc gaa ggt ttc atc tca gcc ttc ggt ttc acc 48

Lys Ala Phe Xaa Gln Arg Glu Gly Phe Ile Ser Ala Phe Gly Phe Thr
 1 5 10 15
 gtc ctc gtg gtc atc gtc tcc gtg atc aca gtc aac atc ttc gcc ttc 96
 Val Leu Val Val Ile Val Ser Val Ile Thr Val Asn Ile Phe Ala Phe
 20 25 30
 ctc ttg gcg tgg ttg ctg acc cgc aaa ctc cgc ggt acc aac ttt ttc 144
 Leu Leu Ala Trp Leu Leu Thr Arg Lys Leu Arg Gly Thr Asn Phe Phe
 35 40 45
 cgc aca gtc ttc ttt atg ccg aac ctt atc ggc ggc att gtg ctg ggt 192
 Arg Thr Val Phe Phe Met Pro Asn Leu Ile Gly Gly Ile Val Leu Gly
 50 55 60
 tat acc tgg cag acc atg atc aac gcc gtg ctt tcg cac tat gcc acg 240
 Tyr Thr Trp Gln Thr Met Ile Asn Ala Val Leu Ser His Tyr Ala Thr
 65 70 75 80
 act att agc gcg gac tgg aaa ttc ggc tac gcc ggc ctc atc atg cta 288
 Thr Ile Ser Ala Asp Trp Lys Phe Gly Tyr Ala Gly Leu Ile Met Leu
 85 90 95
 ctt aac tgg cag ctc atc ggc tac atg atg atc att tac atc gcc ggc 336
 Leu Asn Trp Gln Leu Ile Gly Tyr Met Met Ile Ile Tyr Ile Ala Gly
 100 105 110
 ctg caa aac gtc cca cca gag ctc att gag gct gcc gaa ctc gac ggc 384
 Leu Gln Asn Val Pro Pro Glu Leu Ile Glu Ala Ala Glu Leu Asp Gly
 115 120 125
 gtc aac aag tgg gag atg ctg cgg cac gtc act att ccg atg gtc atg 432
 Val Asn Lys Trp Glu Met Leu Arg His Val Thr Ile Pro Met Val Met
 130 135 140
 cca tcc atc acc atc tgc ctc ttt ttg act ttg tcg aac tcc ttt aag 480
 Pro Ser Ile Thr Ile Cys Leu Phe Leu Thr Leu Ser Asn Ser Phe Lys
 145 150 155 160
 ctc ttc gac cag aac ctg gcg ctg acc aac ggc gct cct ggc ggg caa 528
 Leu Phe Asp Gln Asn Leu Ala Leu Thr Asn Gly Ala Pro Gly Gly Gln
 165 170 175
 act gag atg gtg gcg ctc aac atc atc aac acg ctg ttt aac cgt atg 576
 Thr Glu Met Val Ala Leu Asn Ile Ile Asn Thr Leu Phe Asn Arg Met
 180 185 190
 aat gtc gag ggc gtc ggt 594
 Asn Val Glu Gly Val Gly
 195

<210> 302

<211> 198

<212> PRT

<213> Corynebacterium glutamicum

<400> 302

Lys Ala Phe Xaa Gln Arg Glu Gly Phe Ile Ser Ala Phe Gly Phe Thr
 1 5 10 15

Val Leu Val Val Ile Val Ser Val Ile Thr Val Asn Ile Phe Ala Phe
 20 25 30
 Leu Leu Ala Trp Leu Leu Thr Arg Lys Leu Arg Gly Thr Asn Phe Phe
 35 40 45
 Arg Thr Val Phe Phe Met Pro Asn Leu Ile Gly Gly Ile Val Leu Gly
 50 55 60
 Tyr Thr Trp Gln Thr Met Ile Asn Ala Val Leu Ser His Tyr Ala Thr
 65 70 75 80
 Thr Ile Ser Ala Asp Trp Lys Phe Gly Tyr Ala Gly Leu Ile Met Leu
 85 90 95
 Leu Asn Trp Gln Leu Ile Gly Tyr Met Met Ile Ile Tyr Ile Ala Gly
 100 105 110
 Leu Gln Asn Val Pro Pro Glu Leu Ile Glu Ala Ala Glu Leu Asp Gly
 115 120 125
 Val Asn Lys Trp Glu Met Leu Arg His Val Thr Ile Pro Met Val Met
 130 135 140
 Pro Ser Ile Thr Ile Cys Leu Phe Leu Thr Leu Ser Asn Ser Phe Lys
 145 150 155 160
 Leu Phe Asp Gln Asn Leu Ala Leu Thr Asn Gly Ala Pro Gly Gly Gln
 165 170 175
 Thr Glu Met Val Ala Leu Asn Ile Ile Asn Thr Leu Phe Asn Arg Met
 180 185 190
 Asn Val Glu Gly Val Gly
 195

<210> 303
 <211> 940
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (75)..(917)
 <223> FRXA00193

<400> 303
 cctcagcctc ctctcctcac cgccttcccc gctgggaaac gtgtggcacc acctgaaatt 60
 aaggtttcac caccatg caa gca acg ctg aag aag tac ttc cca gtc ttt 110
 Met Gln Ala Thr Leu Lys Lys Tyr Phe Pro Val Phe
 1 5 10
 gtc ttg ccc acc ctt ctg gca ttc atg att gcc ttc ttg gtg ccg ttc 158
 Val Leu Pro Thr Leu Leu Ala Phe Met Ile Ala Phe Leu Val Pro Phe
 15 20 25
 atc gtg ggt ttc ttc ctc tcc ttt acg aag ttc acc act atc acc aac 206
 Ile Val Gly Phe Phe Leu Ser Phe Thr Lys Phe Thr Thr Ile Thr Asn
 30 35 40

gcc aag tgg gtt ggc ata gac aac tac gtc aaa gct ttc tcc caa cgc 254
 Ala Lys Trp Val Gly Ile Asp Asn Tyr Val Lys Ala Phe Ser Gln Arg
 45 50 55 60

gaa ggt ttc atc tca gcc ttc ggt ttc acc gtc ctc gtg gtc atc gtc 302
 Glu Gly Phe Ile Ser Ala Phe Gly Phe Thr Val Leu Val Val Ile Val
 65 70 75

tcc gtg atc aca gtc aac atc ttc gcc ttc ctc ttg gcg tgg ttg ctg 350
 Ser Val Ile Thr Val Asn Ile Phe Ala Phe Leu Leu Ala Trp Leu Leu
 80 85 90

acc cgc aaa ctc cgc ggt acc aac ttt ttc cgc aca gtc ttc ttt atg 398
 Thr Arg Lys Leu Arg Gly Thr Asn Phe Phe Arg Thr Val Phe Phe Met
 95 100 105

ccg aac ctt atc ggc ggc att gtg ctg ggt tat acc tgg cag acc atg 446
 Pro Asn Leu Ile Gly Gly Ile Val Leu Gly Tyr Thr Trp Gln Thr Met
 110 115 120

atc aac gcc gtg ctt tcg cac tat gcc acg act att agc gcg gac tgg 494
 Ile Asn Ala Val Leu Ser His Tyr Ala Thr Thr Ile Ser Ala Asp Trp
 125 130 135 140

aaa ttc ggc tac gcc ggc ctc atc atg cta ctt aac tgg cag ctc atc 542
 Lys Phe Gly Tyr Ala Gly Leu Ile Met Leu Leu Asn Trp Gln Leu Ile
 145 150 155

ggc tac atg atg atc att tac atc gcc ggc ctg caa aac gtc cca cca 590
 Gly Tyr Met Met Ile Ile Tyr Ile Ala Gly Leu Gln Asn Val Pro Pro
 160 165 170

gag ctc att gag gct gcc gaa ctc gac ggc gtc aac aag tgg gag atg 638
 Glu Leu Ile Glu Ala Ala Glu Leu Asp Gly Val Asn Lys Trp Glu Met
 175 180 185

ctg cgg cac gtc act att ccg atg gtc atg cca tcc atc acc atc tgc 686
 Leu Arg His Val Thr Ile Pro Met Val Met Pro Ser Ile Thr Ile Cys
 190 195 200

ctc ttt ttg act ttg tcg aac tcc ttt aag ctc ttc gac cag aac ctg 734
 Leu Phe Leu Thr Leu Ser Asn Ser Phe Lys Leu Phe Asp Gln Asn Leu
 205 210 215 220

gcg ctg acc aac gcc gct cct ggc ggc caa act gag atg gtg gcg ctc 782
 Ala Leu Thr Asn Gly Ala Pro Gly Gly Gln Thr Glu Met Val Ala Leu
 225 230 235

aac atc atc aac acg ctg ttt aac cgt atg aat gtc gag ggc gtc ggt 830
 Asn Ile Ile Asn Thr Leu Phe Asn Arg Met Asn Val Glu Gly Val Gly
 240 245 250

cag gcc aag gcc gtt atc ttc gtc gtc gtt gtg gtc gtc atc gcg tac 878
 Gln Ala Lys Ala Val Ile Phe Val Val Val Val Val Val Ile Ala Tyr
 255 260 265

ttc cag ctg cgc gcg acc cgc tcc aag gaa atc gag gct taagttatga 927
 Phe Gln Leu Arg Ala Thr Arg Ser Lys Glu Ile Glu Ala
 270 275 280

940

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			20					25					30		
Phe	Leu	Ser	Phe	Thr	Lys	Phe	Thr	Thr	Ile	Thr	Asn	Ala	Lys	Trp	Val
		35					40					45			
Gly	Ile	Asp	Asn	Tyr	Val	Lys	Ala	Phe	Ser	Gln	Arg	Glu	Gly	Phe	Ile
	50					55					60				
Ser	Ala	Phe	Gly	Phe	Thr	Val	Leu	Val	Val	Ile	Val	Ser	Val	Ile	Thr
65					70					75					80
Val	Asn	Ile	Phe	Ala	Phe	Leu	Leu	Ala	Trp	Leu	Leu	Thr	Arg	Lys	Leu
				85					90					95	
Arg	Gly	Thr	Asn	Phe	Phe	Arg	Thr	Val	Phe	Phe	Met	Pro	Asn	Leu	Ile
			100					105					110		
Gly	Gly	Ile	Val	Leu	Gly	Tyr	Thr	Trp	Gln	Thr	Met	Ile	Asn	Ala	Val
		115					120					125			
Leu	Ser	His	Tyr	Ala	Thr	Thr	Ile	Ser	Ala	Asp	Trp	Lys	Phe	Gly	Tyr
	130					135					140				
Ala	Gly	Leu	Ile	Met	Leu	Leu	Asn	Trp	Gln	Leu	Ile	Gly	Tyr	Met	Met
145					150					155					160
Ile	Ile	Tyr	Ile	Ala	Gly	Leu	Gln	Asn	Val	Pro	Pro	Glu	Leu	Ile	Glu
				165					170					175	
Ala	Ala	Glu	Leu	Asp	Gly	Val	Asn	Lys	Trp	Glu	Met	Leu	Arg	His	Val
			180					185					190		
Thr	Ile	Pro	Met	Val	Met	Pro	Ser	Ile	Thr	Ile	Cys	Leu	Phe	Leu	Thr
		195					200					205			
Leu	Ser	Asn	Ser	Phe	Lys	Leu	Phe	Asp	Gln	Asn	Leu	Ala	Leu	Thr	Asn
	210					215					220				
Gly	Ala	Pro	Gly	Gly	Gln	Thr	Glu	Met	Val	Ala	Leu	Asn	Ile	Ile	Asn
225					230					235					240
Thr	Leu	Phe	Asn	Arg	Met	Asn	Val	Glu	Gly	Val	Gly	Gln	Ala	Lys	Ala
			245						250					255	
Val	Ile	Phe	Val	Val	Val	Val	Val	Val	Ile	Ala	Tyr	Phe	Gln	Leu	Arg
			260					265					270		
Ala	Thr	Arg	Ser	Lys	Glu	Ile	Glu	Ala							

280

[illegible]

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Tyr Gln Asn Pro Asn Trp Ala Leu Phe Met Val Thr Phe Thr Phe Val
      170                      175                      180

tgg aag aac ttg ggc tac tcc ttt gtt atc tac ctg gct gca ttg cag 691
Trp Lys Asn Leu Gly Tyr Ser Phe Val Ile Tyr Leu Ala Ala Leu Gln
      185                      190                      195

ggg cta aac aag gat ttg tct gag gcc gca ccg gtg gat ggc gcg agc 739
Gly Leu Asn Lys Asp Leu Ser Glu Ala Ala Pro Val Asp Gly Ala Ser
      200                      205                      210

gcg tgg aca cgt ttt tgg aag gtt act ctt ccg cag ctt cgc cca acc 787
Ala Trp Thr Arg Phe Trp Lys Val Thr Leu Pro Gln Leu Arg Pro Thr
      215                      220                      225

acg ttc ttc ctt tct att act gtc acg ctg aac tcg gtt cag gtc ttc 835
Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn Ser Val Gln Val Phe
      230                      235                      240                      245

gac atc att cac acc atg act cgt ggt ggc ccc ttg ggt aac ggt acg 883
Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro Leu Gly Asn Gly Thr
      250                      255                      260

acc acc ttg gtt tac cag gtg tac acc gag act ttc acc aac tat cgc 931
Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr Phe Thr Asn Tyr Arg
      265                      270                      275

gcg gga tat ggt gca aca atc gca acg att ttg ttc ctg ttg ctg ctg 979
Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu Phe Leu Leu Leu Leu
      280                      285                      290

att atc act gtt atc cag gtt cga tac atg gat aag gag aac aag cag 1027
Ile Ile Thr Val Ile Gln Val Arg Tyr Met Asp Lys Glu Asn Lys Gln
      295                      300                      305

aaa tgatctcgac tgatagaaac gtt 1053
Lys
310

<210> 306
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<212> PRT
<213> Corynebacterium glutamicum

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Ala Lys Arg Ser Arg Arg Thr Glu Trp Trp Leu Ala Ala Ala Leu Leu
  20                      25                      30

Ala Pro Asn Leu Leu Leu Leu Ala Ile Phe Thr Tyr Arg Pro Leu Leu
  35                      40                      45

Asp Asn Phe Arg Leu Ser Phe Phe Asn Trp Asn Ile Ser Ser Pro Thr
  50                      55                      60

Ser Thr Phe Ile Gly Phe Asp Asn Tyr Val Glu Phe Phe Thr Arg Ser
  65                      70                      75                      80

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Asp Thr Leu Gln Val Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala
      85                      90                      95

Val Ile Gly Ser Met Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp
      100                      105                      110

Gln Lys Leu Phe Gly Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro
      115                      120                      125

Phe Val Ile Ser Gly Ala Ala Ile Gly Val Ala Phe Gln Phe Val Phe
      130                      135                      140

Asp Pro Asn Phe Gly Leu Val Gln Asp Leu Leu Gly Arg Ile Gly Val
      145                      150                      155                      160

Asp Ser Pro Gln Phe Tyr Gln Asn Pro Asn Trp Ala Leu Phe Met Val
      165                      170                      175

Thr Phe Thr Phe Val Trp Lys Asn Leu Gly Tyr Ser Phe Val Ile Tyr
      180                      185                      190

Leu Ala Ala Leu Gln Gly Leu Asn Lys Asp Leu Ser Glu Ala Ala Pro
      195                      200                      205

Val Asp Gly Ala Ser Ala Trp Thr Arg Phe Trp Lys Val Thr Leu Pro
      210                      215                      220

Gln Leu Arg Pro Thr Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn
      225                      230                      235                      240

Ser Val Gln Val Phe Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro
      245                      250                      255

Leu Gly Asn Gly Thr Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr
      260                      265                      270

Phe Thr Asn Tyr Arg Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu
      275                      280                      285

Phe Leu Leu Leu Leu Ile Ile Thr Val Ile Gln Val Arg Tyr Met Asp
      290                      295                      300

Lys Glu Asn Lys Gln Lys
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<210> 307
<211> 416
<212> DNA
<213> Corynebacterium glutamicum

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<223> FRXA01298

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      1                      5                      10                      15

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ttg cag ggg cta aac aag gat ttg tct gag gcc gca ccg gtg gat ggc 96
Leu Gln Gly Leu Asn Lys Asp Leu Ser Glu Ala Ala Pro Val Asp Gly
      20                      25                      30

gcg agc gcg tgg aca cgt ttt tgg aag gtt act ctt ccg cag ctt cgc 144
Ala Ser Ala Trp Thr Arg Phe Trp Lys Val Thr Leu Pro Gln Leu Arg
      35                      40                      45

cca acc acg ttc ttc ctt tct att act gtc acg ctg aac tcg gtt cag 192
Pro Thr Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn Ser Val Gln
      50                      55                      60

gtc ttc gac atc att cac acc atg act cgt ggt ggc ccc ttg ggt aac 240
Val Phe Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro Leu Gly Asn
      65                      70                      75                      80

ggg acg acc acc ttg gtt tac cag gtg tac acc gag act ttc acc aac 288
Gly Thr Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr Phe Thr Asn
      85                      90                      95

tat cgc gcg gga tat ggt gca aca atc gca acg att ttg ttc ctg ttg 336
Tyr Arg Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu Phe Leu Leu
      100                      105                      110

ctg ctg att atc act gtt atc cag gtt cga tac atg gat aag gag aac 384
Leu Leu Ile Ile Thr Val Ile Gln Val Arg Tyr Met Asp Lys Glu Asn
      115                      120                      125

aag cag aaa tgatctcgac tgatagaaac gtt 416
Lys Gln Lys
      130

<210> 308
<211> 131
<212> PRT
<213> Corynebacterium glutamicum

<400> 308
Phe Val Trp Lys Asn Leu Gly Tyr Ser Phe Val Ile Tyr Leu Ala Ala
  1          5          10          15

Leu Gln Gly Leu Asn Lys Asp Leu Ser Glu Ala Ala Pro Val Asp Gly
      20                      25                      30

Ala Ser Ala Trp Thr Arg Phe Trp Lys Val Thr Leu Pro Gln Leu Arg
      35                      40                      45

Pro Thr Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn Ser Val Gln
      50                      55                      60

Val Phe Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro Leu Gly Asn
      65                      70                      75                      80

Gly Thr Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr Phe Thr Asn
      85                      90                      95

Tyr Arg Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu Phe Leu Leu
      100                      105                      110

Leu Leu Ile Ile Thr Val Ile Gln Val Arg Tyr Met Asp Lys Glu Asn

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115
Lys Gln Lys
130

120

125

<210> 309
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<212> DNA
<213> Corynebacterium glutamicum

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<223> FRXA02422

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aacactaattc ggacatttag gtcacataac atttccgctc gtg tcc aca tta att 115
Val Ser Thr Leu Ile
1 5
tct gaa ccc gag gtg gat aag cta cgt aaa cgt gcc aag aga tca agg 163
Ser Glu Pro Glu Val Asp Lys Leu Arg Lys Arg Ala Lys Arg Ser Arg
10 15 20
cgg aca gaa tgg tgg ctt gcc gcc gca ctt ctt gcc cca aac ttg ctt 211
Arg Thr Glu Trp Trp Leu Ala Ala Ala Leu Leu Ala Pro Asn Leu Leu
25 30 35
ctc ttg gcc atc ttt acg tat cgg cca ctg tta gat aac ttc cgg ttg 259
Leu Leu Ala Ile Phe Thr Tyr Arg Pro Leu Leu Asp Asn Phe Arg Leu
40 45 50
tcc ttt ttc aac tgg aac att tcc tcg ccc aca tca acc ttc att ggg 307
Ser Phe Phe Asn Trp Asn Ile Ser Ser Pro Thr Ser Thr Phe Ile Gly
55 60 65
ttt gat aac tac gtt gag ttc ttc act cgt agt gac act ctc caa gtt 355
Phe Asp Asn Tyr Val Glu Phe Phe Thr Arg Ser Asp Thr Leu Gln Val
70 75 80 85
gtt tta aac acc gtc atc ttc acg gca tgt gct gtg atc gga tcg atg 403
Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala Val Ile Gly Ser Met
90 95 100
gtg ctc ggt ttg ctc ctg gcc atg ttg ttg gat cag aag ctt ttc ggc 451
Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp Gln Lys Leu Phe Gly
105 110 115
cgt aac ttt gtg cgt tcc atg gtg ttt gcc cgg ttt gtg att tcc ggt 499
Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro Phe Val Ile Ser Gly
120 125 130
gct gcc att ggt ggt gct ttc cag ttc gtt ttt gac 535
Ala Ala Ile Gly Gly Ala Phe Gln Phe Val Phe Asp
135 140 145

<210> 310

<211> 145
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 310
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 20 25 30
 Ala Pro Asn Leu Leu Leu Leu Ala Ile Phe Thr Tyr Arg Pro Leu Leu
 35 40 45
 Asp Asn Phe Arg Leu Ser Phe Phe Asn Trp Asn Ile Ser Ser Pro Thr
 50 55 60
 Ser Thr Phe Ile Gly Phe Asp Asn Tyr Val Glu Phe Phe Thr Arg Ser
 65 70 75 80
 Asp Thr Leu Gln Val Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala
 85 90 95
 Val Ile Gly Ser Met Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp
 100 105 110
 Gln Lys Leu Phe Gly Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro
 115 120 125
 Phe Val Ile Ser Gly Ala Ala Ile Gly Gly Ala Phe Gln Phe Val Phe
 130 135 140
 Asp
 145

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 <211> 879
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(856)
 <223> RXN02515

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 tcagtttaaa attcgcttca accctgaaaag attgtgacag atg agc act ctt gaa 115
 Met Ser Thr Leu Glu
 1 5
 atc cgt aac ctg cac gca cag gtc ctg ccg tcc gat gag tcc gct gag 163
 Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser Asp Glu Ser Ala Glu
 10 15 20
 cct aag gaa atc ctc aag ggc gtc aac ctc acc atc aac tct ggt gag 211
 Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr Ile Asn Ser Gly Glu
 25 30 35

atc cac gcc atc atg ggc cct aac ggt tcc ggc aag tcc act ctt gct 259
 Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ala
 40 45 50

tac acc ctt ggt gga cac cca cgc tac gag gta acc gca ggc gag gtc 307
 Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val Thr Ala Gly Glu Val
 55 60 65

ctc ctc gac ggc gag aac atc ctg gag atg gaa gtt gat gag cgt gca 355
 Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu Val Asp Glu Arg Ala
 70 75 80 85

cgc gct ggt ctc ttc ctg gcc atg cag tat cca act gaa atc cct ggc 403
 Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro Thr Glu Ile Pro Gly
 90 95 100

gtt tcc gtt gct aac ttc ctg cgt tcc gca gcg acc gca atc cgc ggc 451
 Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala Thr Ala Ile Arg Gly
 105 110 115

gag gct cct aag ctt cgc gag tgg gtt aag gaa gtc cgc acc gct cag 499
 Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu Val Arg Thr Ala Gln
 120 125 130

gaa gct ctg gca att gac cct gag ttc tcc aac cgc tca gtc aac gaa 547
 Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn Arg Ser Val Asn Glu
 135 140 145

ggt ttc tcc ggt ggc gag aag aag cgc cac gag gtt ctg cag ctt gat 595
 Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu Val Leu Gln Leu Asp
 150 155 160 165

ctg ctg aag cca aag ttc gcg atc atg gat gag acc gac tcc ggc ctt 643
 Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu Thr Asp Ser Gly Leu
 170 175 180

gac gtg gat gca ctg cgc att gtt tcc gag ggc atc aac tcc tac aag 691
 Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly Ile Asn Ser Tyr Lys
 185 190 195

cag gag acc gaa ggt ggc atc ttg atg atc acc cac tac aag cgc atc 739
 Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr His Tyr Lys Arg Ile
 200 205 210

ctc aac tac gtt aag cct gac ttc att cac gtt ttc gcg aat ggc cag 787
 Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val Phe Ala Asn Gly Gln
 215 220 225

att gtg acc acc ggt ggc gct gag ctt gct gac aag ctc gag gct gac 835
 Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp Lys Leu Glu Ala Asp
 230 235 240 245

ggc tac gac cag ttc atc aag taacatgtcc gatttcctca atg 879
 Gly Tyr Asp Gln Phe Ile Lys
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<210> 312

<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 312

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Asp Glu Ser Ala Glu Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr
          20           25           30

Ile Asn Ser Gly Glu Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly
 35           40           45

Lys Ser Thr Leu Ala Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val
 50           55           60

Thr Ala Gly Glu Val Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu
 65           70           75           80

Val Asp Glu Arg Ala Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro
          85           90           95

Thr Glu Ile Pro Gly Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala
          100          105          110

Thr Ala Ile Arg Gly Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu
          115          120          125

Val Arg Thr Ala Gln Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn
          130          135          140

Arg Ser Val Asn Glu Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu
          145          150          155          160

Val Leu Gln Leu Asp Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu
          165          170          175

Thr Asp Ser Gly Leu Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly
          180          185          190

Ile Asn Ser Tyr Lys Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr
          195          200          205

His Tyr Lys Arg Ile Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val
          210          215          220

Phe Ala Asn Gly Gln Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp
          225          230          235          240

Lys Leu Glu Ala Asp Gly Tyr Asp Gln Phe Ile Lys
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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(856)

<223> FRXA02515

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<211> 549
<212> DNA
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				Met	Glu	Thr	Val	Arg									
				1				5									
acc	gca	acc	gcc	gct	cct	gaa	act	gca	tct	ttg	aag	ctg	cgt	gag	gca	163	
Thr	Ala	Thr	Ala	Ala	Pro	Glu	Thr	Ala	Ser	Leu	Lys	Leu	Arg	Glu	Ala		
			10					15						20			
gaa	agc	cca	gca	aag	tcc	cca	aag	aaa	gcc	gcc	ttg	gcg	tca	ctt	ttg	211	
Glu	Ser	Pro	Ala	Lys	Ser	Pro	Lys	Lys	Ala	Ala	Leu	Ala	Ser	Leu	Leu		
			25					30					35				
ggt	tcg	act	ctg	gag	tac	tac	gac	ttt	gtc	att	tac	ggc	acc	gcc	tcc	259	
Gly	Ser	Thr	Leu	Glu	Tyr	Tyr	Asp	Phe	Val	Ile	Tyr	Gly	Thr	Ala	Ser		
		40					45					50					
gcg	ctg	ctg	ttc	aat	cac	ctc	ttc	ttc	cca	cag	ggc	gac	cca	gtc	gtc	307	
Ala	Leu	Leu	Phe	Asn	His	Leu	Phe	Phe	Pro	Gln	Gly	Asp	Pro	Val	Val		
		55				60					65						
gcg	acg	atc	ggc	tct	ctc	gcc	tca	ttc	ggt	gtt	gcg	tac	att	gcg	cgc	355	
Ala	Thr	Ile	Gly	Ser	Leu	Ala	Ser	Phe	Gly	Val	Ala	Tyr	Ile	Ala	Arg		
	70				75				80						85		
ccc	atc	ggt	ggt	ctg	gtg	atg	gga	cat	gtt	ggc	gat	aag	atc	agt	cgc	403	
Pro	Ile	Gly	Gly	Leu	Val	Met	Gly	His	Val	Gly	Asp	Lys	Ile	Ser	Arg		
				90					95					100			
aaa	acc	gcc	ctc	atg	gtg	acg	ttg	atg	atc	atg	ggt	atc	gcc	tcc	att	451	
Lys	Thr	Ala	Leu	Met	Val	Thr	Leu	Met	Ile	Met	Gly	Ile	Ala	Ser	Ile		
			105					110					115				

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atc cgt aac ctg cac gca cag gtc ctg ccg tcc gat gag tcc gct gag 163
Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser Asp Glu Ser Ala Glu
10 15 20

atc cac gcc atc atg ggc cct aac ggt tcc ggc aag tcc act ctt gct 259
Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ala
40 45 50

ctc ctc gac ggc gag aac atc ctg gag atg gaa gtt gat gag cgt gca 355
Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu Val Asp Glu Arg Ala
70 75 80 85

gtt tcc gtt gct aac ttc ctg cgt tcc gca gcg acc gca atc cgc ggc 451
Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala Thr Ala Ile Arg Gly
105 110 115

gaa gct ctg gca att gac cct gag ttc tcc aac cgc tca gtc aac gaa 547
Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn Arg Ser Val Asn Glu
135 140 145

ctg ctg aag cca aag ttc gcg atc atg gat gag acc gac tcc ggc ctt 643
Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu Thr Asp Ser Gly Leu
170 175 180

cag gag acc gaa ggt ggc atc ttg atg atc acc cac tac aag cgc atc 739
Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr His Tyr Lys Arg Ile
200 205 210

ctc aac tac gtt aag cct gac ttc att cac gtt ttc gcg aat ggc cag 787
Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val Phe Ala Asn Gly Gln

[illegible]

ggc tac gac cag ttc atc aag taacatgtcc gatttcctca atg 879
Gly Tyr Asp Gln Phe Ile Lys
250

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Phe Ala Asn Gly Gln Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp
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Lys Leu Glu Ala Asp Gly Tyr Asp Gln Phe Ile Lys
245 250

<210> 315

<211> 1461

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1438)

<223> RXN01995

<400> 315

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octcgaccat tacggtcgcc ctctcctaaa ggagcctggc atg gat atc cgc caa 115
                                         Met Asp Ile Arg Gln
                                         1 5

aca att aac gac aca gca atg tcg aga tat cag tgg ttc att gta ttt 163
Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln Trp Phe Ile Val Phe
          10          15          20

atc gca gtg ctg ctc aac gca ctg gac ggc ttt gat gtc ctc gcc atg 211
Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe Asp Val Leu Ala Met
          25          30          35

tct ttt act gcg aat gca gtg acc gaa gaa ttt gga ctg agt ggc agc 259
Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe Gly Leu Ser Gly Ser
          40          45          50

cag ctt ggt gtg ctg ctg agt tcc gcg ctg ttc ggc atg acc gct gga 307
Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe Gly Met Thr Ala Gly
          55          60          65

tct ttg ctg ttc ggt ccg atc ggt gac cgt ttc ggc cgt aag aat gcc 355
Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe Gly Arg Lys Asn Ala
          70          75          80          85

ctg atg atc gcg ctg ctg ttc aac gtg gtg gga ttg gta ttg tcc gcc 403
Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly Leu Val Leu Ser Ala
          90          95          100

acc gcg cag tcc gca ggc cag ttg ggc gtg tgg cgt ttg atc act ggt 451
Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp Arg Leu Ile Thr Gly
          105          110          115

atc ggc atc ggc gga atc ctc gcc tgc atc aca gtg gtg atc agt gag 499
Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr Val Val Ile Ser Glu
          120          125          130

ttc tcc aac aac aaa aac cgc ggc atg gcc atg tcc atc tac gct gct 547
Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met Ser Ile Tyr Ala Ala
          135          140          145

ggt tac ggc atc ggc gcg tcc ttg ggc ggt ttc ggc gca gcg cag ctc 595
Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe Gly Ala Ala Gln Leu
          150          155          160          165

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atc cca aca ttt gga tgg cgc tcc gtg ttc gca gcc ggt gcg atc gca	643
Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala Ala Gly Ala Ile Ala	
170 175 180	
act ggt atc gcc acc atc gct act ttc ttc ttc ctg cca gaa tcc gtt	691
Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe Leu Pro Glu Ser Val	
185 190 195	
gat tgg ctg agc act cgc cgc cct gcg ggc gct cgc gac aag atc aat	739
Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala Arg Asp Lys Ile Asn	
200 205 210	
tac att gcg cgc cgc ctg ggc aaa gtc ggt acc ttt gag ctt cca ggc	787
Tyr Ile Ala Arg Arg Leu Gly Lys Val Gly Thr Phe Glu Leu Pro Gly	
215 220 225	
gaa caa agc ttg tcg acg aaa aaa gcc ggt ctc caa tcg tat gca gtg	835
Glu Gln Ser Leu Ser Thr Lys Lys Ala Gly Leu Gln Ser Tyr Ala Val	
230 235 240 245	
ctc gtt aac aaa gag aac cgt gga acc agc atc aag ctg tgg gtt gcg	883
Leu Val Asn Lys Glu Asn Arg Gly Thr Ser Ile Lys Leu Trp Val Ala	
250 255 260	
ttc ggc atc gtg atg ttc ggc ttc tac ttc gcc aac act tgg acc ccg	931
Phe Gly Ile Val Met Phe Gly Phe Tyr Phe Ala Asn Thr Trp Thr Pro	
265 270 275	
aag ctg ctc gtg gaa acc gga atg tca gaa cag cag ggc atc atc ggt	979
Lys Leu Val Glu Thr Gly Met Ser Glu Gln Gln Gly Ile Ile Gly	
280 285 290	
ggt ttg atg ttg tcc atg ggt gga gca ttc ggc tcc ctg ctc tac ggt	1027
Gly Leu Met Leu Ser Met Gly Gly Ala Phe Gly Ser Leu Leu Tyr Gly	
295 300 305	
ttc ctc acc acc aag ttc agc tcc cga aac aca ctg atg acc ttc atg	1075
Phe Leu Thr Thr Lys Phe Ser Ser Arg Asn Thr Leu Met Thr Phe Met	
310 315 320 325	
gtg ctg tcc ggc ctg acg ctg atc ctg ttc att tcc tcc acc tct gtt	1123
Val Leu Ser Gly Leu Thr Leu Ile Leu Phe Ile Ser Ser Thr Ser Val	
330 335 340	
cca tcc atc gcg ttt gcc agc ggc gtt gtc gtg ggc atg ctg atc aat	1171
Pro Ser Ile Ala Phe Ala Ser Gly Val Val Val Gly Met Leu Ile Asn	
345 350 355	
ggt tgt gtg gct ggt ctg tac acc ctg tcc cca cag ctg tac tcc gct	1219
Gly Cys Val Ala Gly Leu Tyr Thr Leu Ser Pro Gln Leu Tyr Ser Ala	
360 365 370	
gaa gta cgc acc act ggt gtg ggc gct gcg att ggt atg ggt cgt gtc	1267
Glu Val Arg Thr Thr Gly Val Gly Ala Ala Ile Gly Met Gly Arg Val	
375 380 385	
ggt gcg att tcc gcg cca ctg ctg gtg ggt ggc ctg ctg gat tct ggc	1315
Gly Ala Ile Ser Ala Pro Leu Leu Val Gly Gly Leu Leu Asp Ser Gly	
390 395 400 405	

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tgg tcc cca acg cag ctg tat gtt ggt gtg gca gtg att gtt att gcc 1363
Trp Ser Pro Thr Gln Leu Tyr Val Gly Val Ala Val Ile Val Ile Ala
          410          415          420

ggt gca acc gca ttg att ggg atg cgc act cag gcg gta gcc gtc gaa 1411
Gly Ala Thr Ala Leu Ile Gly Met Arg Thr Gln Ala Val Ala Val Glu
          425          430          435

aag cag cct gaa gcc cta gcg acc aaa tagggccgcg attcctagca 1458
Lys Gln Pro Glu Ala Leu Ala Thr Lys
          440          445

tgc 1461

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<210> 316
<211> 446
<212> PRT
<213> Corynebacterium glutamicum

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<400> 316
Met Asp Ile Arg Gln Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln
 1          5          10          15

Trp Phe Ile Val Phe Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe
          20          25          30

Asp Val Leu Ala Met Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe
          35          40          45

Gly Leu Ser Gly Ser Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe
          50          55          60

Gly Met Thr Ala Gly Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe
          65          70          75          80

Gly Arg Lys Asn Ala Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly
          85          90          95

Leu Val Leu Ser Ala Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp
          100          105          110

Arg Leu Ile Thr Gly Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr
          115          120          125

Val Val Ile Ser Glu Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met
          130          135          140

Ser Ile Tyr Ala Ala Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe
          145          150          155          160

Gly Ala Ala Gln Leu Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala
          165          170          175

Ala Gly Ala Ile Ala Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe
          180          185          190

Leu Pro Glu Ser Val Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala
          195          200          205

Arg Asp Lys Ile Asn Tyr Ile Ala Arg Arg Leu Gly Lys Val Gly Thr

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210 215 220
 Phe Glu Leu Pro Gly Glu Gln Ser Leu Ser Thr Lys Lys Ala Gly Leu
 225 230 235 240
 Gln Ser Tyr Ala Val Leu Val Asn Lys Glu Asn Arg Gly Thr Ser Ile
 245 250 255
 Lys Leu Trp Val Ala Phe Gly Ile Val Met Phe Gly Phe Tyr Phe Ala
 260 265 270
 Asn Thr Trp Thr Pro Lys Leu Leu Val Glu Thr Gly Met Ser Glu Gln
 275 280 285
 Gln Gly Ile Ile Gly Gly Leu Met Leu Ser Met Gly Gly Ala Phe Gly
 290 295 300
 Ser Leu Leu Tyr Gly Phe Leu Thr Thr Lys Phe Ser Ser Arg Asn Thr
 305 310 315 320
 Leu Met Thr Phe Met Val Leu Ser Gly Leu Thr Leu Ile Leu Phe Ile
 325 330 335
 Ser Ser Thr Ser Val Pro Ser Ile Ala Phe Ala Ser Gly Val Val Val
 340 345 350
 Gly Met Leu Ile Asn Gly Cys Val Ala Gly Leu Tyr Thr Leu Ser Pro
 355 360 365
 Gln Leu Tyr Ser Ala Glu Val Arg Thr Thr Gly Val Gly Ala Ala Ile
 370 375 380
 Gly Met Gly Arg Val Gly Ala Ile Ser Ala Pro Leu Leu Val Gly Gly
 385 390 395 400
 Leu Leu Asp Ser Gly Trp Ser Pro Thr Gln Leu Tyr Val Gly Val Ala
 405 410 415
 Val Ile Val Ile Ala Gly Ala Thr Ala Leu Ile Gly Met Arg Thr Gln
 420 425 430
 Ala Val Ala Val Glu Lys Gln Pro Glu Ala Leu Ala Thr Lys
 435 440 445

<210> 317

<211> 754

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(754)

<223> FRXA01995

<400> 317

ccgacgcacaa ggcattgcgcc tgcgtgtctc gagtagtctc ctccccttcc tcgtcccca 60

cctcgacccat tacggtcgcc ctctcctaaa ggagcctggc atg gat atc cgc caa 115

Met Asp Ile Arg Gln

1

5

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aca att aac gac aca gca atg tcg aga tat cag tgg ttc att gta ttt 163
Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln Trp Phe Ile Val Phe
      10      15      20

atc gca gtg ctg ctc aac gca ctg gac ggc ttt gat gtc ctc gcc atg 211
Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe Asp Val Leu Ala Met
      25      30      35

tct ttt act gcg aat gca gtg acc gaa gaa ttt gga ctg agt ggc agc 259
Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe Gly Leu Ser Gly Ser
      40      45      50

cag ctt ggt gtg ctg ctg agt tcc gcg ctg ttc ggc atg acc gct gga 307
Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe Gly Met Thr Ala Gly
      55      60      65

tct ttg ctg ttc ggt ccg atc ggt gac cgt ttc ggc cgt aag aat gcc 355
Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe Gly Arg Lys Asn Ala
      70      75      80      85

ctg atg atc gcg ctg ctg ttc aac gtg gtg gga ttg gta ttg tcc gcc 403
Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly Leu Val Leu Ser Ala
      90      95      100

acc gcg cag tcc gca ggc cag ttg ggc gtg tgg cgt ttg atc act ggt 451
Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp Arg Leu Ile Thr Gly
      105      110      115

atc ggc atc ggc gga atc ctc gcc tgc atc aca gtg gtg atc agt gag 499
Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr Val Val Ile Ser Glu
      120      125      130

ttc tcc aac aac aaa aac cgc ggc atg gcc atg tcc atc tac gct gct 547
Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met Ser Ile Tyr Ala Ala
      135      140      145

ggg tac ggc atc ggc gcg tcc ttg ggc ggt ttc ggc gca gcg cag ctc 595
Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe Gly Ala Ala Gln Leu
      150      155      160      165

atc cca aca ttt gga tgg cgc tcc gtg ttc gca gcc ggt gcg atc gca 643
Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala Ala Gly Ala Ile Ala
      170      175      180

act ggt atc gcc acc atc gct act ttc ttc ttc ctg cca gaa tcc gtt 691
Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe Leu Pro Glu Ser Val
      185      190      195

gat tgg ctg agc act cgc cgc cct gcg ggc gct cgc gac aag atc aat 739
Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala Arg Asp Lys Ile Asn
      200      205      210

tac att gcg cgc cgc
Tyr Ile Ala Arg Arg
      215

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<210> 318

<211> 218

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 318

Met Asp Ile Arg Gln Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln
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Trp Phe Ile Val Phe Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe
20 25 30

Asp Val Leu Ala Met Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe
35 40 45

Gly Leu Ser Gly Ser Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe
50 55 60

Gly Met Thr Ala Gly Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe
65 70 75 80

Gly Arg Lys Asn Ala Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly
85 90 95

Leu Val Leu Ser Ala Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp
100 105 110

Arg Leu Ile Thr Gly Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr
115 120 125

Val	Val	Ile	Ser	Glu	Phe	Ser	Asn	Asn	Lys	Asn	Arg	Gly	Met	Ala	Met
	130					135					140				

Ser Ile Tyr Ala Ala Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe
145 150 155 160

Gly Ala Ala Gln Leu Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala
165 170 175

Ala Gly Ala Ile Ala Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe
180 185 190

Leu Pro Glu Ser Val Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala
195 200 205

Arg Asp Lys Ile Asn Tyr Ile Ala Arg Arg
210 215

<210> 319

<211> 1227

<212> DNA

<213> Corynebacterium glutamicum

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (1204)

<223> RXA01188

<400> 319

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gctttgtagt tttccctccg gtgtccaaga tgaatatgac atg atg aat ggc gtg 115
Met Met Asn Gly Val

	1	5	
gta cag cct cag gaa cat ctc gat gca acg ttg att gct gca gac ttc			163
Val Gln Pro Gln Glu His Leu Asp Ala Thr Leu Ile Ala Ala Asp Phe			
	10	20	
cac ggc aac ccc gaa aac tct ggt gac cgc aaa gag cgc ctg aat ttt			211
His Gly Asn Pro Glu Asn Ser Gly Asp Arg Lys Glu Arg Leu Asn Phe			
	25	35	
caa ggt tgg aag tat gcc ctt aat cgc acg gtc agg gat gtt ttt cca			259
Gln Gly Trp Lys Tyr Ala Leu Asn Arg Thr Val Arg Asp Val Phe Pro			
	40	50	
gat ggc ctg ctc gat ttg gcg gcc ttg ttg acg ttc ttt tcc att ctg			307
Asp Gly Leu Leu Asp Leu Ala Ala Leu Leu Thr Phe Phe Ser Ile Leu			
	55	65	
tcg atc gcc cct gca gtg ctg ctg ggc tat tcg gtg atc acg att ttt			355
Ser Ile Ala Pro Ala Val Leu Leu Gly Tyr Ser Val Ile Thr Ile Phe			
	70	80	85
ctg gcc agt gac tcc acc gaa atc ctc aac ctt gtc cgc gat gag gta			403
Leu Ala Ser Asp Ser Thr Glu Ile Leu Asn Leu Val Arg Asp Glu Val			
	90	95	100
aat cag tac gtt ccg gaa gat caa tcc cat gtt gtc aac ggc gtg att			451
Asn Gln Tyr Val Pro Glu Asp Gln Ser His Val Val Asn Gly Val Ile			
	105	110	115
gat tcg atc gca ggc tcg gca gct gca ggt cag gtc ggt gtc gcg gtc			499
Asp Ser Ile Ala Gly Ser Ala Ala Ala Gly Gln Val Gly Val Ala Val			
	120	125	130
ggt gtg atc acg gca ttg tgg aca tct tcg gca tat gtg cgc gct ttt			547
Gly Val Ile Thr Ala Leu Trp Thr Ser Ser Ala Tyr Val Arg Ala Phe			
	135	140	145
tcc aga tgt gcc aac gct gtt tat ggc cga agc gaa ggc cgc aca ttg			595
Ser Arg Cys Ala Asn Ala Val Tyr Gly Arg Ser Glu Gly Arg Thr Leu			
	150	155	160
atc aaa cgc tgg gca atg ctg ctt ttc ctc aac ctt gct ttg ctg ctt			643
Ile Lys Arg Trp Ala Met Leu Leu Phe Leu Asn Leu Ala Leu Leu Leu			
	170	175	180
gga atc atc atc att ttg gtc tcc tgg gtg ctc aac gag acc ttg gtg			691
Gly Ile Ile Ile Ile Leu Val Ser Trp Val Leu Asn Glu Thr Leu Val			
	185	190	195
atg gga att ttc gcc ccc atc gcg gaa cca ctt cat ctc acg aat gtg			739
Met Gly Ile Phe Ala Pro Ile Ala Glu Pro Leu His Leu Thr Asn Val			
	200	205	210
ctc agc ttc ctc acg gac cgg ttc atg ccg atc tgg atc tgg gtg cgg			787
Leu Ser Phe Leu Thr Asp Arg Phe Met Pro Ile Trp Ile Trp Val Arg			
	215	220	225
ttc cca gtg att gtg ggg gtg ctc atc atg ttc gtg gcc acg ctg tat			835
Phe Pro Val Ile Val Gly Val Leu Ile Met Phe Val Ala Thr Leu Tyr			
	230	235	240
			245


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tac tgg gcc ccg aac gcc cgc ccg tgg aag ttt cgc tgg ctc agc ctc 883
Tyr Trp Ala Pro Asn Ala Arg Pro Trp Lys Phe Arg Trp Leu Ser Leu
                250                255                260

gga tca ttc ttg gcg atc gtt ggc atc ctg ctc gca ggc gtg ggc ttg 931
Gly Ser Phe Leu Ala Ile Val Gly Ile Leu Leu Ala Gly Val Gly Leu
                265                270                275

aat ttc tac ttc acg ctg ttc gcc gct ttt agt tcc tac ggc gcg gtg 979
Asn Phe Tyr Phe Thr Leu Phe Ala Ala Phe Ser Ser Tyr Gly Ala Val
                280                285                290

ggg tcc ctg ctc gcg gtt ttt att gcg ctg tgg gtg ttc aac att tgc 1027
Gly Ser Leu Leu Ala Val Phe Ile Ala Leu Trp Val Phe Asn Ile Cys
                295                300                305

tta atc atc ggc ctg aaa atc gac gtg gag atc agc cgc gcc aag caa 1075
Leu Ile Ile Gly Leu Lys Ile Asp Val Glu Ile Ser Arg Ala Lys Gln
310                315                320                325

ctg cag gca gga atg ccg gcg gag gat tac agt tta gtg cca cca cgc 1123
Leu Gln Ala Gly Met Pro Ala Glu Asp Tyr Ser Leu Val Pro Pro Arg
                330                335                340

tct atc gag aag gtg gcg aaa atg aag cag cgc cag cag cgc ttg atg 1171
Ser Ile Glu Lys Val Ala Lys Met Lys Gln Arg Gln Gln Arg Leu Met
                345                350                355

gat cag gct gcg gcg atc cgg gag gaa agc aat taaaaaattg cttatcgacg 1224
Asp Gln Ala Ala Ala Ile Arg Glu Glu Ser Asn
                360                365

tcc 1227

<210> 320
<211> 368
<212> PRT
<213> Corynebacterium glutamicum

<400> 320
Met Met Asn Gly Val Val Gln Pro Gln Glu His Leu Asp Ala Thr Leu
  1                5                10                15

Ile Ala Ala Asp Phe His Gly Asn Pro Glu Asn Ser Gly Asp Arg Lys
                20                25                30

Glu Arg Leu Asn Phe Gln Gly Trp Lys Tyr Ala Leu Asn Arg Thr Val
  35                40                45

Arg Asp Val Phe Pro Asp Gly Leu Leu Asp Leu Ala Ala Leu Leu Thr
  50                55                60

Phe Phe Ser Ile Leu Ser Ile Ala Pro Ala Val Leu Leu Gly Tyr Ser
  65                70                75                80

Val Ile Thr Ile Phe Leu Ala Ser Asp Ser Thr Glu Ile Leu Asn Leu
                85                90                95

Val Arg Asp Glu Val Asn Gln Tyr Val Pro Glu Asp Gln Ser His Val

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      100              105              110
Val Asn Gly Val Ile Asp Ser Ile Ala Gly Ser Ala Ala Ala Gly Gln
   115              120              125

Val Gly Val Ala Val Gly Val Ile Thr Ala Leu Trp Thr Ser Ser Ala
   130              135              140

Tyr Val Arg Ala Phe Ser Arg Cys Ala Asn Ala Val Tyr Gly Arg Ser
  145              150              155              160

Glu Gly Arg Thr Leu Ile Lys Arg Trp Ala Met Leu Leu Phe Leu Asn
   165              170              175

Leu Ala Leu Leu Leu Gly Ile Ile Ile Ile Leu Val Ser Trp Val Leu
   180              185              190

Asn Glu Thr Leu Val Met Gly Ile Phe Ala Pro Ile Ala Glu Pro Leu
   195              200              205

His Leu Thr Asn Val Leu Ser Phe Leu Thr Asp Arg Phe Met Pro Ile
   210              215              220

Trp Ile Trp Val Arg Phe Pro Val Ile Val Gly Val Leu Ile Met Phe
  225              230              235              240

Val Ala Thr Leu Tyr Tyr Trp Ala Pro Asn Ala Arg Pro Trp Lys Phe
   245              250              255

Arg Trp Leu Ser Leu Gly Ser Phe Leu Ala Ile Val Gly Ile Leu Leu
   260              265              270

Ala Gly Val Gly Leu Asn Phe Tyr Phe Thr Leu Phe Ala Ala Phe Ser
   275              280              285

Ser Tyr Gly Ala Val Gly Ser Leu Leu Ala Val Phe Ile Ala Leu Trp
   290              295              300

Val Phe Asn Ile Cys Leu Ile Ile Gly Leu Lys Ile Asp Val Glu Ile
  305              310              315              320

Ser Arg Ala Lys Gln Leu Gln Ala Gly Met Pro Ala Glu Asp Tyr Ser
   325              330              335

Leu Val Pro Pro Arg Ser Ile Glu Lys Val Ala Lys Met Lys Gln Arg
   340              345              350

Gln Gln Arg Leu Met Asp Gln Ala Ala Ala Ile Arg Glu Glu Ser Asn
   355              360              365

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<210> 321

<211> 717

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<223> RXA01972

acgcgttgct ggatatcacc ctggccgtcg atgacaacgc cgaatgcac c qacgccggat 60

ctg tcg gcg att ggt ctg ttt atc gcc acc aat atc gac gac atc atc 163
Leu Ser Ala Ile Gly Leu Phe Ile Ala Thr Asn Ile Asp Asp Ile Ile
10 15 20

ctt cgg att ctg gct ggt cag tac ctc gcc ttc atg gcc atc ctc gcg 259
Leu Arg Ile Leu Ala Gly Gln Tyr Leu Gly Phe Met Gly Ile Leu Ala
 40 45 50

gcg atc ccg tac ttc gga cta att ccc ctg gcc ctg gga cta tgg gcg 355
Ala Ile Pro Tyr Phe Gly Leu Ile Pro Leu Ala Leu Gly Leu Trp Ala
70 75 80 85

atc gcc ggg aaa aag gtg ggt gtg ctg acc gtc gcc ggt gtg acg ttt 451
Ile Ala Gly Lys Lys Val Gly Val Leu Thr Val Ala Gly Val Thr Phe
105 110 115

gtg gac act gcc gcc gtc atc atc tac tgc atc gtt ttc ctc gtc ctg 547
Val Asp Thr Ala Ala Val Ile Ile Tyr Cys Ile Val Phe Leu Val Leu
135 140 145

atc gca gaa gtc ctt gag cgc tgg gag cac gtg ctg ttc ccg atc gtc 643
Ile Ala Glu Val Leu Glu Arg Trp Glu His Val Leu Phe Pro Ile Val
170 175 180

ctc taataagccc atcccgagcg ccc 717
Leu

Country	Year	Population (millions)	GDP (billion USD)	Urban population (millions)	Urban population (%)	Population density (per sq km)	Life expectancy (years)	Infant mortality (per 1,000 live births)	Health expenditure (billion USD)	Health expenditure (%)
Algeria	2000	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2001	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2002	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2003	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2004	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2005	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2006	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2007	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2008	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2009	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2010	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2011	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2012	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2013	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2014	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2015	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2016	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2017	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2018	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2019	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2020	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2021	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2022	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2023	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2024	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2025	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2026	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2027	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2028	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2029	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2030	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2031	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2032	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2033	24.0	10.0	10.0	41.7	10.0	72.0	10.0	0.5	0.5
Algeria	2034	24.0	10.0	10.0	41.7	10.0	72.0			

<210> 322
 <211> 198
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 322
 Val Ala Thr Gly Leu Leu Ser Ala Ile Gly Leu Phe Ile Ala Thr Asn
 1 5 10 15
 Ile Asp Asp Ile Ile Val Leu Ser Leu Phe Phe Ala Arg Gly Ala Gly
 20 25 30
 Gln Lys Gly Thr Thr Leu Arg Ile Leu Ala Gly Gln Tyr Leu Gly Phe
 35 40 45
 Met Gly Ile Leu Ala Ala Ala Val Leu Val Thr Leu Gly Ala Gly Ala
 50 55 60
 Phe Leu Pro Ala Glu Ala Ile Pro Tyr Phe Gly Leu Ile Pro Leu Ala
 65 70 75 80
 Leu Gly Leu Trp Ala Ala Trp Gln Ala Trp Arg Ser Asp Asp Asp Asp
 85 90 95
 Asp Asp Asp Ala Glu Ile Ala Gly Lys Lys Val Gly Val Leu Thr Val
 100 105 110
 Ala Gly Val Thr Phe Ala Asn Gly Gly Asp Asn Ile Gly Val Tyr Val
 115 120 125
 Pro Val Phe Leu Asn Val Asp Thr Ala Ala Val Ile Ile Tyr Cys Ile
 130 135 140
 Val Phe Leu Val Leu Val Ala Gly Leu Val Leu Leu Ala Lys Phe Val
 145 150 155 160
 Ala Thr Arg Pro Pro Ile Ala Glu Val Leu Glu Arg Trp Glu His Val
 165 170 175
 Leu Phe Pro Ile Val Leu Ile Gly Leu Gly Ile Phe Ile Leu Val Ser
 180 185 190
 Gly Gly Ala Phe Gly Leu
 195

<210> 323
 <211> 978
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(955)
 <223> RXA00311

<400> 323
 cggacagatc ggcatttggg cgaccgtgct gttgatgac gcccgcatcg catagggatt 60

ctctgcagtc	gcagaagctg	caggtgc	atc	cacactgacc	atg	gaa	cat	tct	cct	115
					Met	Glu	His	Ser	Pro	
					1				5	
gaa ggc aag cgt gga ttc ttc acc tca tcg gtg atg gcg ggt tgc tca	163									
Glu Gly Lys Arg Gly Phe Phe Thr Ser Ser Val Met Ala Gly Cys Ser										
	10									
	15									
	20									
gtt gga aac gtc ctg gct ggc ttg gta ttt atc ccg ttc ttg atg ctg	211									
Val Gly Asn Val Leu Ala Gly Leu Val Phe Ile Pro Phe Leu Met Leu										
	25									
	30									
	35									
ccg gaa gaa cac ctc atg tca tgg ggc tgg cgc gta cct ttc ctg ctt	259									
Pro Glu Glu His Leu Met Ser Trp Gly Trp Arg Val Pro Phe Leu Leu										
	40									
	45									
	50									
tcc gca ctg gtt tta gtt gtc gca tac ttc gtg cgc acc cga ctg gag	307									
Ser Ala Leu Val Leu Val Val Ala Tyr Phe Val Arg Thr Arg Leu Glu										
	55									
	60									
	65									
gaa gca tca act gag aag gcc gaa gag gac gca ggc gct ccg gct ttg	355									
Glu Ala Ser Thr Glu Lys Ala Glu Glu Asp Ala Gly Ala Pro Ala Leu										
	70									
	75									
	80									
	85									
gct gtg ctg cgc acc cag ggc att gat gtc gca cga gtt ttc ctg atc	403									
Ala Val Leu Arg Thr Gln Gly Ile Asp Val Ala Arg Val Phe Leu Ile										
	90									
	95									
	100									
acc ttc ttc gcc gtt gtt cag acc act ttc aac gtt tac gca ctg gca	451									
Thr Phe Phe Ala Val Val Gln Thr Thr Phe Asn Val Tyr Ala Leu Ala										
	105									
	110									
	115									
tac gcc gcc aac gaa atc ggc atc gat cgt tcc ttc atg gtg atg gtg	499									
Tyr Ala Ala Asn Glu Ile Gly Ile Asp Arg Ser Phe Met Val Met Val										
	120									
	125									
	130									
aac acc atc gcg ctg ggg ctt tcc atc gga acg att cct ttg gcc gcg	547									
Asn Thr Ile Ala Leu Gly Leu Ser Ile Gly Thr Ile Pro Leu Ala Ala										
	135									
	140									
	145									
tgg gtc tct gac cgc att ggc cgc aag cca gtc ttg ctg ttc ggg gcc	595									
Trp Val Ser Asp Arg Ile Gly Arg Lys Pro Val Leu Leu Phe Gly Ala										
	150									
	155									
	160									
	165									
atc acc tgt gca atc acc acc tac ttc tac ttc cag gca atc tct gaa	643									
Ile Thr Cys Ala Ile Thr Thr Tyr Phe Tyr Phe Gln Ala Ile Ser Glu										
	170									
	175									
	180									
gct gac ctt gtg ctg atc ttc gca ctg tgc ttg gtc aac caa ggt ttg	691									
Ala Asp Leu Val Leu Ile Phe Ala Leu Cys Leu Val Asn Gln Gly Leu										
	185									
	190									
	195									
ttc tac tcc tgc tgg aac ggc gtg tgg acc att ttc ttc cca gaa atg	739									
Phe Tyr Ser Cys Trp Asn Gly Val Trp Thr Thr Ile Phe Phe Pro Glu Met										
	200									
	205									
	210									
ttc gca tct tcc gtg cgc tac acc ggc atg gct atg ggc aac cag ctc	787									
Phe Ala Ser Ser Val Arg Tyr Thr Gly Met Ala Met Met Gly Asn Gln Leu										
	215									
	220									
	225									
ggg ctg atc atc gtt ggt ttc gca cca acc atc gcc acc gcc ctg tac	835									

gtg ctg ttg atg atc gcc cgc atc gca tagggattct ctgcagtcgc 546
Val Leu Leu Met Ile Ala Arg Ile Ala
135 140

aga 549

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<210> 326
<211> 142
<212> PRT
<213> Corynebacterium glutamicum
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<400> 326
Met Glu Thr Val Arg Thr Ala Thr Ala Ala Pro Glu Thr Ala Ser Leu
   1                   5             10              15
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Lys Leu Arg Glu Ala Glu Ser Pro Ala Lys Ser Pro Lys Lys Ala Ala
20 25 30

Leu Ala Ser Leu Leu Gly Ser Thr Leu Glu Tyr Tyr Asp Phe Val Ile
35 40 45

Tyr Gly Thr Ala Ser Ala Leu Leu Phe Asn His Leu Phe Phe Pro Gln
50 55 60

Gly Asp Pro Val Val Ala Thr Ile Gly Ser Leu Ala Ser Phe Gly Val
65 70 75 80

Ala Tyr Ile Ala Arg Pro Ile Gly Gly Leu Val Met Gly His Val Gly
85 90 95

Asp Lys Ile Ser Arg Lys Thr Ala Leu Met Val Thr Leu Met Ile Met
100 105 110

Gly Ile Ala Ser Ile Ser Ile Gly Leu Leu Pro Thr Tyr Gly Gln Ile
115 120 125

Gly Ile Trp Ala Thr Val Leu Leu Met Ile Ala Arg Ile Ala
130 135 140

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<210> 327
<211> 888
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(865)  
<223> RXN01411
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<400> 327
cttatcgacg tccccatccc cctcgccaat gcttcggcga ggggttctat ttattgtgtg 60

tgctagcctt ttcgcaatcg ttcagcccgc cccgacgtca atg ttg gga gtg ggc 115
                Met Leu Gly Val Gly
                1             5

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tgg cgc att cca ttc ctg atg gcc gtg cca cta ggg ctt atc ggc tgg	163
Trp Arg Ile Pro Phe Leu Met Ala Val Pro Leu Gly Leu Ile Gly Trp	
10 15 20	
tgg atc cgc acc ggt gcc cag gaa aat gta cgc ccc gca tcc gaa cgc	211
Trp Ile Arg Thr Gly Ala Gln Glu Asn Val Arg Pro Ala Ser Glu Arg	
25 30 35	
ccc gaa gct cct att aag cag gca ttg cgt act gag tgg aag atg atg	259
Pro Glu Ala Pro Ile Lys Gln Ala Leu Arg Thr Glu Trp Lys Met Met	
40 45 50	
ttg cgg gta ggt ggc ttt atc tct tgc acc ggt ctg agc ttc tac att	307
Leu Arg Val Gly Gly Phe Ile Ser Cys Thr Gly Leu Ser Phe Tyr Ile	
55 60 65	
ttc acc acg tac atg acc act ttc ctg cgc agc acc gtc gga ctg gag	355
Phe Thr Thr Tyr Met Thr Thr Phe Leu Arg Ser Thr Val Gly Leu Glu	
70 75 80 85	
ggc acg tta gtg ctg gct gga aac atc atc gct ctc agc atg gca gca	403
Gly Thr Leu Val Leu Ala Gly Asn Ile Ile Ala Leu Ser Met Ala Ala	
90 95 100	
att gtg gcc cca ttt gtt ggc cgc gca att gat aaa ttc ccc cgc cgg	451
Ile Val Ala Pro Phe Val Gly Arg Ala Ile Asp Lys Phe Pro Arg Arg	
105 110 115	
aac atc atg gct ttc gct acc tta agc aca gta att atg gcg atc ccg	499
Asn Ile Met Ala Phe Ala Thr Leu Ser Thr Val Ile Met Ala Ile Pro	
120 125 130	
gcc tac atc att gca ggt caa ggt act ttg act gct tct ttg att gcg	547
Ala Tyr Ile Ile Ala Gly Gln Gly Thr Leu Thr Ala Ser Leu Ile Ala	
135 140 145	
cag gta atg ctt gga atc ggc gcg gtt acc gct aac tgc gtt acc tca	595
Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala Asn Cys Val Thr Ser	
150 155 160 165	
gta atg atg gcc gag gtc ttc caa gag gtc acc cgc ggt act tcc gcc	643
Val Met Met Ala Glu Val Phe Gln Glu Val Thr Arg Gly Thr Ser Ala	
170 175 180	
ggc att acc tac aac gtc act tac gca atc ttc ggc ggc tcg gct cca	691
Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly Ser Ala Pro	
185 190 195	
ttt atc tcc acc gca ttg gtc tcc tgg acc ggc agc ccg ctg gcc cct	739
Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly Ser Pro Leu Ala Pro	
200 205 210	
gcg gta tac atg atc atc att gcg ctc ttc gcc ttc acc gcg tcc cgc	787
Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala Phe Thr Ala Ser Arg	
215 220 225	
ttc att cct gaa acc tcc cca gtt ttt gtc acc gca acc ccg gcc att	835
Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr Ala Thr Pro Ala Ile	
230 235 240 245	

885

888

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<400> 328
Met Leu Gly Val Gly Trp Arg Ile Pro Phe Leu Met Ala Val Pro Leu
  1             5             10             15
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Pro Ala Ser Glu Arg Pro Glu Ala Pro Ile Lys Gln Ala Leu Arg Thr
35 40 45

Glu Trp Lys Met Met Leu Arg Val Gly Gly Phe Ile Ser Cys Thr Gly
50 55 60

Leu Ser Phe Tyr Ile Phe Thr Thr Tyr Met Thr Thr Phe Leu Arg Ser
65 70 75 80

Thr Val Gly Leu Glu Gly Thr Leu Val Leu Ala Gly Asn Ile Ile Ala
85 90 95

Leu Ser Met Ala Ala Ile Val Ala Pro Phe Val Gly Arg Ala Ile Asp
100 105 110

Lys Phe Pro Arg Arg Asn Ile Met Ala Phe Ala Thr Leu Ser Thr Val
115 120 125

Ile Met Ala Ile Pro Ala Tyr Ile Ile Ala Gly Gln Gly Thr Leu Thr
130 135 140

Ala Ser Leu Ile Ala Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala
145 150 155 160

Asn Cys Val Thr Ser Val Met Met Ala Glu Val Phe Gln Glu Val Thr
165 170 175

Arg Gly Thr Ser Ala Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe
180 185 190

Gly Gly Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly
195 200 205

Ser Pro Leu Ala Pro Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala
210 215 220

Phe Thr Ala Ser Arg Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr
225 230 235 240

Ala Thr Pro Ala Ile Lys Ala Pro Lys Val Leu Val Asn Pro Gly
245 250 255

<210> 329
 <211> 350
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(327)
 <223> FRXA01411

<400> 329
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 Phe Ile Ala Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala Asn Cys
 1 5 10 15
 gtt acc tca gta atg atg gcc gag gtc ttc caa gag gtc acc cgc ggt 96
 Val Thr Ser Val Met Met Ala Glu Val Phe Gln Glu Val Thr Arg Gly
 20 25 30
 act tcc gcc ggc att acc tac aac gtc act tac gca atc ttc ggc ggc 144
 Thr Ser Ala Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly
 35 40 45
 tcg gct cca ttt atc tcc acc gca ttg gtc tcc tgg acc ggc agc ccg 192
 Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly Ser Pro
 50 55 60
 ctg gcc cct gcg gta tac atg atc atc att gcg ctc ttc gcc ttc acc 240
 Leu Ala Pro Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala Phe Thr
 65 70 75 80
 gcg tcc cgc ttc att cct gaa acc tcc cca gtt ttt gtc acc gca acc 288
 Ala Ser Arg Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr Ala Thr
 85 90 95
 ccg gcc att aag gca cca aag gtg ctg gtc aac ccg ggt taaaccacgc 337
 Pro Ala Ile Lys Ala Pro Lys Val Leu Val Asn Pro Gly
 100 105
 ttttcgacga aaa 350

<210> 330
 <211> 109
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 330
 Phe Ile Ala Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala Asn Cys
 1 5 10 15
 Val Thr Ser Val Met Met Ala Glu Val Phe Gln Glu Val Thr Arg Gly
 20 25 30
 Thr Ser Ala Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly
 35 40 45
 Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly Ser Pro
 50 55 60

Leu Ala Pro Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala Phe Thr
 65 70 75 80
 Ala Ser Arg Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr Ala Thr
 85 90 95
 Pro Ala Ile Lys Ala Pro Lys Val Leu Val Asn Pro Gly
 100 105

<210> 331
 <211> 1422
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1399)
 <223> RXA01900

<400> 331
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 cccgttttact cccgcggtcc gtttcagaga agaggtcacc atg aca acc gca gta 115
 Met Thr Thr Ala Val
 1 5
 gat caa aac tca ccg ccc aag cag caa ctc aac aag cgc gtc ctg ctg 163
 Asp Gln Asn Ser Pro Pro Lys Gln Gln Leu Asn Lys Arg Val Leu Leu
 10 15 20
 ggc agc ttg agt ggc agc gtt atc gaa tgg ttc gac ttc ctg gtt tac 211
 Gly Ser Leu Ser Gly Ser Val Ile Glu Trp Phe Asp Phe Leu Val Tyr
 25 30 35
 gga acc gtc gcc gcg ctg gtc ttc aac aag atg tac ttc ccc agc ggc 259
 Gly Thr Val Ala Ala Leu Val Phe Asn Lys Met Tyr Phe Pro Ser Gly
 40 45 50
 aac gag ttc ctc tcc aca atc ctg gcg tac gca tcc ttc tcc ctg acc 307
 Asn Glu Phe Leu Ser Thr Ile Leu Ala Tyr Ala Ser Phe Ser Leu Thr
 55 60 65
 ttc ttc ttc cgc ccc att ggt ggc gtc atc ttc gcc cac atc ggc gac 355
 Phe Phe Phe Arg Pro Ile Gly Gly Val Ile Phe Ala His Ile Gly Asp
 70 75 80 85
 cgc att ggg cgt aag aag acc ctg ttc atc acc ttg atg ctc atg ggt 403
 Arg Ile Gly Arg Lys Lys Thr Leu Phe Ile Thr Leu Met Leu Met Gly
 90 95 100
 ggc ggc acc gtc gcc att ggt ttg ctg ccc gac tac aac gcc atc ggc 451
 Gly Gly Thr Val Ala Ile Gly Leu Leu Pro Asp Tyr Asn Ala Ile Gly
 105 110 115
 att tgg gca cca atc ctt ctg atg ttc ctc cgc att ttg cag ggc atc 499
 Ile Trp Ala Pro Ile Leu Leu Met Phe Leu Arg Ile Leu Gln Gly Ile
 120 125 130
 gga att ggc ggc gaa tgg ggt ggc gca ctg ctc ctg gca tac gaa tac 547
 Gly Ile Gly Gly Glu Trp Gly Gly Ala Leu Leu Leu Ala Tyr Glu Tyr

135					140					145						
gct	cca	aag	aag	cag	cgt	ggg	ctc	tac	ggc	gca	gtt	cct	caa	atg	ggc	595
Ala	Pro	Lys	Lys	Gln	Arg	Gly	Leu	Tyr	Gly	Ala	Val	Pro	Gln	Met	Gly	
150					155					160					165	
att	tcc	ctg	ggc	atg	ctg	ctt	gca	gct	ggc	gtg	atc	tct	ctg	ctc	acc	643
Ile	Ser	Leu	Gly	Met	Leu	Leu	Ala	Ala	Gly	Val	Ile	Ser	Leu	Leu	Thr	
				170					175					180		
ctc	atg	ccg	gaa	gat	cag	ttc	ctc	acc	tgg	ggc	tgg	cgc	atc	cca	ttc	691
Leu	Met	Pro	Glu	Asp	Gln	Phe	Leu	Thr	Trp	Gly	Trp	Arg	Ile	Pro	Phe	
			185					190					195			
gtc	gga	tcc	atc	ctc	cta	gtg	ttc	atc	ggc	ctg	ttc	atc	cga	aac	ggc	739
Val	Gly	Ser	Ile	Leu	Leu	Val	Phe	Ile	Gly	Leu	Phe	Ile	Arg	Asn	Gly	
		200					205					210				
ctt	gat	gaa	acc	ccc	gag	ttc	aag	cgt	atc	cgc	gat	tcc	ggc	cag	cag	787
Leu	Asp	Glu	Thr	Pro	Glu	Phe	Lys	Arg	Ile	Arg	Asp	Ser	Gly	Gln	Gln	
	215					220					225					
gta	aag	atg	cct	ctg	aag	gaa	gtt	ctg	acc	aag	tac	tgg	cca	gcc	gtt	835
Val	Lys	Met	Pro	Leu	Lys	Glu	Val	Leu	Thr	Lys	Tyr	Trp	Pro	Ala	Val	
230					235					240					245	
ctg	gtc	tcc	atc	ggc	gca	aaa	gct	gcc	gag	acc	ggc	ccc	ttc	tac	atc	883
Leu	Val	Ser	Ile	Gly	Ala	Lys	Ala	Ala	Glu	Thr	Gly	Pro	Phe	Tyr	Ile	
				250					255					260		
ttc	ggc	acc	tac	atc	gtt	gct	tac	gca	acc	aac	ttc	ctg	aac	atc	cgc	931
Phe	Gly	Thr	Tyr	Ile	Val	Ala	Tyr	Ala	Thr	Asn	Phe	Leu	Asn	Ile	Arg	
			265				270						275			
gac	aac	att	gtc	ctt	ctg	gca	gtt	gct	tgc	gcc	gcc	ctc	gtt	gcc	acc	979
Asp	Asn	Ile	Val	Leu	Leu	Ala	Val	Ala	Cys	Ala	Ala	Leu	Val	Ala	Thr	
		280					285					290				
atc	tgg	atg	cca	ctg	ttc	gga	tcc	ttc	tcc	gac	cgc	gtc	aac	cgt	gca	1027
Ile	Trp	Met	Pro	Leu	Phe	Gly	Ser	Phe	Ser	Asp	Arg	Val	Asn	Arg	Ala	
	295					300					305					
gtg	ctc	tac	agg	atc	tgt	gca	tcc	gca	acc	atc	gtg	ctg	att	gtc	cct	1075
Val	Leu	Tyr	Arg	Ile	Cys	Ala	Ser	Ala	Thr	Ile	Val	Leu	Ile	Val	Pro	
310					315					320					325	
tac	tac	ttg	gtc	ctc	aac	acc	ggc	gaa	att	tgg	gca	ctg	ttt	atc	act	1123
Tyr	Tyr	Leu	Val	Leu	Asn	Thr	Gly	Glu	Ile	Trp	Ala	Leu	Phe	Ile	Thr	
				330					335					340		
acc	gtg	att	ggc	ttc	ggc	atc	ctc									

gtaaaacccc tcc 1422

<213> Corynebacterium glutamicum

Trp Arg Ile Pro Phe Val Gly Ser Ile Leu Leu Val Phe Ile Gly Leu
195 200 205

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Phe Ile Arg Asn Gly Leu Asp Glu Thr Pro Glu Phe Lys Arg Ile Arg
 210                      215                      220

Asp Ser Gly Gln Gln Val Lys Met Pro Leu Lys Glu Val Leu Thr Lys
225                      230                      235                      240

Tyr Trp Pro Ala Val Leu Val Ser Ile Gly Ala Lys Ala Ala Glu Thr
                245                      250                      255

Gly Pro Phe Tyr Ile Phe Gly Thr Tyr Ile Val Ala Tyr Ala Thr Asn
                260                      265                      270

Phe Leu Asn Ile Arg Asp Asn Ile Val Leu Leu Ala Val Ala Cys Ala
                275                      280                      285

Ala Leu Val Ala Thr Ile Trp Met Pro Leu Phe Gly Ser Phe Ser Asp
                290                      295                      300

Arg Val Asn Arg Ala Val Leu Tyr Arg Ile Cys Ala Ser Ala Thr Ile
305                      310                      315                      320

Val Leu Ile Val Pro Tyr Tyr Leu Val Leu Asn Thr Gly Glu Ile Trp
                325                      330                      335

Ala Leu Phe Ile Thr Thr Val Ile Gly Phe Gly Ile Leu Trp Gly Ser
                340                      345                      350

Val Asn Ala Ile Leu Gly Thr Val Ile Ala Glu Asn Phe Ala Pro Glu
                355                      360                      365

Val Arg Tyr Thr Gly Ala Thr Leu Gly Tyr Gln Val Gly Ala Ala Leu
370                      375                      380

Phe Gly Gly Thr Ala Pro Ile Ile Ala Ala Trp Leu Phe Glu Ile Ser
385                      390                      395                      400

Gly Gly Gln Trp Trp Pro Ile Ala Val Tyr Val Ala Ala Cys Cys Leu
                405                      410                      415

Leu Ser Val Ile Ala Ser Phe Phe Ile Gln Arg Val Ala His Gln Glu
                420                      425                      430

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Asn

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<210> 333
<211> 1524
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1501)
<223> RXA02507

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<400> 333
attaccacac atttcaatcg gtttatacaa ccagcctcta actggcaaca ggactgcaga 60

cagaaactgt tgctggaacc ttcgatgaac aggatcgaca atg agc gaa caa ctt      115
                Met Ser Glu Gln Leu

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	1	5	
cag ggt gta act cac tcc gaa tca act ccg ggc aag acg ccc aag cga	10	20	163
Gln Gly Val Thr His Ser Glu Ser Thr Pro Gly Lys Thr Pro Lys Arg			
gca gca cta tcc agc tgg atc ggc tca gct ctc gaa tac tac gac ttc	25	35	211
Ala Ala Leu Ser Ser Trp Ile Gly Ser Ala Leu Glu Tyr Tyr Asp Phe			
gct gtt tac gga acc gct gca gcg ctg gtt ctt aac cac ctc ttc ttc	40	50	259
Ala Val Tyr Gly Thr Ala Ala Ala Leu Val Leu Asn His Leu Phe Phe			
cca gct gat act tca cca ggc atc gca att ttg gct gcg atg ggt acc	55	65	307
Pro Ala Asp Thr Ser Pro Gly Ile Ala Ile Leu Ala Ala Met Gly Thr			
gtg ggt gtt gct tat gtg gtt cgc cct ctt ggt gcg ctg atc atg ggt	70	80	355
Val Gly Val Ala Tyr Val Val Arg Pro Leu Gly Ala Leu Ile Met Gly			
cca tta ggt gac cgt tac gga cgt aaa ttt gtc ctc atg ctg tgc ctc	90	95	403
Pro Leu Gly Asp Arg Tyr Gly Arg Lys Phe Val Leu Met Leu Cys Leu			
ttc ctg att gga gca tcc act ttc gca gtt ggc tgc ttg cca aca ttt	105	110	451
Phe Leu Ile Gly Ala Ser Thr Phe Ala Val Gly Cys Leu Pro Thr Phe			
gat cag gtc ggt tac ttg gct ccg gca ctg ttg gtg ctg tgc cgt gtg	120	125	499
Asp Gln Val Gly Tyr Leu Ala Pro Ala Leu Leu Val Leu Cys Arg Val			
atc cag gga ctg tct gca tcc ggt gag cag tcc agt gcg att tcc gtt	135	140	547
Ile Gln Gly Leu Ser Ala Ser Gly Glu Gln Ser Ser Ala Ile Ser Val			
tct ttg gag cac gcc gat gag cgt cac cgc gca ttt act gct agc tgg	150	155	595
Ser Leu Glu His Ala Asp Glu Arg His Arg Ala Phe Thr Ala Ser Trp			
act ctt cac gga acc cag ttc ggt acc ttg ctg gca acc gga gta ttt	170	175	643
Thr Leu His Gly Thr Gln Phe Gly Thr Leu Leu Ala Thr Gly Val Phe			
atc cca ttc acc ttg ttc ctg agt gaa gat gct cta atg tca tgg ggt	185	190	691
Ile Pro Phe Thr Leu Phe Leu Ser Glu Asp Ala Leu Met Ser Trp Gly			
tgg cgc gtt ccg ttc tgg ctg tcc gct gct gtt gtt ttg gtt gct ttc	200	205	739
Trp Arg Val Pro Phe Trp Leu Ser Ala Ala Val Val Leu Val Ala Phe			
ctc atc cgt cgt gga ctg gaa gag cca cca gca ttc cgt gaa aac aag	215	220	787
Leu Ile Arg Arg Gly Leu Glu Glu Pro Pro Ala Phe Arg Glu Asn Lys			
gaa gca gtt gca ggc gca gca tct cca ctg gcg atg acc ttg cgt tac	230	235	835
Glu Ala Val Ala Gly Ala Ala Ser Pro Leu Ala Met Thr Leu Arg Tyr			

cac aag gcg gcg gtt gct cgc gtt gct att gct gcg atg atc aac tcc 883
 His Lys Ala Ala Val Ala Arg Val Ala Ile Ala Ala Met Ile Asn Ser
 250 255 260

gtg aac att gtg ttt act gtg tgg gca ctg tcg ttc gcc acc aac att 931
 Val Asn Ile Val Phe Thr Val Trp Ala Leu Ser Phe Ala Thr Asn Ile
 265 270 275

gtt ggc ctg gat cgt tca act gtt ttg ctg gtt cca gtt gtt gcg aac 979
 Val Gly Leu Asp Arg Ser Thr Val Leu Leu Val Pro Val Val Ala Asn
 280 285 290

ttg gtt gca ctg att gcg att cct ttg tcc ggc atg ctg gct gac cgc 1027
 Leu Val Ala Leu Ile Ala Ile Pro Leu Ser Gly Met Leu Ala Asp Arg
 295 300 305

att ggt cgc cga cca gtg ttc atc atg ggt gcc att ggt ggt ggc ctg 1075
 Ile Gly Arg Arg Pro Val Phe Ile Met Gly Ala Ile Gly Gly Gly Leu
 310 315 320 325

gcc atg aac ggt tac ctg gga gct atc tac tcc ggc aat tgg acc atg 1123
 Ala Met Asn Gly Tyr Leu Gly Ala Ile Tyr Ser Gly Asn Trp Thr Met
 330 335 340

atc ttc ttc atg ggc gtg ttg atg tct ggt ctg ctg tac tcc atg ggt 1171
 Ile Phe Phe Met Gly Val Leu Met Ser Gly Leu Leu Tyr Ser Met Gly
 345 350 355

aat gcc gtg tgg cca gcg ttc tac gca gaa atg ttc cca acc tct gtg 1219
 Asn Ala Val Trp Pro Ala Phe Tyr Ala Glu Met Phe Pro Thr Ser Val
 360 365 370

cgt gtc acc ggc ttg gct ctt gga act cag att ggt ttc gca gtc tct 1267
 Arg Val Thr Gly Leu Ala Leu Gly Thr Gln Ile Gly Phe Ala Val Ser
 375 380 385

ggt ggt ttc gtc cca gtt atc gca tcc gcg ctt gct ggt gat cag ggt 1315
 Gly Gly Phe Val Pro Val Ile Ala Ser Ala Leu Ala Gly Asp Gln Gly
 390 395 400 405

gac cag tgg atg aag gtg tcc atc ttc gtt ggt gtt gtt tgt gtg att 1363
 Asp Gln Trp Met Lys Val Ser Ile Phe Val Gly Val Val Cys Val Ile
 410 415 420

tct gca ctg gtt gcc atg acc gct aag gaa acc aag gct ctg act ctg 1411
 Ser Ala Leu Val Ala Met Thr Ala Lys Glu Thr Lys Ala Leu Thr Leu
 425 430 435

gat gag atc gat gct ctg cac act gct ggt ggt gag gcc gca gac ctg 1459
 Asp Glu Ile Asp Ala Leu His Thr Ala Gly Gly Glu Ala Ala Asp Leu
 440 445 450

gca gcc gca agc aaa gcc tcc gag gcc caa ctc gcg gct cag 1501
 Ala Ala Ala Ser Lys Ala Ser Glu Ala Gln Leu Ala Ala Gln
 455 460 465

taaaacaaaa aggaatcttt gac 1524

<210> 334

<212> PRT

<213> Corynebacterium glutamicum

Met Ser Glu Gln Leu Gln Gly Val Thr His Ser Glu Ser Thr Pro Gly
1 5 10 15

Lys Thr Pro Lys Arg Ala Ala Leu Ser Ser Trp Ile Gly Ser Ala Leu
20 25 30

Glu Tyr Tyr Asp Phe Ala Val Tyr Gly Thr Ala Ala Ala Leu Val Leu
35 40 45

Asn His Leu Phe Phe Pro Ala Asp Thr Ser Pro Gly Ile Ala Ile Leu
50 55 60

Ala Ala Met Gly Thr Val Gly Val Ala Tyr Val Val Arg Pro Leu Gly
65 70 75 80

Ala Leu Ile Met Gly Pro Leu Gly Asp Arg Tyr Gly Arg Lys Phe Val
85 90 95

Leu Met Leu Cys Leu Phe Leu Ile Gly Ala Ser Thr Phe Ala Val Gly
100 105 110

Cys Leu Pro Thr Phe Asp Gln Val Gly Tyr Leu Ala Pro Ala Leu Leu
115 120 125

Val Leu Cys Arg Val Ile Gln Gly Leu Ser Ala Ser Gly Glu Gln Ser
130 135 140

Ser Ala Ile Ser Val Ser Leu Glu His Ala Asp Glu Arg His Arg Ala
145 150 155 160

Phe Thr Ala Ser Trp Thr Leu His Gly Thr Gln Phe Gly Thr Leu Leu
165 170 175

Ala Thr Gly Val Phe Ile Pro Phe Thr Leu Phe Leu Ser Glu Asp Ala
180 185 190

Leu Met Ser Trp Gly Trp Arg Val Pro Phe Trp Leu Ser Ala Ala Val
195 200 205

Val Leu Val Ala Phe Leu Ile Arg Arg Gly Leu Glu Glu Pro Pro Ala
210 215 220

Phe Arg Glu Asn Lys Glu Ala Val Ala Gly Ala Ala Ser Pro Leu Ala
225 230 235 240

Met Thr Leu Arg Tyr His Lys Ala Ala Val Ala Arg Val Ala Ile Ala
245 250 255

Ala Met Ile Asn Ser Val Asn Ile Val Phe Thr Val Trp Ala Leu Ser
260 265 270

Phe Ala Thr Asn Ile Val Gly Leu Asp Arg Ser Thr Val Leu Leu Val
275 280 285

Pro Val Val Ala Asn Leu Val Ala Leu Ile Ala Ile Pro Leu Ser Gly
290 295 300[illegible]

Met Leu Ala Asp Arg Ile Gly Arg Arg Pro Val Phe Ile Met Gly Ala
305 310 315 320

Ile Gly Gly Gly Leu Ala Met Asn Gly Tyr Leu Gly Ala Ile Tyr Ser
325 330 335

Gly Asn Trp Thr Met Ile Phe Phe Met Gly Val Leu Met Ser Gly Leu
340 345 350

Leu Tyr Ser Met Gly Asn Ala Val Trp Pro Ala Phe Tyr Ala Glu Met
355 360 365

Phe Pro Thr Ser Val Arg Val Thr Gly Leu Ala Leu Gly Thr Gln Ile
370 375 380

Gly Phe Ala Val Ser Gly Gly Phe Val Pro Val Ile Ala Ser Ala Leu
385 390 395 400

Ala Gly Asp Gln Gly Asp Gln Trp Met Lys Val Ser Ile Phe Val Gly
405 410 415

Val Val Cys Val Ile Ser Ala Leu Val Ala Met Thr Ala Lys Glu Thr
420 425 430

Lys Ala Leu Thr Leu Asp Glu Ile Asp Ala Leu His Thr Ala Gly Gly
435 440 445

Glu Ala Ala Asp Leu Ala Ala Ala Ser Lys Ala Ser Glu Ala Gln Leu
450 455 460

Ala Ala Gln
465

<210> 335

<211> 955

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (21)..(932)

<223> RXA00445

<400> 335

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Met Ala Asp Leu Ser Ile Glu His Val Ser Arg
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ttt ttc ggc gat gcc atc gcc ttg aac gat gtg tca ttg acc gtc ccc 101
Phe Phe Gly Asp Ala Ile Ala Leu Asn Asp Val Ser Leu Thr Val Pro
15 20 25

tca ggc tcc atc acc gcc atc atc ggg ccg tcc ggg agc ggt aaa acc 149
Ser Gly Ser Ile Thr Ala Ile Ile Gly Pro Ser Gly Ser Gly Lys Thr
30 35 40

acg tta ctg cgt ttg ctg gca ggc ctt gat tca ccc gat gaa ggc acc 197
Thr Leu Leu Arg Leu Leu Ala Gly Leu Asp Ser Pro Asp Glu Gly Thr
45 50 55

ggtgcaaaaaaggactaaccatg gcg gat ctg agc att gaa cac gta tca agg 53

gtg agc att ggg aat aag atc gcc aag ctg ggt gac act gcg ctg tgt	245
Val Ser Ile Gly Asn Lys Ile Ala Lys Leu Gly Asp Thr Ala Leu Cys	
60 65 70 75	
ttc cag gat tcg cct ttg tat ccg cac ctt aat gtg tgg gaa aac gtg	293
Phe Gln Asp Ser Pro Leu Tyr Pro His Leu Asn Val Trp Glu Asn Val	
80 85 90	
gca ttt ccg ctc aag ctc aaa gcc acc aat act gca gat gag gtg gtg	341
Ala Phe Pro Leu Lys Leu Lys Ala Thr Asn Thr Ala Asp Glu Val Val	
95 100 105	
aaa aag cgg gtg agt gat gtt ttg gaa atg ctc gaa att gct ccc ctc	389
Lys Lys Arg Val Ser Asp Val Leu Glu Met Leu Glu Ile Ala Pro Leu	
110 115 120	
gcc cgc cgg aaa att acc gaa ctc tcc ggc ggg caa aaa cag cgc gtc	437
Ala Arg Arg Lys Ile Thr Glu Leu Ser Gly Gly Gln Lys Gln Arg Val	
125 130 135	
ggc att gct cga gca ctg gtc aga gac gta gag gtt tac ctt ttc gac	485
Gly Ile Ala Arg Ala Leu Val Arg Asp Val Glu Val Tyr Leu Phe Asp	
140 145 150 155	
gaa ccg atg gcc cac ctc gac caa gcc tta gcc cgc gat att gtg gcc	533
Glu Pro Met Ala His Leu Asp Gln Ala Leu Ala Arg Asp Ile Val Ala	
160 165 170	
gat ctg cgc aaa att caa caa tcg ttg gga ctg acg ttt gta tac gtc	581
Asp Leu Arg Lys Ile Gln Gln Ser Leu Gly Leu Thr Phe Val Tyr Val	
175 180 185	
acc cac agc aaa tcc gag gca ttc gcg ctc gcc gac caa att gtc gtg	629
Thr His Ser Lys Ser Glu Ala Phe Ala Leu Ala Asp Gln Ile Val Val	
190 195 200	
ctg gta gat ggc caa gtc gcg cag gtt ggt gag gcg gag gag ctc gtc	677
Leu Val Asp Gly Gln Val Ala Gln Val Gly Glu Ala Glu Glu Leu Val	
205 210 215	
gaa aag cca aaa acc cta gaa ata gcc gag ttc ctc tcc ccc acc gag	725
Glu Lys Pro Lys Thr Leu Glu Ile Ala Glu Phe Leu Ser Pro Thr Glu	
220 225 230 235	
ctc aat gtg cgc cgg cgt ggg gac gcc gtg gag gca tgg cga ccc gaa	773
Leu Asn Val Arg Arg Gly Asp Ala Val Glu Ala Trp Arg Pro Glu	
240 245 250	
gac acc cag ctc gcc cgc ggt ggc act gcg acc gtg gaa gcc gtg acg	821
Asp Thr Gln Leu Ala Arg Gly Gly Thr Ala Thr Val Glu Ala Val Thr	
255 260 265	
tat ttg ggc cgc gag tgg ctt gta caa acc acc gag ggg cac gcc gtg	869
Tyr Leu Gly Arg Glu Trp Leu Val Gln Thr Thr Glu Gly His Ala Val	
270 275 280	
tcg gag gaa aaa ttc gac gtc ggc gaa agc gtc acg cta acc cag aag	917
Ser Glu Glu Lys Phe Asp Val Gly Glu Ser Val Thr Leu Thr Gln Lys	
285 290 295	

955

<400> 336

Met	Ala	Asp	Leu	Ser	Ile	Glu	His	Val	Ser	Arg	Phe	Phe	Gly	Asp	Ala
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Ile	Ala	Leu	Asn	Asp	Val	Ser	Leu	Thr	Val	Pro	Ser	Gly	Ser	Ile	Thr
			20					25					30		
Ala	Ile	Ile	Gly	Pro	Ser	Gly	Ser	Gly	Lys	Thr	Thr	Leu	Leu	Arg	Leu
		35					40					45			
Leu	Ala	Gly	Leu	Asp	Ser	Pro	Asp	Glu	Gly	Thr	Val	Ser	Ile	Gly	Asn
	50					55					60				
Lys	Ile	Ala	Lys	Leu	Gly	Asp	Thr	Ala	Leu	Cys	Phe	Gln	Asp	Ser	Pro
65					70					75					80
Leu	Tyr	Pro	His	Leu	Asn	Val	Trp	Glu	Asn	Val	Ala	Phe	Pro	Leu	Lys
				85					90					95	
Leu	Lys	Ala	Thr	Asn	Thr	Ala	Asp	Glu	Val	Val	Lys	Lys	Arg	Val	Ser
			100					105					110		
Asp	Val	Leu	Glu	Met	Leu	Glu	Ile	Ala	Pro	Leu	Ala	Arg	Arg	Lys	Ile
		115					120					125			
Thr	Glu	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Val	Gly	Ile	Ala	Arg	Ala
	130					135					140				
Leu	Val	Arg	Asp	Val	Glu	Val	Tyr	Leu	Phe	Asp	Glu	Pro	Met	Ala	His
145					150					155					160
Leu	Asp	Gln	Ala	Leu	Ala	Arg	Asp	Ile	Val	Ala	Asp	Leu	Arg	Lys	Ile
				165					170					175	
Gln	Gln	Ser	Leu	Gly	Leu	Thr	Phe	Val	Tyr	Val	Thr	His	Ser	Lys	Ser
			180					185					190		
Glu	Ala	Phe	Ala	Leu	Ala	Asp	Gln	Ile	Val	Val	Leu	Val	Asp	Gly	Gln
		195					200					205			
Val	Ala	Gln	Val	Gly	Glu	Ala	Glu	Glu	Leu	Val	Glu	Lys	Pro	Lys	Thr
	210					215					220				
Leu	Glu	Ile	Ala	Glu	Phe	Leu	Ser	Pro	Thr	Glu	Leu	Asn	Val	Arg	Arg
225					230					235					240
Arg	Gly	Asp	Ala	Val	Glu	Ala	Trp	Arg	Pro	Glu	Asp	Thr	Gln	Leu	Ala
				245					250					255	
Arg	Gly	Gly	Thr	Ala	Thr	Val	Glu	Ala	Val	Thr	Tyr	Leu	Gly	Arg	Glu
			260					265					270		

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<210> 337
<211> 491
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(468)
<223> RXA02353
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<400> 337																	
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Met	Ala	Leu	Leu	Ile	Leu	Ala	Gly	Leu	Gln	Met	Ile	Pro	Lys	Glu	Thr		
1				5				10						15			
tac	gaa	gca	gcc	cgc	gtc	gat	ggc	gca	acc	gcg	tgg	cag	caa	ttc	acc	96	
Tyr	Glu	Ala	Ala	Arg	Val	Asp	Gly	Ala	Thr	Ala	Trp	Gln	Gln	Phe	Thr		
			20					25					30				
aag	atc	acc	ctc	ccg	ctg	gtg	cgc	cca	gct	ttg	atg	gtg	gca	gta	ctc	144	
Lys	Ile	Thr	Leu	Pro	Leu	Val	Arg	Pro	Ala	Leu	Met	Val	Ala	Val	Leu		
		35					40					45					
ttc	cgc	acc	ctc	gat	gcg	cta	cgc	atg	tat	gac	ctc	ccc	gtc	atc	atg	192	
Phe	Arg	Thr	Leu	Asp	Ala	Leu	Arg	Met	Tyr	Asp	Leu	Pro	Val	Ile	Met		
	50					55					60						
atc	tcc	agc	tcc	tcc	aac	tcc	ccc	acc	gct	gtt	atc	tcc	cag	ctg	gtt	240	
Ile	Ser	Ser	Ser	Ser	Asn	Ser	Pro	Thr	Ala	Val	Ile	Ser	Gln	Leu	Val		
65					70					75					80		
gtg	gaa	gac	atg	cgc	caa	aac	aac	ttc	aac	tcc	gct	tcc	gcc	ctt	tcc	288	
Val	Glu	Asp	Met	Arg	Gln	Asn	Asn	Phe	Asn	Ser	Ala	Ser	Ala	Leu	Ser		
				85					90					95			
aca	ctg	atc	ttc	ctg	ctg	atc	ttc	ttc	gtg	gcg	ttc	atc	atg	atc	cga	336	
Thr	Leu	Ile	Phe	Leu	Leu	Ile	Phe	Phe	Val	Ala	Phe	Ile	Met	Ile	Arg		
			100					105					110				
ttc	ctc	ggc	gca	gat	gtt	tcg	ggc	caa	cgc	gga	ata	aag	aaa	aag	aaa	384	
Phe	Leu	Gly	Ala	Asp	Val	Ser	Gly	Gln	Arg	Gly	Ile	Lys	Lys	Lys	Lys		
		115					120					125					
ctg	ggc	gga	acc	aag	gat	gag	aaa	ccc	acc	gct	aag	gat	gct	gtt	gta	432	
Leu	Gly	Gly	Thr	Lys	Asp	Glu	Lys	Pro	Thr	Ala	Lys	Asp	Ala	Val	Val		
	130					135					140						
aag	gcc	gat	tct	gct	gtg	aag	gaa	gcc	gct	aag	cca	tgactaaacg				478	
Lys	Ala	Asp	Ser	Ala	Val	Lys	Glu	Ala	Ala	Lys	Pro						
145					150				155								

aacaaaagga ctc

491

<210> 338

<211> 156

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Met Ala Leu Leu Ile Leu Ala Gly Leu Gln Met Ile Pro Lys Glu Thr
1 5 10 15

Tyr Glu Ala Ala Arg Val Asp Gly Ala Thr Ala Trp Gln Gln Phe Thr
20 25 30

Lys Ile Thr Leu Pro Leu Val Arg Pro Ala Leu Met Val Ala Val Leu
35 40 45

Phe Arg Thr Leu Asp Ala Leu Arg Met Tyr Asp Leu Pro Val Ile Met
50 55 60

Ile Ser Ser Ser Ser Asn Ser Pro Thr Ala Val Ile Ser Gln Leu Val
65 70 75 80

Val Glu Asp Met Arg Gln Asn Asn Phe Asn Ser Ala Ser Ala Leu Ser
85 90 95

Thr Leu Ile Phe Leu Leu Ile Phe Phe Val Ala Phe Ile Met Ile Arg
100 105 110

Phe Leu Gly Ala Asp Val Ser Gly Gln Arg Gly Ile Lys Lys Lys Lys
115 120 125

Leu Gly Gly Thr Lys Asp Glu Lys Pro Thr Ala Lys Asp Ala Val Val
130 135 140

Lys Ala Asp Ser Ala Val Lys Glu Ala Ala Lys Pro
145 150 155

<210> 339

<211> 921

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101) .. (898)

<223> RXA01297

<400> 339

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agaaatgata tcgactgata gaaacgtttt ggtcaaaatc atg ggc tat gtc ggc 115
Met Gly Tyr Val Gly
1 5

atg gtt ctt gcc atc ttg ttc att ggc ctt ccg ctg gta ttt att gtg 163
Met Val Leu Ala Ile Leu Phe Ile Gly Leu Pro Leu Val Phe Ile Val
10 15 20

ctg act agc ttc aag cag cag tca gag att tac acc cag ccg gtc acg	211
Leu Thr Ser Phe Lys Gln Gln Ser Glu Ile Tyr Thr Gln Pro Val Thr	
25 30 35	
tgg ttc cct tcg gaa ttt aat ttc gat aac tat gca aat gtt ttc gag	259
Trp Phe Pro Ser Glu Phe Asn Phe Asp Asn Tyr Ala Asn Val Phe Glu	
40 45 50	
cgg gtt ccg ttc ctg aac tac ttc cgc aac tcg atc atc atc acg gtt	307
Arg Val Pro Phe Leu Asn Tyr Phe Arg Asn Ser Ile Ile Ile Thr Val	
55 60 65	
att ttg tgt ctg gtg aag att atc ttg ggt gtg atc tct gca tat gcg	355
Ile Leu Cys Leu Val Lys Ile Ile Leu Gly Val Ile Ser Ala Tyr Ala	
70 75 80 85	
ttg tcg att ttg cgc ttc ccg ggt cga aac ctt gtg ttc ttg ctg gtt	403
Leu Ser Ile Leu Arg Phe Pro Gly Arg Asn Leu Val Phe Leu Leu Val	
90 95 100	
atc tcc gcg ctg atg gtg cct tcc gaa gtg act gtt att tcc aac tat	451
Ile Ser Ala Leu Met Val Pro Ser Glu Val Thr Val Ile Ser Asn Tyr	
105 110 115	
gcg ttg gtc agt cag ctt ggt tgg cgc gat acc tac cag gcc atc atc	499
Ala Leu Val Ser Gln Leu Gly Trp Arg Asp Thr Tyr Gln Gly Ile Ile	
120 125 130	
gtt ccg cta gcg ggt att gct ttc gga acg ttc ctc atg cgt aac cac	547
Val Pro Leu Ala Gly Ile Ala Phe Gly Thr Phe Leu Met Arg Asn His	
135 140 145	
ttc atg tct att cct tct gag ctc att gaa gct gcg cga atg gat cac	595
Phe Met Ser Ile Pro Ser Glu Leu Ile Glu Ala Ala Arg Met Asp His	
150 155 160 165	
tgt gga cac ttc agg ttg ctc tgg aag gtt ttg ctt cca atc tct atg	643
Cys Gly His Phe Arg Leu Leu Trp Lys Val Leu Leu Pro Ile Ser Met	
170 175 180	
cct acg ttg gtg gcg ttc tcc atg atc acc gtg gtg aat gaa tgg aac	691
Pro Thr Leu Val Ala Phe Ser Met Ile Thr Val Val Asn Glu Trp Asn	
185 190 195	
caa tac ctg tgg cct ttc ctg atg gca gaa acc gat aat tca gca act	739
Gln Tyr Leu Trp Pro Phe Leu Met Ala Glu Thr Asp Asn Ser Ala Thr	
200 205 210	
ctg ccc att ggt ttg acc atg ctt caa aac aat gag ggt gtc tcc aac	787
Leu Pro Ile Gly Leu Thr Met Leu Gln Asn Asn Glu Gly Val Ser Asn	
215 220 225	
tgg gga cct gtc atg gcc gca acg atc atg acc atg ttg cct gtg ctt	835
Trp Gly Pro Val Met Ala Ala Thr Ile Met Thr Met Leu Pro Val Leu	
230 235 240 245	
gtg atg ttc ttg gca ctg cag gag tac atg atc aag gga ctt atc tcc	883
Val Met Phe Leu Ala Leu Gln Glu Tyr Met Ile Lys Gly Leu Ile Ser	
250 255 260	

921

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<210> 340
<211> 266
<212> PRT
<213> Corynebacterium glutamicum
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<400> 340
Met Gly Tyr Val Gly Met Val Leu Ala Ile Leu Phe Ile Gly Leu Pro
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Leu Val Phe Ile Val Leu Thr Ser Phe Lys Gln Gln Ser Glu Ile Tyr
20 25 30

Thr Gln Pro Val Thr Trp Phe Pro Ser Glu Phe Asn Phe Asp Asn Tyr
35 40 45

Ala Asn Val Phe Glu Arg Val Pro Phe Leu Asn Tyr Phe Arg Asn Ser
50 55 60

Ile Ile Ile Thr Val Ile Leu Cys Leu Val Lys Ile Ile Leu Gly Val
65 70 75 80

Ile Ser Ala Tyr Ala Leu Ser Ile Leu Arg Phe Pro Gly Arg Asn Leu
85 90 95

Val Phe Leu Leu Val Ile Ser Ala Leu Met Val Pro Ser Glu Val Thr
100 105 110

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Val Ile Ser Asn Tyr Ala Leu Val Ser Gln Leu Gly Trp Arg Asp Thr
      115                      120                      125
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Tyr Gln Gly Ile Ile Val Pro Leu Ala Gly Ile Ala Phe Gly Thr Phe
130 135 140

Leu Met Arg Asn His Phe Met Ser Ile Pro Ser Glu Leu Ile Glu Ala
145 150 155 160

Ala Arg Met Asp His Cys Gly His Phe Arg Leu Leu Trp Lys Val Leu
165 170 175

Leu Pro Ile Ser Met Pro Thr Leu Val Ala Phe Ser Met Ile Thr Val
180 185 190

Val Asn Glu Trp Asn Gln Tyr Leu Trp Pro Phe Leu Met Ala Glu Thr
195 200 205

Asp Asn Ser Ala Thr Leu Pro Ile Gly Leu Thr Met Leu Gln Asn Asn
210 215 220

Glu Gly Val Ser Asn Trp Gly Pro Val Met Ala Ala Thr Ile Met Thr
225 230 235 240

Met Leu Pro Val Leu Val Met Phe Leu Ala Leu Gln Glu Tyr Met Ile
245 250 255

Lys Gly Leu Ile Ser Gly Ala Val Lys Gly
260 265

<210> 341
 <211> 899
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(876)
 <223> RXS00088

<400> 341

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gtc gct gcg acc gac aac cgc gca ttc gaa ctg ctt gat cgc tgg ggt	96
Val Ala Ala Thr Asp Asn Arg Ala Phe Glu Leu Leu Asp Arg Trp Gly	
20 25 30	
gta gag ctc gtt gca gct cca ctt cag ctg gtt cca ttt acc gtt acg	144
Val Glu Leu Val Ala Ala Pro Leu Gln Leu Val Pro Phe Thr Val Thr	
35 40 45	
ggc tac acc gaa gag ggc ggc gtc gct aac ctt ggc tcc cac cgc gag	192
Gly Tyr Thr Glu Glu Gly Gly Val Ala Asn Leu Gly Ser His Arg Glu	
50 55 60	
cca gac ctg gaa gca ctt gct gct gca cag cct tcc ctg atc atc aac	240
Pro Asp Leu Glu Ala Leu Ala Ala Ala Gln Pro Ser Leu Ile Ile Asn	
65 70 75 80	
ggc cag cgc ttc gct cag tac tac gat gac atc att gcc ctg aac cct	288
Gly Gln Arg Phe Ala Gln Tyr Tyr Asp Asp Ile Ile Ala Leu Asn Pro	
85 90 95	
gac gca acc gtt gtt gag cta gac cca cgc gat ggc gag cca ctt gac	336
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Gln Glu Leu Ile Arg Gln Ala Glu Thr Leu Gly Glu Ile Phe Gly Glu	
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Glu Glu Asp Ala Ala Lys Ile Val Ala Asp Phe Glu Ser Ala Leu Glu	
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Glu Ala Ile Ala Ala Ala Asn Pro Asp Leu Ile Leu Val Met Asp Arg
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245 250 255

Asp Gly Tyr Val Tyr Tyr Ala Pro Ala Asp Thr Tyr Thr Asn Glu Asn
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Met Ser Ser Lys His
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 Pro Glu Glu Lys Val Asp Glu Ile Asn Lys Ala Phe Met Glu Ala Asn
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Asn Gln Pro Met Ile Ala Gln Ser Asn Gly Pro Thr Ser Gln Glu Ile
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Ala Gly Gly Gly His Pro Val Gly Ile Val Val Asp Tyr Leu Val Arg
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Asp Leu Ala Ala Ala Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu
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Gly Ser Pro Tyr Ile Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu
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Gly Gln Glu Ile Ala Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp
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Tyr	Gly	Ile	Ile	Met	Gly	Ile	Phe	Thr	Ile	Pro	Leu	Gly	Ala	Ile	Ala		
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Thr	Trp	Trp	Ala	Ser	Thr	Phe	Pro	Val	Gly	Thr	Leu	Ser	Leu	Gly	Ala		
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His	Phe	Leu	Ser	Gln	Ser	Thr	Gly	Val	Glu	Trp	Phe	Asn	Tyr	Phe	Ser		
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BGI-131CP

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<213> Corynebacterium glutamicum

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355              360              365
Asp Glu Ile Ser Pro Trp Ser Gly Glu Phe Ser Ile Ser Tyr Asn Ala
370              375              380

Asp Gly Gly His Gln Ala Trp Val Asp Ala Thr Ala Asn Ser Ile Arg
385              390              395

Asn Thr Leu Gly Ile Asp Ala Ile Gly Asn Pro Tyr Pro Asp Phe Lys
405              410              415

Ser Leu Arg Asp Asp Val Thr Asn Arg Thr Ile Asn Gly Ala Phe Arg
420              425              430

Thr Gly Trp Gln Ala Asp Tyr Pro Ser Leu Gly Asn Phe Leu Gly Pro
435              440              445

Leu Tyr Gly Thr Gly Ala Gly Ser Asn Asp Gly Asp Tyr Ser Asn Pro
450              455              460

Asp Phe Asp Ala Lys Leu Ala Glu Ala Ala Asn Ala Ala Asp Val Asp
465              470              475

Ala Ser Thr Pro Leu Tyr Asn Glu Ala Gln Glu Ile Leu Leu Gln Asp
485              490              495

Leu Pro Ala Ile Pro Thr Trp Tyr Ser Asn Ala Val Gly Gly Tyr Ser
500              505              510

Thr Asn Val Asp Asn Val Glu Phe Gln Trp Asn Ser Gln Pro Ala Tyr
515              520              525

Tyr Gln Ile Thr Lys Asn
530

```

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<210> 349
<211> 1698
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1675)
<223> RXS01346

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<400> 349
aaggtgtggt gagtcactgg ctagatttga ttgtgtggcc ataccaaatc ggccacaca 60

ggcacgttgc aaacagcaac gctcacccat aggagattta atg cgc aca gcc aca 115
Met Arg Thr Ala Thr
1 5

aaa gtc atc gca aca gtg atg gcc tca acc ctg gct atc ggg ctg gca 163
Lys Val Ile Ala Thr Val Met Ala Ser Thr Leu Ala Ile Gly Leu Ala
10 15 20

tct tgt tcc agc tct agt ggc acc cca gac gtg aat tac gta tcc gtc 211
Ser Cys Ser Ser Ser Ser Gly Thr Pro Asp Val Asn Tyr Val Ser Val
25 30 35

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aac ggc acc gaa cct cag cgc gga ctc atc ccg ggc gac acc aat gaa	259
Asn Gly Thr Glu Pro Gln Arg Gly Leu Ile Pro Gly Asp Thr Asn Glu	
40 45 50	
aac ggc ggt ggg cga gtg gtg gac atg ctg tac tct ggg ctc gtc tac	307
Asn Gly Gly Gly Arg Val Val Asp Met Leu Tyr Ser Gly Leu Val Tyr	
55 60 65	
ttt gat gaa gct ggc gtt gct caa aat gac ctg gcg gca tca att gac	355
Phe Asp Glu Ala Gly Val Ala Gln Asn Asp Leu Ala Ala Ser Ile Asp	
70 75 80 85	
cag gaa aca gac acc acc tac aaa atc act ttg cgt gat ggc atc aaa	403
Gln Glu Thr Asp Thr Thr Tyr Lys Ile Thr Leu Arg Asp Gly Ile Lys	
90 95 100	
ttc agt gac gga tcg gat att act gcc act gat ttt gtg gat acc tgg	451
Phe Ser Asp Gly Ser Asp Ile Thr Ala Thr Asp Phe Val Asp Thr Trp	
105 110 115	
aat ttt gta gtg gaa aat gga ctg ctc aac act tct ttc ttc tca ccg	499
Asn Phe Val Val Glu Asn Gly Leu Leu Asn Thr Ser Phe Phe Ser Pro	
120 125 130	
att aaa ggg tat gag gag ggc gtg gaa acg ctc gag ggt ttg aat gtg	547
Ile Lys Gly Tyr Glu Glu Gly Val Glu Thr Leu Glu Gly Leu Asn Val	
135 140 145	
gtg gat gat cgc aca ttt acc atc gag ctt gcc caa ccg gat tct gag	595
Val Asp Asp Arg Thr Phe Thr Ile Glu Leu Ala Gln Pro Asp Ser Glu	
150 155 160 165	
ttc acc caa cgc att ggc tac tac ggt ttt gca ccg atg cca gct tcg	643
Phe Thr Gln Arg Ile Gly Tyr Tyr Gly Phe Ala Pro Met Pro Ala Ser	
170 175 180	
gct cgc gat gat att gac gcc ttt ggt gaa aac ccc gtg tcc tct ggc	691
Ala Arg Asp Asp Ile Asp Ala Phe Gly Glu Asn Pro Val Ser Ser Gly	
185 190 195	
cct tac aaa cta gag cag tgg gat cac aac gca gaa ctg aaa gtg gtg	739
Pro Tyr Lys Leu Glu Gln Trp Asp His Asn Ala Glu Leu Lys Val Val	
200 205 210	
gcc aat gaa cac tac gat ggc ccg cgc gca gcc aac aac gat ggc ttg	787
Ala Asn Glu His Tyr Asp Gly Pro Arg Ala Ala Asn Asn Asp Gly Leu	
215 220 225	
aag tac gtg ttc tac gcc caa aat gat gca gct tat tca gat ctg ttg	835
Lys Tyr Val Phe Tyr Ala Gln Asn Asp Ala Ala Tyr Ser Asp Leu Leu	
230 235 240 245	
gct gga aac cta gat gtg ctg gat ctc att cca cca tcg gcg tac acc	883
Ala Gly Asn Leu Asp Val Leu Asp Leu Ile Pro Pro Ser Ala Tyr Thr	
250 255 260	
acc tat gaa gag gaa ctg tcg ggt cga tcc att aat caa cct gcg gcc	931
Thr Tyr Glu Glu Glu Leu Ser Gly Arg Ser Ile Asn Gln Pro Ala Ala	
265 270 275	
tcc tat ctg gaa ctc tcc att cgc atg gaa tcc ccc aac ttt gaa ggg	979

Ser	Tyr	Leu	Glu	Leu	Ser	Ile	Arg	Met	Glu	Ser	Pro	Asn	Phe	Glu	Gly	
		280					285					290				
caa	cag	gga	cag	ttg	cgt	cga	caa	gca	att	tct	atg	gcg	att	aac	cgt	1027
Gln	Gln	Gly	Gln	Leu	Arg	Arg	Gln	Ala	Ile	Ser	Met	Ala	Ile	Asn	Arg	
		295				300					305					
gaa	gaa	atc	gct	gag	cag	atc	ttc	gcc	ggc	acc	tac	acg	cct	gcg	ctc	1075
Glu	Glu	Ile	Ala	Glu	Gln	Ile	Phe	Ala	Gly	Thr	Tyr	Thr	Pro	Ala	Leu	
310					315					320					325	
gac	ttc	acc	gcg	ccc	gtg	ctc	gac	ggc	tgg	cgc	gat	gat	ttg	aac	ggc	1123
Asp	Phe	Thr	Ala	Pro	Val	Leu	Asp	Gly	Trp	Arg	Asp	Asp	Leu	Asn	Gly	
				330					335					340		
aat	gac	gtg	ctg	act	ttc	cag	cct	gac	aag	gcc	cgt	gag	ctg	tgg	gaa	1171
Asn	Asp	Val	Leu	Thr	Phe	Gln	Pro	Asp	Lys	Ala	Arg	Glu	Leu	Trp	Glu	
			345					350					355			
gac	gct	gag	gag	atc	gca	cct	ttt	gag	ggc	gaa	ttg	cag	atc	agt	tac	1219
Asp	Ala	Glu	Glu	Ile	Ala	Pro	Phe	Glu	Gly	Glu	Leu	Gln	Ile	Ser	Tyr	
		360					365					370				
aac	gcg	gat	gtt	ccc	aac	cgg	gaa	tgg	gtg	gat	gcg	gta	gca	aac	agc	1267
Asn	Ala	Asp	Val	Pro	Asn	Arg	Glu	Trp	Val	Asp	Ala	Val	Ala	Asn	Ser	
		375				380					385					
atc	agc	aac	gaa	tta	gac	gtc	aac	gcc	act	ggc	aat	cct	ttc	ccc	gat	1315
Ile	Ser	Asn	Glu	Leu	Asp	Val	Asn	Ala	Thr	Gly	Asn	Pro	Phe	Pro	Asp	
390					395					400					405	
ttt	aaa	tcc	ttc	cgc	gac	aca	tac	cgc	acc	acc	gga	ttg	gat	ggc	gcc	1363
Phe	Lys	Ser	Phe	Arg	Asp	Thr	Tyr	Arg	Thr	Thr	Gly	Leu	Asp	Gly	Ala	
				410					415					420		
tac	cgc	acc	gcg	tgg	ttt	gcg	gac	tac	cca	agc	atc	ggc	aac	ttc	ctt	1411
Tyr	Arg	Thr	Ala	Trp	Phe	Ala	Asp	Tyr	Pro	Ser	Ile	Gly	Asn	Phe	Leu	
			425					430				435				
gga	cct	aac	tac	acc	tcg	ggc	gtg	gcc	tcc	aac	gat	gcc	aag	tac	gaa	1459
Gly	Pro	Asn	Tyr	Thr	Ser	Gly	Val	Ala	Ser	Asn	Asp	Ala	Lys	Tyr	Glu	
		440				445						450				
aac	cca	gaa	ttt	gat	caa	ttg	att	gcc	gac	gcc	gca	gca	gcc	tcc	acc	1507
Asn	Pro	Glu	Phe	Asp	Gln	Leu	Ile	Ala	Asp	Ala	Ala	Ala	Ala	Ser	Thr	
		455				460					465					
aag	gag	gaa	acc	ttc	cag	gca	tat	gcg	cag	gcc	cag	gaa	atg	ttg	ttg	1555
Lys	Glu	Glu	Thr	Phe	Gln	Ala	Tyr	Ala	Gln	Ala	Gln	Glu	Met	Leu	Leu	
470					475					480					485	
cgc	gat	ctt	ccc	gca	atc	cca	ctg	tgg	tac	ccg	aat	gtg	gtt	ggc	ggc	1603
Arg	Asp	Leu	Pro	Ala												

520

525

<210> 350

<211> 525

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

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Met Arg Thr Ala Thr Lys Val Ile Ala Thr Val Met Ala Ser Thr Leu
  1           5           10           15

Ala Ile Gly Leu Ala Ser Cys Ser Ser Ser Gly Thr Pro Asp Val
      20           25           30

Asn Tyr Val Ser Val Asn Gly Thr Glu Pro Gln Arg Gly Leu Ile Pro
      35           40           45

Gly Asp Thr Asn Glu Asn Gly Gly Gly Arg Val Val Asp Met Leu Tyr
      50           55           60

Ser Gly Leu Val Tyr Phe Asp Glu Ala Gly Val Ala Gln Asn Asp Leu
      65           70           75

Ala Ala Ser Ile Asp Gln Glu Thr Asp Thr Thr Tyr Lys Ile Thr Leu
      85           90           95

Arg Asp Gly Ile Lys Phe Ser Asp Gly Ser Asp Ile Thr Ala Thr Asp
      100          105          110

Phe Val Asp Thr Trp Asn Phe Val Val Glu Asn Gly Leu Leu Asn Thr
      115          120          125

Ser Phe Phe Ser Pro Ile Lys Gly Tyr Glu Glu Gly Val Glu Thr Leu
      130          135          140

Glu Gly Leu Asn Val Val Asp Asp Arg Thr Phe Thr Ile Glu Leu Ala
      145          150          155          160

Gln Pro Asp Ser Glu Phe Thr Gln Arg Ile Gly Tyr Tyr Gly Phe Ala
      165          170          175

Pro Met Pro Ala Ser Ala Arg Asp Asp Ile Asp Ala Phe Gly Glu Asn
      180          185          190

Pro Val Ser Ser Gly Pro Tyr Lys Leu Glu Gln Trp Asp His Asn Ala
      195          200          205

Glu Leu Lys Val Val Ala Asn Glu His Tyr Asp Gly Pro Arg Ala Ala
      210          215          220

Asn Asn Asp Gly Leu Lys Tyr Val Phe Tyr Ala Gln Asn Asp Ala Ala
      225          230          235          240

Tyr Ser Asp Leu Leu Ala Gly Asn Leu Asp Val Leu Asp Leu Ile Pro
      245          250          255

Pro Ser Ala Tyr Thr Thr Tyr Glu Glu Glu Leu Ser Gly Arg Ser Ile
      260          265          270

Asn Gln Pro Ala Ala Ser Tyr Leu Glu Leu Ser Ile Arg Met Glu Ser

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                275                280                285
Pro Asn Phe Glu Gly Gln Gln Gly Gln Leu Arg Arg Gln Ala Ile Ser
 290                295                300

Met Ala Ile Asn Arg Glu Glu Ile Ala Glu Gln Ile Phe Ala Gly Thr
305                310                315

Tyr Thr Pro Ala Leu Asp Phe Thr Ala Pro Val Leu Asp Gly Trp Arg
      325                330                335

Asp Asp Leu Asn Gly Asn Asp Val Leu Thr Phe Gln Pro Asp Lys Ala
      340                345                350

Arg Glu Leu Trp Glu Asp Ala Glu Glu Ile Ala Pro Phe Glu Gly Glu
      355                360                365

Leu Gln Ile Ser Tyr Asn Ala Asp Val Pro Asn Arg Glu Trp Val Asp
      370                375                380

Ala Val Ala Asn Ser Ile Ser Asn Glu Leu Asp Val Asn Ala Thr Gly
385                390                395

Asn Pro Phe Pro Asp Phe Lys Ser Phe Arg Asp Thr Tyr Arg Thr Thr
      405                410                415

Gly Leu Asp Gly Ala Tyr Arg Thr Ala Trp Phe Ala Asp Tyr Pro Ser
      420                425                430

Ile Gly Asn Phe Leu Gly Pro Asn Tyr Thr Ser Gly Val Ala Ser Asn
      435                440                445

Asp Ala Lys Tyr Glu Asn Pro Glu Phe Asp Gln Leu Ile Ala Asp Ala
      450                455                460

Ala Ala Ala Ser Thr Lys Glu Glu Thr Phe Gln Ala Tyr Ala Gln Ala
465                470                475

Gln Glu Met Leu Leu Arg Asp Leu Pro Ala Ile Pro Leu Trp Tyr Pro
      485                490                495

Asn Val Val Gly Gly Tyr Ser Glu Ser Val Asp Asn Val Ser Val Asn
      500                505                510

Trp Lys Ala Ile Pro Val Tyr Trp Ala Ile Thr Lys Gln
      515                520                525

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<210> 351
<211> 321
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (26)..(298)
<223> RXS00912

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<400> 351
ccacaccttt gaaaggagct aagcgatg gac aac acc ctc tac aca gca ggc
          Met Asp Asn Thr Leu Tyr Thr Ala Gly

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              1              5
ctc aca atc gca gct gcc ttt ttc atg ctg tcg ttc atc ttc acc atc 100
Leu Thr Ile Ala Ala Phe Phe Met Leu Ser Phe Ile Phe Thr Ile
 10              15              20              25

tac cgc atc atc gtc ggg ccc aac tcc atc gat cgc cta ctc ggc ctg 148
Tyr Arg Ile Ile Val Gly Pro Asn Ser Ile Asp Arg Leu Leu Gly Leu
              30              35              40

gac gga acc gtc tcc atg att caa tgc tcc atg gcc acc tac atc tgc 196
Asp Gly Thr Val Ser Met Ile Gln Cys Ser Met Ala Thr Tyr Ile Cys
              45              50              55

tgg aca ctc gac acc acc gtc acc aac ttc atg atg gtc atc gca ctc 244
Trp Thr Leu Asp Thr Thr Val Thr Asn Phe Met Met Val Ile Ala Leu
              60              65              70

tta gga ttc atc agc tct gta tcc gta gcc cgc ttc cgc aag agg gat 292
Leu Gly Phe Ile Ser Ser Val Ser Val Ala Arg Phe Arg Lys Arg Asp
              75              80              85

ggt gcc taaatgaccc tgcaactatt cac 321
Gly Ala
 90

<210> 352
<211> 91
<212> PRT
<213> Corynebacterium glutamicum

<400> 352
Met Asp Asn Thr Leu Tyr Thr Ala Gly Leu Thr Ile Ala Ala Ala Phe
 1              5              10              15

Phe Met Leu Ser Phe Ile Phe Thr Ile Tyr Arg Ile Ile Val Gly Pro
              20              25              30

Asn Ser Ile Asp Arg Leu Leu Gly Leu Asp Gly Thr Val Ser Met Ile
              35              40              45

Gln Cys Ser Met Ala Thr Tyr Ile Cys Trp Thr Leu Asp Thr Thr Val
              50              55              60

Thr Asn Phe Met Met Val Ile Ala Leu Leu Gly Phe Ile Ser Ser Val
 65              70              75              80

Ser Val Ala Arg Phe Arg Lys Arg Asp Gly Ala
              85              90

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<210> 353
<211> 2472
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(2449)
<223> RXS00453

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<400> 353

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attcaggttg gggcgatggt cctataatcg caagtggatt gtg att tcg gca tgg 115
                                   Val Ile Ser Ala Trp
                                   1 5

cta ctt att ttg gcc att gtt ggt ggt ctg gcc ctg acg atg cag aag 163
Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala Leu Thr Met Gln Lys
                                   10 15 20

ggg ttc agt aac tct ttc act att gaa gac acc cct tcg att gat gcc 211
Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr Pro Ser Ile Asp Ala
                                   25 30 35

act gtt tct ctg gtt gaa aat ttc cct gat cag acg aac ccg gtg acg 259
Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln Thr Asn Pro Val Thr
                                   40 45 50

gcc gcc gga gtt aac gtg gtt ttc caa tcc ccg gaa gga acc acg ctt 307
Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro Glu Gly Thr Thr Leu
                                   55 60 65

gat gat cct cag atg atg act gcg atg gat gca gtc gtt gat tac att 355
Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala Val Val Asp Tyr Ile
                                   70 75 80 85

gag gac aat ttg cct gat ttt ggt ggg gga gag cgc ttc ggc aat cct 403
Glu Asp Asn Leu Pro Asp Phe Gly Gly Glu Arg Phe Gly Asn Pro
                                   90 95 100

gtt gag gtg tct cct gcg ttg gaa gag atg gtc atc gag cag atg acc 451
Val Glu Val Ser Pro Ala Leu Glu Glu Met Val Ile Glu Gln Met Thr
                                   105 110 115

agc atg ggg ctt cct gag gaa acc gct gca aag gat gct gcc aat ctg 499
Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys Asp Ala Ala Asn Leu
                                   120 125 130

gcg gtg ttg agc gaa gac aaa acc att ggc tac acc tct ttc aac att 547
Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr Thr Ser Phe Asn Ile
                                   135 140 145

gat gtt gag gcc gca gaa tat gtg gag caa aaa cac cgc gat gtg atc 595
Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys His Arg Asp Val Ile
                                   150 155 160 165

aac gaa gcg atg caa atc ggt gaa gat tta ggt gtc cgg gtg gaa gcc 643
Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly Val Arg Val Glu Ala
                                   170 175 180

ggt gga cct gct ttc ggt gat cca att cag att gaa acc acc agt gag 691
Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile Glu Thr Thr Ser Glu
                                   185 190 195

atc atc ggt att ggc atc gcg ttc atc gtg ttg att ttc acc ttt ggt 739
Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu Ile Phe Thr Phe Gly
                                   200 205 210

tct ttg att gct gca ggc ttg cct ttg att acc gcg gtg atc ggc gtg 787

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Ser	Leu	Ile	Ala	Ala	Gly	Leu	Pro	Leu	Ile	Thr	Ala	Val	Ile	Gly	Val	
215						220					225					
ggc	att	ggt	gcg	ctg	gca	att	gtg	ctg	gcc	acg	gcg	ttt	act	gat	ctc	835
Gly	Ile	Gly	Ala	Leu	Ala	Ile	Val	Leu	Ala	Thr	Ala	Phe	Thr	Asp	Leu	
230					235					240					245	
aac	aat	gtg	act	cca	gtg	ctc	gca	gtg	atg	att	ggc	ctg	gcc	gtg	ggc	883
Asn	Asn	Val	Thr	Pro	Val	Leu	Ala	Val	Met	Ile	Gly	Leu	Ala	Val	Gly	
				250					255					260		
att	gac	tac	gcg	ctg	ttt	att	ttg	tct	agg	tac	cgt	gcg	gag	tat	aag	931
Ile	Asp	Tyr	Ala	Leu	Phe	Ile	Leu	Ser	Arg	Tyr	Arg	Ala	Glu	Tyr	Lys	
			265					270					275			
cgc	atg	cca	cgt	gcc	gat	gct	gcc	gga	atg	gcg	gtg	ggc	aca	gct	ggt	979
Arg	Met	Pro	Arg	Ala	Asp	Ala	Ala	Gly	Met	Ala	Val	Gly	Thr	Ala	Gly	
		280					285					290				
agt	gcg	gtg	gtg	ttt	gct	ggc	gcg	acg	gtg	att	atc	gcg	ctg	gta	gcc	1027
Ser	Ala	Val	Val	Phe	Ala	Gly	Ala	Thr	Val	Ile	Ile	Ala	Leu	Val	Ala	
	295					300					305					
ctc	atc	att	gcg	gat	atc	gga	ttc	ctc	acg	gcc	atg	ggt	att	tct	gcg	1075
Leu	Ile	Ile	Ala	Asp	Ile	Gly	Phe	Leu	Thr	Ala	Met	Gly	Ile	Ser	Ala	
310					315					320					325	
gcg	ttt	acg	gtg	ttc	gtg	gct	gtg	ctc	att	gcg	ttg	acg	ttt	atc	ccg	1123
Ala	Phe	Thr	Val	Phe	Val	Ala	Val	Leu	Ile	Ala	Leu	Thr	Phe	Ile	Pro	
				330					335					340		
gcg	ctg	ttg	ggt	gtg	ttt	ggt	ggt	cat	gcg	ttc	aag	ggc	aag	atc	cct	1171
Ala	Leu	Leu	Gly	Val	Phe	Gly	Gly	His	Ala	Phe	Lys	Gly	Lys	Ile	Pro	
			345					350					355			
gga	att	ggt	gga	aac	cca	acg	cca	aag	cag	acg	tgg	gag	caa	gcg	ctt	1219
Gly	Ile	Gly	Gly	Asn	Pro	Thr	Pro	Lys	Gln	Thr	Trp	Glu	Gln	Ala	Leu	
		360					365					370				
aat	cgt	cgt	tcc	aag	ggt	cgc	tca	tgg	gtc	aag	ctt	gta	cag	aaa	gca	1267
Asn	Arg	Arg	Ser	Lys	Gly	Arg	Ser	Trp	Val	Lys	Leu	Val	Gln	Lys	Ala	
	375					380					385					
ccg	ggt	ctt	gtg	gtg	gca	gtg	gtg	gtc	ttg	ggt	ctt	ggt	gcc	ttg	acc	1315
Pro	Gly	Leu	Val	Val	Ala	Val	Val	Val	Leu	Gly	Leu	Gly	Ala	Leu	Thr	
390					395					400					405	
att	cct	gca	atg	aac	ctg	cag	ttg	tca	ctg	cct	tct	gac	tcc	acc	tcc	1363
Ile	Pro	Ala	Met	Asn	Leu	Gln	Leu	Ser	Leu	Pro	Ser	Asp	Ser	Thr	Ser	
				410					415					420		
aat	att	gat	acc	act	cag	cgt	cag	tcg	gct	gat	ttg	atg	gca	gag	ggc	1411
Asn	Ile	Asp	Thr	Thr	Gln	Arg	Gln	Ser	Ala	Asp	Leu	Met	Ala	Glu	Gly	
			425					430					435			
ttt	ggc	gcg	ggc	gtt	aat	gcg	ccg	ttc	ttg	gtc	atc	gtc	gat	acg	cat	1459
Phe	Gly	Ala	Gly	Val	Asn	Ala	Pro	Phe	Leu	Val	Ile	Val	Asp	Thr	His	
		440					445					450				
gag	gtc	aat	gct	gat	tcc	acc	gca	ttg	cag	cca	ctg	att	gag	gca	cag	1507
Glu	Val	Asn	Ala	Asp	Ser	Thr	Ala	Leu	Gln	Pro	Leu	Ile	Glu	Ala	Gln	

455					460					465										
gag Glu 470	cct Pro	gaa Glu	gag Glu	ggc Gly	gag Glu	ttc Phe	gat Asp	cgg Arg	gag Glu	cag Gln	gcg Ala	gct Ala	cgt Arg	ttt Phe	gct Ala	1555				
acc Thr	tat Tyr	atg Met	tat Tyr	gtc Val	acc Thr	cag Gln	acc Thr	tac Tyr	aat Asn	tcc Ser	aac Asn	atc Ile	gat Asp	gtg Val	aag Lys	1603				
aat Asn	gcg Ala	cag Gln	atc Ile	atc Ile	agc Ser	gtc Val	aat Asn	gat Asp	gat Asp	ttc Phe	act Thr	gcg Ala	gcg Ala	cag Gln	att Ile	1651				
ctc Leu	gtg Val	act Thr	cca Pro	tac Tyr	acc Thr	gga Gly	cct Pro	gcg Ala	gat Asp	aaa Lys	gag Glu	acc Thr	cct Pro	gag Glu	ttg Leu	1699				
atg Met	cac His	gtg Val	ctg Leu	cgt Arg	gcg Ala	cag Gln	gaa Glu	gct Ala	cag Gln	att Ile	gag Glu	gat Asp	gtt Val	acg Thr	gga Gly	1747				
act Thr	gaa Glu	ctg Leu	ggc Gly	acc Thr	act Thr	ggg Gly	ttt Phe	acg Thr	gcg Ala	gtt Val	cag Gln	ttg Leu	gac Asp	att Ile	act Thr	1795				
gag Glu	cag Gln	ctg Leu	gaa Glu	gac Asp	gca Ala	atg Met	ccg Pro	gtt Val	tac Tyr	ctc Leu	gct Ala	gtg Val	gtt Val	gtt Val	ggc Gly	1843				
ttg Leu	gct Ala	att Ile	ttc Phe	ctc Leu	ctc Leu	att Ile	ctg Leu	gtg Val	ttc Phe	cgt Arg	tcc Ser	ctg Leu	ctt Leu	gtt Val	ccg Pro	1891				
ctg Leu	gtt Val	gct Ala	ggc Gly	ctt Leu	ggc Gly	ttc Phe	ttg Leu	ttg Leu	tct Ser	gtg Val	ggc Gly	gcc Ala	ttc Ala	ggc Phe	1939					
gag Ala	acg Thr	gtg Val	ttg Leu	gtc Val	tgg Trp	cag Gln	gag Glu	ggc Gly	ttc Phe	ggc Gly	ggt Phe	ttt Val	gtg Val	aac Asn	acc Thr	1987				
cct Pro	ggc Gly	ccg Pro	ctg Leu	att Ile	tcc Ser	ttc Phe	atg Met	ccg Pro	atc Ile	ttc Phe	ctc Leu	atc Ile	ggc Gly	gtg Val	acc Thr	2035				
ttc Phe	ggc Gly	ttg Leu	gcc Ala	atg Met	gac Asp	tat Tyr	cag Gln	gtg Val	ttc Phe	ctt Leu	gtg Val	act Thr	cgc Arg	atg Met	cgc Arg	2083				
gag Glu	cac His	tac Tyr	acc Thr	cac His	cac His	aat Asn	ggc Gly	aag Lys	gga Gly	cag Gln	cct Pro	ggc Gly	tcc Ser	aag Lys	tac Tyr	2131				
acc Thr	ccg Pro	gtt Val	gag Glu	cag Gln	tca Ser	gtg Val	att Ile	gaa Glu	ggc Gly	ttc Phe	acg Thr	cag Gln	ggc Gly	tcc Ser	cgc Arg	2179				
gtg Val	gtt Val	aca Thr	gca Ala	gcg Ala	gca Ala	ctg Leu	atc Ile	atg Met	att Ile	gcc Ala	gtg Val	ttc Phe	gtg Val	gcg Ala	ttt Phe	2227				

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att gat cag ccg ttg cca ttt att aag atc ttc ggt ttc gcg ttg ggt 2275
Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe Gly Phe Ala Leu Gly
710 715 720 725

gcg ggc gtg ttt ttc gat gct ttc ttc att cgc atg ggt ctg gtc ccc 2323
Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg Met Gly Leu Val Pro
730 735 740

gcg tcg atg ttc ctg atg ggc aag gcc acg tgg tgg atg cct aag tgg 2371
Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp Trp Met Pro Lys Trp
745 750 755

ctg gat cga att ctg cca agt ttg gac att gaa ggc acc gca ctg gag 2419
Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu Gly Thr Ala Leu Glu
760 765 770

aag gaa tgg gag gag aag cag gct gca cgt tagacttggc acctatgtca 2469
Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg
775 780

gat 2472

<210> 354
<211> 783
<212> PRT
<213> Corynebacterium glutamicum

<400> 354
Val Ile Ser Ala Trp Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala
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Leu Thr Met Gln Lys Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr
20 25 30

Pro Ser Ile Asp Ala Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln
35 40 45

Thr Asn Pro Val Thr Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro
50 55 60

Glu Gly Thr Thr Leu Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala
65 70 75 80

Val Val Asp Tyr Ile Glu Asp Asn Leu Pro Asp Phe Gly Gly Gly Glu
85 90 95

Arg Phe Gly Asn Pro Val Glu Val Ser Pro Ala Leu Glu Glu Met Val
100 105 110

Ile Glu Gln Met Thr Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys
115 120 125

Asp Ala Ala Asn Leu Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr
130 135 140

Thr Ser Phe Asn Ile Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys
145 150 155 160

His Arg Asp Val Ile Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly

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165										170					175				
Val	Arg	Val	Glu	Ala	Gly	Gly	Pro	Ala	Phe	Gly	Asp	Pro	Ile	Gln	Ile				
			180					185					190						
Glu	Thr	Thr	Ser	Glu	Ile	Ile	Gly	Ile	Gly	Ile	Ala	Phe	Ile	Val	Leu				
		195					200					205							
Ile	Phe	Thr	Phe	Gly	Ser	Leu	Ile	Ala	Ala	Gly	Leu	Pro	Leu	Ile	Thr				
	210					215					220								
Ala	Val	Ile	Gly	Val	Gly	Ile	Gly	Ala	Leu	Ala	Ile	Val	Leu	Ala	Thr				
225					230					235					240				
Ala	Phe	Thr	Asp	Leu	Asn	Asn	Val	Thr	Pro	Val	Leu	Ala	Val	Met	Ile				
				245					250					255					
Gly	Leu	Ala	Val	Gly	Ile	Asp	Tyr	Ala	Leu	Phe	Ile	Leu	Ser	Arg	Tyr				
			260					265					270						
Arg	Ala	Glu	Tyr	Lys	Arg	Met	Pro	Arg	Ala	Asp	Ala	Ala	Gly	Met	Ala				
		275					280					285							
Val	Gly	Thr	Ala	Gly	Ser	Ala	Val	Val	Phe	Ala	Gly	Ala	Thr	Val	Ile				
	290					295					300								
Ile	Ala	Leu	Val	Ala	Leu	Ile	Ile	Ala	Asp	Ile	Gly	Phe	Leu	Thr	Ala				
305					310					315					320				
Met	Gly	Ile	Ser	Ala	Ala	Phe	Thr	Val	Phe	Val	Ala	Val	Leu	Ile	Ala				
				325					330					335					
Leu	Thr	Phe	Ile	Pro	Ala	Leu	Leu	Gly	Val	Phe	Gly	Gly	His	Ala	Phe				
			340					345					350						
Lys	Gly	Lys	Ile	Pro	Gly	Ile	Gly	Gly	Asn	Pro	Thr	Pro	Lys	Gln	Thr				
		355					360					365							
Trp	Glu	Gln	Ala	Leu	Asn	Arg	Arg	Ser	Lys	Gly	Arg	Ser	Trp	Val	Lys				
	370					375					380								
Leu	Val	Gln	Lys	Ala	Pro	Gly	Leu	Val	Val	Ala	Val	Val	Val	Leu	Gly				
385					390					395					400				
Leu	Gly	Ala	Leu	Thr	Ile	Pro	Ala	Met	Asn	Leu	Gln	Leu	Ser	Leu	Pro				
				405					410					415					
Ser	Asp	Ser	Thr	Ser	Asn	Ile	Asp	Thr	Thr	Gln	Arg	Gln	Ser	Ala	Asp				
			420					425					430						
Leu	Met	Ala	Glu	Gly	Phe	Gly	Ala	Gly	Val	Asn	Ala	Pro	Phe	Leu	Val				
		435					440					445							
Ile	Val	Asp	Thr	His	Glu	Val	Asn	Ala	Asp	Ser	Thr	Ala	Leu	Gln	Pro				
	450					455					460								
Leu	Ile	Glu	Ala	Gln	Glu	Pro	Glu	Glu	Gly	Glu	Phe	Asp	Arg	Glu	Gln				
465					470					475					480				
Ala	Ala	Arg	Phe	Ala	Thr	Tyr	Met	Tyr	Val	Thr	Gln	Thr	Tyr	Asn	Ser				
				485					490					495					

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Asn Ile Asp Val Lys Asn Ala Gln Ile Ile Ser Val Asn Asp Asp Phe
      500                               505                      510

Thr Ala Ala Gln Ile Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys
      515                               520                      525

Glu Thr Pro Glu Leu Met His Val Leu Arg Ala Gln Glu Ala Gln Ile
      530                               535                      540

Glu Asp Val Thr Gly Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val
      545                               550                      555                      560

Gln Leu Asp Ile Thr Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu
      565                               570                      575

Ala Val Val Val Gly Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg
      580                               585                      590

Ser Leu Leu Val Pro Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val
      595                               600                      605

Gly Ala Ala Phe Gly Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly
      610                               615                      620

Gly Phe Val Asn Thr Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe
      625                               630                      635                      640

Leu Ile Gly Val Thr Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu
      645                               650                      655

Val Thr Arg Met Arg Glu His Tyr Thr His His Asn Gly Lys Gly Gln
      660                               665                      670

Pro Gly Ser Lys Tyr Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe
      675                               680                      685

Thr Gln Gly Ser Arg Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala
      690                               695                      700

Val Phe Val Ala Phe Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe
      705                               710                      715                      720

Gly Phe Ala Leu Gly Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg
      725                               730                      735

Met Gly Leu Val Pro Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp
      740                               745                      750

Trp Met Pro Lys Trp Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu
      755                               760                      765

Gly Thr Ala Leu Glu Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg
      770                               775                      780

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<210> 355

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

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ctt cac cgt ttt gca gcc ctt tta gaa atg ggt acc tgg acc ctg ctg 163
Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly Thr Trp Thr Leu Leu
 10 15 20

cct att gcc ggc ggt atc cac ggc ttt ggc ttc ctc tgt ttt gca gcc 259
Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe Leu Cys Phe Ala Ala
40 45 50

atc acc atc acc gtg tgg atc aat aat aag tgg aca ttc ccg cag ggt 307
Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp Thr Phe Pro Gln Gly
55 60 65

atc gca ggt ttg atc gtc tct gtt atc ccg tgg gct gca ttg cca ttt 355
Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp Ala Ala Leu Pro Phe
70 75 80 85

gca ttg tgg gca gac aag aag ggc ctc gtt gcc ggc gga tgg cgc ttt 403
Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala Gly Gly Trp Arg Phe
90 95 100

tca	gat	ccg	tcc	gaa	aag	cca	cac	act	ttc	ttt	gac	aag	atc	ttg	gct	451
Ser	Asp	Pro	Ser	Glu	Lys	Pro	His	Thr	Phe	Phe	Asp	Lys	Ile	Leu	Ala	
			105					110					115			

caa ttg gtc agg cac cca atc cga tcc att tta att ctg ctg gtg att 499
Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu Ile Leu Leu Val Ile
120 125 130

atc gcc gtc gtc ttc tct atc ttg ctg gcg atg gga cca cct tat gat 547
Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met Gly Pro Pro Tyr Asp
135 140 145

cca gat gcc atc gca aac act gtg gat taaacaacag cctccttcac 594
Pro Asp Ala Ile Ala Asn Thr Val Asp
150 155

atq 597

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<210> 356
<211> 158
<212> PRT
<213> Corynebacterium glutamicum
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<400> 356

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Met Thr Pro Gln Lys Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly
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Thr Trp Thr Leu Leu Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val
              20              25              30

Thr Asp Ala Val Thr Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe
              35              40              45

Leu Cys Phe Ala Ala Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp
 50              55              60

Thr Phe Pro Gln Gly Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp
 65              70              75              80

Ala Ala Leu Pro Phe Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala
              85              90              95

Gly Gly Trp Arg Phe Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe
100              105              110

Asp Lys Ile Leu Ala Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu
115              120              125

Ile Leu Leu Val Ile Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met
130              135              140

Gly Pro Pro Tyr Asp Pro Asp Ala Ile Ala Asn Thr Val Asp
145              150              155

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<210> 357
<211> 2313
<212> DNA
<213> Corynebacterium glutamicum

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<220>
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<222> (101)..(2290)
<223> RXS00479

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<400> 357
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cttagaacta acctttacgc cttaaacgga agtgaatttg atg tct act agc atc 115
                               Met Ser Thr Ser Ile
                               1              5

aca aca gag aac aag aag aaa tct ggt cct cct cgc ttg atg aga atc 163
Thr Thr Glu Asn Lys Lys Lys Ser Gly Pro Pro Arg Leu Met Arg Ile
              10              15              20

ttt ctg ccc gcc ttg cta att tta gtt tgg ctt gta gga gct gga gtc 211
Phe Leu Pro Ala Leu Leu Ile Leu Val Trp Leu Val Gly Ala Gly Val
              25              30              35

ggc ggt cct tat ttt ggc aag gtt agt gag gtc tcc tcc aac agc cag 259
Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val Ser Ser Asn Ser Gln
              40              45              50

acc aca tat ctg cca gaa tct gcc gat gcc act caa gta cag gaa cag 307

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G E N E B A N K

Thr Thr Tyr Leu Pro Glu Ser Ala Asp Ala Thr Gln Val Gln Glu Gln
 55 60 65
 ttg gga gat ttt act gat tct gaa tcc atc cca gcc att gtc gta atg 355
 Leu Gly Asp Phe Thr Asp Ser Glu Ser Ile Pro Ala Ile Val Val Met
 70 75 80 85
 gtc agc gat gaa ccc tta aca cag caa gac atc aca caa ctc aat gaa 403
 Val Ser Asp Glu Pro Leu Thr Gln Gln Asp Ile Thr Gln Leu Asn Glu
 90 95 100
 gtt gtt gct ggg ctt tca gaa tta gac ata gtt tcc gat gaa gtc tcc 451
 Val Val Ala Gly Leu Ser Glu Leu Asp Ile Val Ser Asp Glu Val Ser
 105 110 115
 cct gct att cca tcc gag gac ggc aga gct gtc caa gtg ttt gtc ccc 499
 Pro Ala Ile Pro Ser Glu Asp Gly Arg Ala Val Gln Val Phe Val Pro
 120 125 130
 ctc aat cca tca gcg gag ctg acg gaa agc gtc gag aag ctc tct gag 547
 Leu Asn Pro Ser Ala Glu Leu Thr Glu Ser Val Glu Lys Leu Ser Glu
 135 140 145
 acc ttg acc cag caa acg ccg gac tat gtg agc acc tat gtg acc gga 595
 Thr Leu Thr Gln Gln Thr Pro Asp Tyr Val Ser Thr Tyr Val Thr Gly
 150 155 160 165
 ccg gct ggg ttt acc gct gat ctc agc gca gct ttc gcg ggt att gat 643
 Pro Ala Gly Phe Thr Ala Asp Leu Ser Ala Ala Phe Ala Gly Ile Asp
 170 175 180
 ggg cta ctc cta gca gtc gcc ttg gct gcc gtc ctt gtc att ctt gtc 691
 Gly Leu Leu Leu Ala Val Ala Leu Ala Ala Val Leu Val Ile Leu Val
 185 190 195
 atc gtc tat cgc tcc ttc att ctg ccc atc gcc gtg ctt gcc acc agt 739
 Ile Val Tyr Arg Ser Phe Ile Leu Pro Ile Ala Val Leu Ala Thr Ser
 200 205 210
 ttg ttt gcg ctg act gta gct cta ttg gtg gtg tgg tgg cta gct aag 787
 Leu Phe Ala Leu Thr Val Ala Leu Leu Val Val Trp Trp Leu Ala Lys
 215 220 225
 tgg gac atc ctg ctg ctt tcg ggt cag act caa gcc atc ctc ttc att 835
 Trp Asp Ile Leu Leu Leu Ser Gly Gln Thr Gln Gly Ile Leu Phe Ile
 230 235 240 245
 ctg gtc att gcc gcc gcc acc gac tac tca ttg cta tac gtt gct cgt 883
 Leu Val Ile Gly Ala Ala Thr Asp Tyr Ser Leu Leu Tyr Val Ala Arg
 250 255 260
 ttc cgt gaa gag tta cgc gtt caa caa gat aaa ggg ata gcc aca ggg 931
 Phe Arg Glu Glu Leu Arg Val Gln Gln Asp Lys Gly Ile Ala Thr Gly
 265 270 275
 aaa gcc atc cgg gca tcg gtg gaa ccc att ctt gcc tcg gcc agc act 979
 Lys Ala Ile Arg Ala Ser Val Glu Pro Ile Leu Ala Ser Gly Ser Thr
 280 285 290
 gtt att gcg gcc ctc ctt tgt ttg cta ttt agt gat ttg aaa tct aac 1027
 Val Ile Ala Gly Leu Leu Cys Leu Leu Phe Ser Asp Leu Lys Ser Asn

295	300	305	
tcc acg cta ggt cca gta gct tgc gtg ggc att att ttt gca atg ctt			1075
Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile Ile Phe Ala Met Leu			
310	315	320	325
tct gct ctt act ctg cta cca gcc ctg ctg ttt gta ttc ggt cgg gtg			1123
Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe Val Phe Gly Arg Val			
	330	335	340
gcc ttt tgg ccc aag cga cca aaa tac gaa cct gaa aaa gcc cgt gcg			1171
Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro Glu Lys Ala Arg Ala			
	345	350	355
aaa aac gac atc ccc gcc agc ggg atc tgg tca aaa gtg gct gat tta			1219
Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser Lys Val Ala Asp Leu			
	360	365	370
gtg gag cag cat cct cgt gca atc tgg gta tct aca ctt att gtg ctt			1267
Val Glu Gln His Pro Arg Ala Ile Trp Val Ser Thr Leu Ile Val Leu			
	375	380	385
ctc ttg ggt gcg gct ttc gtt ccc aca cta aaa gcg gac ggt gtg tcc			1315
Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys Ala Asp Gly Val Ser			
	390	395	400
caa tcc gac cta gtt ctg ggt tcc tct gaa gca cgt gat ggc cag cag			1363
Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala Arg Asp Gly Gln Gln			
	410	415	420
gct tta ggc gaa cac ttc ccc ggt gga tcc ggc agt cct gct tat att			1411
Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly Ser Pro Ala Tyr Ile			
	425	430	435
atc gtt gat gaa aca cag gca gca cag gct gct gac gta gtc ctt aac			1459
Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala Asp Val Val Leu Asn			
	440	445	450
aac gac aat ttc gag act gta act gta act agt gct gac tcc ccc tct			1507
Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser Ala Asp Ser Pro Ser			
	455	460	465
ggc tca gcc cca atc acc gct gac ggt att gtg ccg tta ggt tct ggt			1555
Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val Pro Leu Gly Ser Gly			
	470	475	480
aca gct cca ggc ccg gta gtt gta gaa ggg caa gtc ctt tta caa gca			1603
Thr Ala Pro Gly Pro Val Val Val Glu Gly Gln Val Leu Leu Gln Ala			
	490	495	500
aca ctt gtc gaa gca cca gat tcc gaa gaa gct caa aaa gct att cgc			1651
Thr Leu Val Glu Ala Pro Asp Ser Glu Glu Ala Gln Lys Ala Ile Arg			
	505	510	515
agt atc cgc caa act ttt gca gat gaa aat ata tca gcg gta gta ggc			1699
Ser Ile Arg Gln Thr Phe Ala Asp Glu Asn Ile Ser Ala Val Val Gly			
	520	525	530
ggg gtc act gca act tcc gta gac act aac gat gcc tcc atc cat gac			1747
Gly Val Thr Ala Thr Ser Val Asp Thr Asn Asp Ala Ser Ile His Asp			
	535	540	545

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cgc aac ctg atc atc cca att gta ttg ctg gtc att ttg gtt att ctc 1795
Arg Asn Leu Ile Ile Pro Ile Val Leu Leu Val Ile Leu Val Ile Leu
550          555          560          565

atg ctg ttg ctg cgg tct att gtc gca cca ctc ctg cta gta gtc acc 1843
Met Leu Leu Leu Arg Ser Ile Val Ala Pro Leu Leu Leu Val Val Thr
          570          575          580

acc gtg gtg tct ttt gct act gct tta ggc gtg gct gct tta ctt ttc 1891
Thr Val Val Ser Phe Ala Thr Ala Leu Gly Val Ala Ala Leu Leu Phe
          585          590          595

aat cac gtt ttc agt ttc cca gga gca gac ccc gca gta cct ctc tac 1939
Asn His Val Phe Ser Phe Pro Gly Ala Asp Pro Ala Val Pro Leu Tyr
          600          605          610

gga ttt gta ttt tta gta gcc ttg ggc atc gac tac aac att ttc tta 1987
Gly Phe Val Phe Leu Val Ala Leu Gly Ile Asp Tyr Asn Ile Phe Leu
          615          620          625

gtc acc cga atc cgt gaa gaa acc aaa acc cac ggc aca aga ctt gga 2035
Val Thr Arg Ile Arg Glu Glu Thr Lys Thr His Gly Thr Arg Leu Gly
630          635          640          645

att ctt cga ggc ctg aca gta acc ggc gga gta att acc tca gct gga 2083
Ile Leu Arg Gly Leu Thr Val Thr Gly Gly Val Ile Thr Ser Ala Gly
          650          655          660

gta gtt ctc gcc gca acg ttc gca gca ctc tat gtc atc cca att cta 2131
Val Val Leu Ala Ala Thr Phe Ala Ala Leu Tyr Val Ile Pro Ile Leu
          665          670          675

ttc ctg gca caa att gcc ttc att gtc gct ttt gga gtt ctt att gat 2179
Phe Leu Ala Gln Ile Ala Phe Ile Val Ala Phe Gly Val Leu Ile Asp
          680          685          690

acc ctg ctc gtt cgc gcc ttc ttg gtg cct gct ttg ttc tac gac atc 2227
Thr Leu Leu Val Arg Ala Phe Leu Val Pro Ala Leu Phe Tyr Asp Ile
          695          700          705

gga ccg aaa atc tgg tgg ccg tca aaa ttg tcc aat cag aaa tac cag 2275
Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser Asn Gln Lys Tyr Gln
710          715          720          725

aag cag cct cag cta tgacacacca aaattcgct ctc 2313
Lys Gln Pro Gln Leu
          730

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<210> 358

<211> 730

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

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Met Ser Thr Ser Ile Thr Thr Glu Asn Lys Lys Lys Ser Gly Pro Pro
  1          5          10          15

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Arg Leu Met Arg Ile Phe Leu Pro Ala Leu Leu Ile Leu Val Trp Leu
  20          25          30

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Val	Gly	Ala	Gly	Val	Gly	Gly	Pro	Tyr	Phe	Gly	Lys	Val	Ser	Glu	Val
		35					40					45			
Ser	Ser	Asn	Ser	Gln	Thr	Thr	Tyr	Leu	Pro	Glu	Ser	Ala	Asp	Ala	Thr
	50					55					60				
Gln	Val	Gln	Glu	Gln	Leu	Gly	Asp	Phe	Thr	Asp	Ser	Glu	Ser	Ile	Pro
	65				70					75					80
Ala	Ile	Val	Val	Met	Val	Ser	Asp	Glu	Pro	Leu	Thr	Gln	Gln	Asp	Ile
				85					90					95	
Thr	Gln	Leu	Asn	Glu	Val	Val	Ala	Gly	Leu	Ser	Glu	Leu	Asp	Ile	Val
			100					105					110		
Ser	Asp	Glu	Val	Ser	Pro	Ala	Ile	Pro	Ser	Glu	Asp	Gly	Arg	Ala	Val
		115					120					125			
Gln	Val	Phe	Val	Pro	Leu	Asn	Pro	Ser	Ala	Glu	Leu	Thr	Glu	Ser	Val
	130					135					140				
Glu	Lys	Leu	Ser	Glu	Thr	Leu	Thr	Gln	Gln	Thr	Pro	Asp	Tyr	Val	Ser
145					150					155					160
Thr	Tyr	Val	Thr	Gly	Pro	Ala	Gly	Phe	Thr	Ala	Asp	Leu	Ser	Ala	Ala
				165					170					175	
Phe	Ala	Gly	Ile	Asp	Gly	Leu	Leu	Leu	Ala	Val	Ala	Leu	Ala	Ala	Val
			180					185					190		
Leu	Val	Ile	Leu	Val	Ile	Val	Tyr	Arg	Ser	Phe	Ile	Leu	Pro	Ile	Ala
		195					200					205			
Val	Leu	Ala	Thr	Ser	Leu	Phe	Ala	Leu	Thr	Val	Ala	Leu	Leu	Val	Val
	210					215					220				
Trp	Trp	Leu	Ala	Lys	Trp	Asp	Ile	Leu	Leu	Leu	Ser	Gly	Gln	Thr	Gln
225					230					235					240
Gly	Ile	Leu	Phe	Ile	Leu	Val	Ile	Gly	Ala	Ala	Thr	Asp	Tyr	Ser	Leu
				245					250					255	
Leu	Tyr	Val	Ala	Arg	Phe	Arg	Glu	Glu	Leu	Arg	Val	Gln	Gln	Asp	Lys
			260					265					270		
Gly	Ile	Ala	Thr	Gly	Lys	Ala	Ile	Arg	Ala	Ser	Val	Glu	Pro	Ile	Leu
		275					280					285			
Ala	Ser	Gly	Ser	Thr	Val	Ile	Ala	Gly	Leu	Leu	Cys	Leu	Leu	Phe	Ser
		290				295					300				
Asp	Leu	Lys	Ser	Asn	Ser	Thr	Leu	Gly	Pro	Val	Ala	Ser	Val	Gly	Ile
305					310					315					320
Ile	Phe	Ala	Met	Leu	Ser	Ala	Leu	Thr	Leu	Leu	Pro	Ala	Leu	Leu	Phe
				325					330					335	
Val	Phe	Gly	Arg	Val	Ala	Phe	Trp	Pro	Lys	Arg	Pro	Lys	Tyr	Glu	Pro
			340					345					350		

Glu 355	Lys 360	Ala 365	Arg 370	Ala 375	Lys 380	Asn 385	Asp 390	Ile 395	Pro 400	Ala 405	Ser 410	Gly 415	Ile 420	Trp 425	Ser 430
Lys 370	Val 375	Ala 380	Asp 385	Leu 390	Val 395	Glu 400	Gln 405	His 410	Pro 415	Arg 420	Ala 425	Ile 430	Trp 435	Val 440	Ser 445
Thr 385	Leu 390	Ile 395	Val 400	Leu 405	Leu 410	Leu 415	Gly 420	Ala 425	Ala 430	Phe 435	Val 440	Pro 445	Thr 450	Leu 455	Lys 460
Ala 405	Asp 410	Gly 415	Val 420	Ser 425	Gln 430	Ser 435	Asp 440	Leu 445	Val 450	Leu 455	Gly 460	Ser 465	Ser 470	Glu 475	Ala 480
Arg 420	Asp 425	Gly 430	Gln 435	Gln 440	Ala 445	Leu 450	Gly 455	Glu 460	His 465	Phe 470	Pro 475	Gly 480	Gly 485	Ser 490	Gly 495
Ser 435	Pro 440	Ala 445	Tyr 450	Ile 455	Ile 460	Val 465	Asp 470	Glu 475	Thr 480	Gln 485	Ala 490	Ala 495	Gln 500	Ala 505	Ala 510
Asp 450	Val 455	Val 460	Leu 465	Asn 470	Asn 475	Asp 480	Asn 485	Phe 490	Glu 495	Thr 500	Val 505	Thr 510	Val 515	Thr 520	Ser 525
Ala 465	Asp 470	Ser 475	Pro 480	Ser 485	Gly 490	Ser 495	Ala 500	Pro 505	Ile 510	Thr 515	Ala 520	Asp 525	Gly 530	Ile 535	Val 540
Pro 480	Leu 485	Gly 490	Ser 495	Gly 500	Thr 505	Ala 510	Pro 515	Gly 520	Pro 525	Val 530	Val 535	Val 540	Glu 545	Gly 550	Gln 555
Val 500	Leu 505	Leu 510	Gln 515	Ala 520	Thr 525	Leu 530	Val 535	Glu 540	Ala 545	Pro 550	Asp 555	Ser 560	Glu 565	Glu 570	Ala 575
Gln 515	Lys 520	Ala 525	Ile 530	Arg 535	Ser 540	Ile 545	Arg 550	Gln 555	Thr 560	Phe 565	Ala 570	Asp 575	Glu 580	Asn 585	Ile 590
Ser 530	Ala 535	Val 540	Val 545	Gly 550	Gly 555	Val 560	Thr 565	Ala 570	Thr 575	Ser 580	Val 585	Asp 590	Thr 595	Asn 600	Asp 605
Ala 545	Ser 550	Ile 555	His 560	Asp 565	Arg 570	Asn 575	Leu 580	Ile 585	Ile 590	Pro 595	Ile 600	Val 605	Leu 610	Leu 615	Val 620
Ile 560	Leu 565	Val 570	Ile 575	Leu 580	Met 585	Leu 590	Leu 595	Leu 600	Arg 605	Ser 610	Ile 615	Val 620	Ala 625	Pro 630	Leu 635
Leu 580	Leu 585	Val 590	Val 595	Thr 600	Thr 605	Val 610	Val 615	Ser 620	Phe 625	Ala 630	Thr 635	Ala 640	Leu 645	Gly 650	Val 655
Ala 595	Ala 600	Leu 605	Leu 610	Phe 615	Asn 620	His 625	Val 630	Phe 635	Ser 640	Phe 645	Pro 650	Gly 655	Ala 660	Asp 665	Pro 670
Ala 610	Val 615	Pro 620	Leu 625	Tyr 630	Gly 635	Phe 640	Val 645	Phe 650	Leu 655	Val 660	Ala 665	Leu 670	Gly 675	Ile 680	Asp 685
Tyr 625	Asn 630	Ile 635	Phe 640	Leu 645	Val 650	Thr 655	Arg 660	Ile 665	Arg 670	Glu 675	Glu 680	Thr 685	Lys 690	Thr 695	His 700
Gly 645	Thr 650	Arg 655	Leu 660	Gly 665	Ile 670	Leu 675	Arg 680	Gly 685	Leu 690	Thr 695	Val 700	Thr 705	Gly 710	Gly 715	Val 720
Ile 660	Thr 665	Ser 670	Ala 675	Gly 680	Val 685	Val 690	Leu 695	Ala 700	Ala 705	Thr 710	Phe 715	Ala 720	Ala 725	Leu 730	Tyr 735
Val 680	Ile 685	Pro 690	Ile 695	Leu 700	Phe 705	Leu 710	Ala 715	Gln 720	Ile 725	Ala 730	Phe 735	Ile 740	Val 745	Ala 750	Ph 755

675						680					685					
Gly	Val	Leu	Ile	Asp	Thr	Leu	Leu	Val	Arg	Ala	Phe	Leu	Val	Pro	Ala	
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Leu	Phe	Tyr	Asp	Ile	Gly	Pro	Lys	Ile	Trp	Trp	Pro	Ser	Lys	Leu	Ser	
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Asn	Gln	Lys	Tyr	Gln	Lys	Gln	Pro	Gln	Leu							
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										Met	His	Leu	Leu	Arg											
										1						5									
gac gac aac tgg tgg gca ccc ggc ttc gtt aaa aag gcc tac acc gtc																	163								
Asp	Asp	Asn	Trp	Trp	Ala	Pro	Gly	Phe	Val	Lys	Lys	Ala	Tyr	Thr	Val										
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atg ggt cac ggc tct gag gtg gag gaa gca cct cgc cca acc acc cgt																	211								
Met	Gly	His	Gly	Ser	Glu	Val	Glu	Glu	Ala	Pro	Arg	Pro	Thr	Thr	Arg										
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cgc ctc aac gac gat gag gaa gtc acc gtg cat gaa gca gtt gtc gct																	259								
Arg	Leu	Asn	Asp	Asp	Glu	Glu	Val	Thr	Val	His	Glu	Ala	Val	Val	Ala										
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ggc gat acc gtg gca tct cgc ggt ggt ttg agc acg cag gaa aac cgt																	307								
Gly	Asp	Thr	Val	Ala	Ser	Arg	Gly	Gly	Leu	Ser	Thr	Gln	Glu	Asn	Arg										
			55							60					65										
gat ctg gtg tcc ttc gtg gaa ctt aag gct cgt ttg gaa aag cgc agg																	355								
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		70							75					80			85								
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Leu	Glu	Asp	Leu	Asp																					
				90																					

<210> 360
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 360
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Arg Pro Thr Thr Arg Arg Leu Asn Asp Asp Glu Glu Val Thr Val His
      35           40           45
Glu Ala Val Val Ala Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser
      50           55           60
Thr Gln Glu Asn Arg Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg
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Leu Glu Lys Arg Arg Leu Glu Asp Leu Asp
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<213> Corynebacterium glutamicum

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<223> RXS02587

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Gly His Phe Ala Tyr Arg Phe Arg Arg Ile Val Pro Leu Val Val Ile
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gcc gcg att ttg gct ttg ttt gtc att ttc ggc acc aag ctg ggc gac 211
Ala Ala Ile Leu Ala Leu Phe Val Ile Phe Gly Thr Lys Leu Gly Asp
      25           30           35

cgc atg agc cag gaa gga tgg gat gat cct ggt tct tcc tcg acc gct 259
Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly Ser Ser Ser Thr Ala
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gcg gcg cgc atc gag ttg gag acc ttt ggg cgt gac aat gac ggc gat 307
Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg Asp Asn Asp Gly Asp
      55           60           65

gtc gtg ttg ctg ttt act gcg cct gaa ggc act tct ttc gat gat gca 355
Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr Ser Phe Asp Asp Ala
      70           75           80           85

gag gtg ttc tcc agc atc tct ggc tac tta gat ggg cta atc gag aac 403
Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp Gly Leu Ile Glu Asn
      90           95           100

aac cct gat gaa gtc agc cac atc aac agc tac ttt gac act cgt aat 451
Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr Phe Asp Thr Arg Asn

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ctc	aaa	ggg	gac	ggc	gag	caa	acg	ctg	aag	gac	ttc	cgg	gag	att	gaa	547				
Leu	Lys	Gly	Asp	Gly	Glu	Gln	Thr	Leu	Lys	Asp	Phe	Arg	Glu	Ile	Glu					
	135					140					145									
gat	cag	ctc	cat	ccg	gac	aac	ctt	gcc	ggg	ggc	gtc	acc	act	gag	gtc	595				
Asp	Gln	Leu	His	Pro	Asp	Asn	Leu	Ala	Gly	Gly	Val	Thr	Thr	Glu	Val					
150					155					160					165					
gcg	ggg	gcc	acc	gct	gta	gcc	gac	gca	ctc	gat	gag	ggc	atg	gct	ggc	643				
Ala	Gly	Ala	Thr	Ala	Val	Ala	Asp	Ala	Leu	Asp	Glu	Gly	Met	Ala	Gly					
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gat	att	tca	cgc	gcc	gaa	gtt	ttt	gcg	ctg	cct	ttc	gtg	gct	atc	ttg	691				
Asp	Ile	Ser	Arg	Ala	Glu	Val	Phe	Ala	Leu	Pro	Phe	Val	Ala	Ile	Leu					
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Leu	Leu	Ile	Val	Phe	Gly	Ser	Val	Val	Ala	Ala	Ala	Met	Pro	Leu	Ile					
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gct	gga	ttc	ttc	cag	gtc	aac	gta	ttt	gca	caa	tct	gtt	gtg	acc	ctt	835				
Ala	Gly	Phe	Phe	Gln	Val	Asn	Val	Phe	Ala	Gln	Ser	Val	Val	Thr	Leu					
230					235					240					245					
ctg	ggc	ttg	ggg	ctt	gcc	att	gac	tat	ggc	tta	ttc	atg	gtc	tct	cgt	883				
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Phe	Arg	Glu	Glu	Met	Asp	Lys	Gly	Thr	Pro	Val	Glu	Gln	Ala	Val	Ala					
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acc	act	acg	gcg	acc	gcg	ggg	aag	act	gtg	gtg	ttc	tct	gca	gcg	atg	979				
Thr	Thr	Thr	Ala	Thr	Ala	Gly	Lys	Thr	Val	Val	Phe	Ser	Ala	Ala	Met					
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Lys	Ser	Val	Ala	Phe	Gly	Ala	Ile	Ser	Ala	Val	Gly	Leu	Ala	Ala	Leu					
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atg	tcg	gtg	acg	gtg	ttg	ccg	tcg	ctg	ttc	agc	atg	ttg	ggg	aag	aat	1123				
Met	Ser	Val	Thr	Val	Leu	Pro	Ser	Leu	Phe	Ser	Met	Leu	Gly	Lys	Asn					
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atc	gat	aag	tgg	agt	ttg	cgt	cgc	act	gct	cga	aca	gcg	cgc	cgt	ttg	1171				
Ile	Asp	Lys	Trp	Ser	Leu	Arg	Arg	Thr	Ala	Arg	Thr	Ala	Arg	Arg	Leu					
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Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp Ala Met Arg His Ala	
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Lys Ala Val Thr Val Gly Val Val Leu Leu Leu Leu Ala Leu Thr Val	
375 380 385	
ccg ttg acg ggc gtg aaa ttc ggc ggc atc aat gaa acg tat ctg cca	1315
Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn Glu Thr Tyr Leu Pro	
390 395 400 405	
cca gct aac gac acc cgc gtc gcc caa gag cgt ttc gac gag gcg ttt	1363
Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg Phe Asp Glu Ala Phe	
410 415 420	
ccc gcc ttc cgc acc gag ccg gtc aag ctt gtg gtc acc ggg gcg gac	1411
Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val Val Thr Gly Ala Asp	
425 430 435	
aac aac cag ctg atc gat atc tat gtt cag gcc aac gaa gtt gag gga	1459
Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala Asn Glu Val Glu Gly	
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Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr Asp Asp Gly Thr Thr	
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gtg ttg tct act ggt att cag gat cgt tcc ctc aat gag cag gta gtg	1555
Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu Asn Glu Gln Val Val	
470 475 480 485	
gag cag ctt cgc gct att tcc gtc cct gag ggc gtt gag gtg cag atc	1603
Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly Val Glu Val Gln Ile	
490 495 500	
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Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile Glu Ala Leu Phe Glu	
505 510 515	
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Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu Ala Thr Phe Ile Leu	
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Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro Ala Lys Ala Ile Ile	
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Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly Ile Leu Thr Leu Met	
550 555 560 565	
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Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn Phe Ser Pro Gly Pro	
570 575 580	
ctg atg agt cca gtg ctg gtg ctg atc atg gct att att tac gga ctt	1891
Leu Met Ser Pro Val Leu Val Leu Ile Met Ala Ile Ile Tyr Gly Leu	
585 590 595	

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Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg Met Val Glu Ala Arg
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gat aaa ggc gaa tcc acc gac gac gcc atc aga tac ggc act gca cac 1987
Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg Tyr Gly Thr Ala His
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acc gga tct atc atc acc gcg gcc gca ctg atc atg att gtg gtc tgt 2035
Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile Met Ile Val Val Cys
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gga gcg ttt ggt ttc tct gag atc gtc atg atg aag tac atc gcg ttc 2083
Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met Lys Tyr Ile Ala Phe
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Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr Ile Ile Arg Met Leu
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ctt gtc ccc cgc cgt gat gca cct gct tcg cga cga caa ctg gtg ggc 2179
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<212> PRT
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Thr Lys Leu Gly Asp Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly
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Ser Ser Ser Thr Ala Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg
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Asp Asn Asp Gly Asp Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr
      65              70              75              80

Ser Phe Asp Asp Ala Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp
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Gly Leu Ile Glu Asn Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr
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Phe Asp Thr Arg Asn Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr
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Phe Ala Ala Leu Gly Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp
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Glu	Gly	Met	Ala 180	Gly	Asp	Ile	Ser	Arg 185	Ala	Glu	Val	Phe	Ala 190	Leu	Pro
Phe	Val	Ala 195	Ile	Leu	Leu	Leu	Ile 200	Val	Phe	Gly	Ser	Val 205	Val	Ala	Ala
Ala	Met 210	Pro	Leu	Ile	Val	Gly 215	Ile	Leu	Ser	Ile	Leu 220	Gly	Ser	Leu	Gly
Ile 225	Leu	Ala	Ile	Leu 230	Ala	Gly	Phe	Phe	Gln	Val 235	Asn	Val	Phe	Ala	Gln 240
Ser	Val	Val	Thr 245	Leu	Leu	Gly	Leu	Gly	Leu 250	Ala	Ile	Asp	Tyr	Gly 255	Leu
Phe	Met	Val	Ser 260	Arg	Phe	Arg	Glu	Glu 265	Met	Asp	Lys	Gly	Thr 270	Pro	Val
Glu	Gln 275	Ala	Val	Ala	Thr	Thr	Thr 280	Ala	Thr	Ala	Gly	Lys 285	Thr	Val	Val
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Pro 305	Gln	Ala	Phe	Leu	Lys 310	Ser	Val	Ala	Phe	Gly 315	Ala	Ile	Ser	Ala	Val 320
Gly	Leu	Ala	Ala 325	Leu	Met	Ser	Val	Thr	Val 330	Leu	Pro	Ser	Leu	Phe 335	Ser
Met	Leu	Gly	Lys 340	Asn	Ile	Asp	Lys	Trp 345	Ser	Leu	Arg	Arg	Thr 350	Ala	Arg
Thr	Ala 355	Arg	Arg	Leu	Glu	Asp	Thr 360	Ile	Trp	Tyr	Arg	Val 365	Pro	Ala	Trp
Ala 370	Met	Arg	His	Ala	Lys	Ala 375	Val	Thr	Val	Gly	Val 380	Val	Leu	Leu	Leu
Leu 385	Ala	Leu	Thr	Val	Pro 390	Leu	Thr	Gly	Val	Lys 395	Phe	Gly	Gly	Ile	Asn 400
Glu	Thr	Tyr	Leu 405	Pro	Pro	Ala	Asn	Asp	Thr 410	Arg	Val	Ala	Gln	Glu 415	Arg
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 500 505 510
 Glu Ala Leu Phe Glu Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu
 515 520 525
 Ala Thr Phe Ile Leu Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro
 530 535 540
 Ala Lys Ala Ile Ile Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly
 545 550 555 560
 Ile Leu Thr Leu Met Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn
 565 570 575
 Phe Ser Pro Gly Pro Leu Met Ser Pro Val Leu Val Leu Ile Met Ala
 580 585 590
 Ile Ile Tyr Gly Leu Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg
 595 600 605
 Met Val Glu Ala Arg Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg
 610 615 620
 Tyr Gly Thr Ala His Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile
 625 630 635 640
 Met Ile Val Val Cys Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met
 645 650 655
 Lys Tyr Ile Ala Phe Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(706)

<223> RXS03042

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 Leu Val Leu Ala Phe

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	10	20	
gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg			211
Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val			
	25	35	
gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca			259
Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro			
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ctg ctg tcc ttc ttg ccg atc atg ctc atc ggc ctg gta ttt ggt ctg			307
Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly Leu Val Phe Gly Leu			
	55	65	
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Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg Met Arg Glu Gly Phe			
	70	80	85
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Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser Asn Gly Phe Lys His			
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Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile Met Val Ser Val Phe			
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Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile Lys Thr Met Gly Phe			
	120	125	130
gct ctg gcc gtt gct gtg ttc ttc gat gcc ttc gtt gtt cgc atg atg			547
Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe Val Val Arg Met Met			
	135	140	145
att atc cct gca aca atg ttc ctg ctt gat gac aag gct tgg tgg cta			595
Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp Lys Ala Trp Trp Leu			
	150	155	160
cct aag tgg ttg gat aag att ctt ccc aac gtt gat gtt gaa ggt gag			643
Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val Asp Val Glu Gly Glu			
	170	175	180
ggt ctt agt gaa cta cat gag gct cgc acc gag gaa ctg aag gaa aat			691
Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu Glu Leu Lys Glu Asn			
	185	190	195
gta ggt gtc ggg gct tagagaaaca aaaaaggctg cta			729
Val Gly Val Gly Ala			
	200		

<210> 364

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

Leu Val Leu Ala Phe Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp
 1 5 10 15
 Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr
 20 25 30
 Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
 35 40 45
 Asp Asp Pro Gln Pro Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly
 50 55 60
 Leu Val Phe Gly Leu Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg
 65 70 75 80
 Met Arg Glu Gly Phe Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser
 85 90 95
 Asn Gly Phe Lys His Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile
 100 105 110
 Met Val Ser Val Phe Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile
 115 120 125
 Lys Thr Met Gly Phe Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe
 130 135 140
 Val Val Arg Met Met Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp
 145 150 155 160
 Lys Ala Trp Trp Leu Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val
 165 170 175
 Asp Val Glu Gly Glu Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu
 180 185 190
 Glu Leu Lys Glu Asn Val Gly Val Gly Ala
 195 200

<210> 365

<211> 826

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(826)

<223> RXS03075

<400> 365

tgtgcaaaat tgcattcagg ctgaaaaatt cctaaaggga ctccgtccga ataattggaa 60

 agcccagaag aacagtcaac tcctagatta aaggataatc gtg gcg aaa ttc ctg 115
 Val Ala Lys Phe Leu
 1 5

 tat aag tta ggc tcc acg gcc tat caa aag aaa tgg ccg ttt ctt gcg 163
 Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys Trp Pro Phe Leu Ala
 10 15 20


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gtc tgg ctc gtg att ctc ata ggt atc acg acg ctg gcg ggg ctg tat 211
Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr Leu Ala Gly Leu Tyr
      25                      30                      35

gcc aag cca acg tcg agt agc ttc tct atc cct ggt ctt gat tct gtc 259
Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro Gly Leu Asp Ser Val
      40                      45                      50

acg acc atg gag aag atg cag gag cgt ttc cct ggt tcg gat gat gca 307
Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro Gly Ser Asp Asp Ala
      55                      60                      65

aca tcg gct ccc act ggt tct gtc gtc att cag gca ccg gaa ggc aag 355
Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln Ala Pro Glu Gly Lys
      70                      75                      80                      85

acc ctc act gat cct gag gtt ggg gct gaa gta aac cag atg ctt gat 403
Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val Asn Gln Met Leu Asp
      90                      95                      100

gag gtt cgg gcg act ggt gtg ctg aag gat gct gat tcc gtt gtg gat 451
Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala Asp Ser Val Val Asp
      105                      110                      115

cct gtg ttg gct gcg cag ggt gtg gct gct cag atg acc cca gcc ctg 499
Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln Met Thr Pro Ala Leu
      120                      125                      130

gag gct cag ggt gta cct gcg gag aag atc gcc gca gat att gag tcg 547
Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala Ala Asp Ile Glu Ser
      135                      140                      145

att agt cca ctg agt gca gat gag act acc ggc atc atc tcg atg act 595
Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly Ile Ile Ser Met Thr
      150                      155                      160                      165

ttt gat gca gat tct gcc atg gat ata tcc gca gag gat cgt gag aag 643
Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala Glu Asp Arg Glu Lys
      170                      175                      180

gtc acc aat att ctt gat gaa tac gat gac ggc gat ctg act gtt gtc 691
Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly Asp Leu Thr Val Val
      185                      190                      195

tac aac ggc aac gtg ttt ggc gca gct gca acc ago ttg gac atg acc 739
Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr Ser Leu Asp Met Thr
      200                      205                      210

tct gag ctc atc ggc ctg ctg gtg gct gcg gtc gtt ctt atc gtg acc 787
Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr
      215                      220                      225

ttc ggt tcg ttc atc gct gcc ggt atg ccg ctg atc tct 826
Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu Ile Ser
      230                      235                      240

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<210> 366

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

Val Ala Lys Phe Leu Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys
1 5 10 15

Trp Pro Phe Leu Ala Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr
20 25 30

Leu Ala Gly Leu Tyr Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro
35 40 45

Gly Leu Asp Ser Val Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro
50 55 60

Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln
65 70 75 80

Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val
85 90 95

Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala
100 105 110

Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln
115 120 125

Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala
130 135 140

Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly
145 150 155 160

Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala
165 170 175

Glu Asp Arg Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly
180 185 190

Asp Leu Thr Val Val Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr
195 200 205

Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val
210 215 220

Val Leu Ile Val Thr Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu
225 230 235 240

Ile Ser

<211> 983

<213> Corynebacterium glutamicum

<221> CDS

<223> RXS03124

<400> 367

atg act cct acc ctg gcg tcg atg att ggt ctg gct gtc ggt atc gac	48
Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp	
1 5 10 15	
tac gcg cta ttt atc gtg tcc cgt ttc cgc aat gag ttg att tct cag	96
Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln	
20 25 30	
act ggc gct aat gat ctg gag cca aag gaa ttg gct gag cgt ctg cgc	144
Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg	
35 40 45	
acc atg ccg ttg gct gct cgt gcg cat gcg atg gga atg gct gtg ggc	192
Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly	
50 55 60	
act gcg ggt tct gcg gtt gta ttc gcg ggt acc acg gtg ctg atc gct	240
Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala	
65 70 75 80	
ctg gtt gct ctg tcg atc att aat att cca ttt cta acc gtg atg gcc	288
Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala	
85 90 95	
att gct gcc gca atc acc gtt gcc atc gca gtt ctg gtt gct ctg tcc	336
Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser	
100 105 110	
ttc ctc cca gct ctg ctt ggc ctg ctt ggc act cgc atc ttc gca gca	384
Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala	
115 120 125	
cgc gtg cct gga cct aag gtt ccg gat cct gag gac gag aag cca acg	432
Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr	
130 135 140	
atg ggt ctg aag tgg gtc cgc ctt gtg cgc aag atg ccg gtg gct tac	480
Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr	
145 150 155 160	
ctg ctg gtt ggc gtc gtt ttg ctt ggt gca atc gca att cct gcg acc	528
Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr	
165 170 175	
aat atg cgc ctg gcc atg ccg act gat ggc acc tcc acg ctg ggc acc	576
Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr	
180 185 190	
gcg ccg cgc acg ggg tat gac atg acg gca gat gcg ttc ggc ccg ggc	624
Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly	
195 200 205	
cgc aac gcg ccc atg att gcg ctt atc gac gca acc gac gtc cct gag	672
Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu	
210 215 220	
gaa gaa cgc cca ttg gtg ttt gga cag gcg gtg gag caa ttc ttg aac	720
Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn	
225 230 235 240	

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act gat ggt gtg aag aat gct cag atc act cag acc acg gag aat ttc 768
Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe
245 250 255

gat acc gcg cag atc ctg tta ccc cag aat ttg atg cga tcg atg agc 816
Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser
260 265 270

gca cct ctg aga ctc tgc caa ctc ttc gtg cag atg ctg aga cct tgc 864
Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser
275 280 285

ctg atg aca ccg gcg cga cgt atg gca tta ctg gcg tca ccc caa ttt 912
Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe
290 295 300

acg atg aca tct ctg ctc gcc tgg gcg acg tcc tgg ttc ctt acg ttc 960
Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe
305 310 315 320

tgatcgtttt ggttctagcg ttc 983

<210> 368

 $\langle 211 \rangle$ 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 368

Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp
1 5 10 15

Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
20 25 30

Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
35 40 45

Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
50 55 60

Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
65 70 75 80

Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
85 90 95

Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
100 105 110

Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
115 120 125

Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
130 135 140

Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
145 150 155 160

Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
165 170 175

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Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
      180                      185                      190

Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
      195                      200                      205

Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
      210                      215                      220

Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
      225                      230                      235                      240

Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe
      245                      250                      255

Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser
      260                      265                      270

Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser
      275                      280                      285

Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe
      290                      295                      300

Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe
      305                      310                      315                      320

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<210> 369
<211> 271
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(271)
<223> RXS03125

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<400> 369
tgacaccggc gcgacgtatg gcattactgg cgtcacccca atttacgatg acatctctgc 60

tcgcctcggc gacgtcctgg ttccttacgt tctgatcggt ttg gtt cta gcg ttc 115
                                   Leu Val Leu Ala Phe
                                   1           5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163
Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
      10                      15                      20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg 211
Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val
      25                      30                      35

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca 259
Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro
      40                      45                      50

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BGI-131CP-485

ctg ctg tgc ttc
 Leu Leu Cys Phe
 55

271

<210> 370
 <211> 57
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 370
 Leu Val Leu Ala Phe Leu Val Leu Leu Val Phe Arg Ser Ile Trp
 1 5 10 15

Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr
 20 25 30

Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
 35 40 45

Asp Asp Pro Gln Pro Leu Leu Cys Phe
 50 55

<210> 371
 <211> 576
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(553)
 <223> RXA00596

<400> 371
 ccgccaccga cggcctcttg aacaccgatg cataccaaca ggctgtgctc ggtgaaaatg 60
 ccacgcggagt gccaaagccct agctaccagg gaggaacta atg ctt aac gcc ctg 115
 Met Leu Asn Ala Leu
 1 5
 aaa ttc atc cca tgg ctg atc ggc cag att ttc ctc tct ggc ttc agc 163
 Lys Phe Ile Pro Trp Leu Ile Gly Gln Ile Phe Leu Ser Gly Phe Ser
 10 15 20
 gtg atc acc gct gcg gta aaa aag gac acc ggc ttc aac ccc gtt gtt 211
 Val Ile Thr Ala Ala Val Lys Lys Asp Thr Gly Phe Asn Pro Val Val
 25 30 35
 atc cgc tac cca ctt cga gtg acc acg gac ttc cag atc gca gcc ctg 259
 Ile Arg Tyr Pro Leu Arg Val Thr Thr Asp Phe Gln Ile Ala Ala Leu
 40 45 50
 tca acg tgc atc acc gcg act cct tcc acc ctg tcc ctt ggc cta cgc 307
 Ser Thr Cys Ile Thr Ala Thr Pro Ser Thr Leu Ser Leu Gly Leu Arg
 55 60 65
 gaa ccc cgc aag ccc ggc gac ccc acc att ttg ctg atc caa gca gtg 355
 Glu Pro Arg Lys Pro Gly Asp Pro Thr Ile Leu Leu Ile Gln Ala Val
 70 75 80 85

ttt ggt tcc gat cca gta gaa gtt ttt gaa tcc atc gcc gat atg gaa 403
 Phe Gly Ser Asp Pro Val Glu Val Phe Glu Ser Ile Ala Asp Met Glu
 90 95 100

 caa cgc ctc gtc cct tcg gtc gct tca att gac cac ggc gtc cca ggc 451
 Gln Arg Leu Val Pro Ser Val Ala Ser Ile Asp His Gly Val Pro Gly
 105 110 115

 caa ggc cct tac aag gag atc cgc ccc agc gat gct gag tgg cca agt 499
 Gln Gly Pro Tyr Lys Glu Ile Arg Pro Ser Asp Ala Glu Trp Pro Ser
 120 125 130

 cgc gag atc gct gac acc gcc caa aac acc gtc agc caa gac aag agg 547
 Arg Glu Ile Ala Asp Thr Ala Gln Asn Thr Val Ser Gln Asp Lys Arg
 135 140 145

 gag ttt taaaacaaca tgactgcttt tgg 576
 Glu Phe
 150

<210> 372
 <211> 151
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 372
 Met Leu Asn Ala Leu Lys Phe Ile Pro Trp Leu Ile Gly Gln Ile Phe
 1 5 10 15

 Leu Ser Gly Phe Ser Val Ile Thr Ala Ala Val Lys Lys Asp Thr Gly
 20 25 30

 Phe Asn Pro Val Val Ile Arg Tyr Pro Leu Arg Val Thr Thr Asp Phe
 35 40 45

 Gln Ile Ala Ala Leu Ser Thr Cys Ile Thr Ala Thr Pro Ser Thr Leu
 50 55 60

 Ser Leu Gly Leu Arg Glu Pro Arg Lys Pro Gly Asp Pro Thr Ile Leu
 65 70 75 80

 Leu Ile Gln Ala Val Phe Gly Ser Asp Pro Val Glu Val Phe Glu Ser
 85 90 95

 Ile Ala Asp Met Glu Gln Arg Leu Val Pro Ser Val Ala Ser Ile Asp
 100 105 110

 His Gly Val Pro Gly Gln Gly Pro Tyr Lys Glu Ile Arg Pro Ser Asp
 115 120 125

 Ala Glu Trp Pro Ser Arg Glu Ile Ala Asp Thr Ala Gln Asn Thr Val
 130 135 140

 Ser Gln Asp Lys Arg Glu Phe
 145 150

<210> 373
 <211> 738
 <212> DNA

BGI-131CP

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(715)

<223> RXA02079

<400> 373

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ctcccactac tgcccaaact gccagaagcg gcgctagctg atg agc gaa gct ttt 115
 Met Ser Glu Ala Phe
 1 5

gat gca acc aaa gtg cgc aaa gct gtg ctc acc gtc gcg ctg ctt aac 163
 Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr Val Ala Leu Leu Asn
 10 15 20

ttc gct tat ttc ttt gta gaa ttc ttt att gca tta agc gca ggc tcc 211
 Phe Ala Tyr Phe Phe Val Glu Phe Phe Ile Ala Leu Ser Ala Gly Ser
 25 30 35

gtt tct cta ctg gct gac agt gtc gat ttt ctt gaa gac acc tcc atc 259
 Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu Glu Asp Thr Ser Ile
 40 45 50

aac ctg ctc att ttc att gcc cta gga tgg ccg ttg gcg agg cgc gca 307
 Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro Leu Ala Arg Arg Ala
 55 60 65

gtg atg ggc aaa ctt atg gcg att gtg att ctt gca cct gct gct ttt 355
 Val Met Gly Lys Leu Met Ala Ile Val Ile Leu Ala Pro Ala Ala Phe
 70 75 80 85

gct gcg tgg gca gcg att caa cgg ttt tcc gca ccg caa gcg ccc gaa 403
 Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala Pro Gln Ala Pro Glu
 90 95 100

gtg ttt ccg atc atc gtc gct tct ctg ggc gcc gtc gtg atc aac ggc 451
 Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala Val Val Ile Asn Gly
 105 110 115

gcg agt gcc atc att att tct cga gtg cga caa cat ggt ggc tcg ctt 499
 Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln His Gly Gly Ser Leu
 120 125 130

ggc caa gct gcc ttc cta tcc gcc cga aat gac gtc ctg atc aac att 547
 Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp Val Leu Ile Asn Ile
 135 140 145

gcc atc atc atg atg gcc tta att acc gca tgg acg acg tct gga tgg 595
 Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp Thr Thr Ser Gly Trp
 150 155 160 165

cca gat ttg atc cta ggt tgt ttc atc att ctg ctc gca ctg cac gcc 643
 Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu Leu Ala Leu His Ala
 170 175 180

gct cac gag gtg tgg gaa gtc agt gag gaa gaa cgc ctc gcc tcc aaa 691
 Ala His Glu Val Trp Glu Val Ser Glu Glu Glu Arg Leu Ala Ser Lys
 185 190 195

CGCGGACGCT GC

gcc ctt gct ggg gaa gcc atc gat taggggagca gtatgagctt ttc
 Ala Leu Ala Gly Glu Ala Ile Asp
 200 205

738

<210> 374
 <211> 205
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 374
 Met Ser Glu Ala Phe Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr
 1 5 10 15
 Val Ala Leu Leu Asn Phe Ala Tyr Phe Phe Val Glu Phe Phe Ile Ala
 20 25 30
 Leu Ser Ala Gly Ser Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu
 35 40 45
 Glu Asp Thr Ser Ile Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro
 50 55 60
 Leu Ala Arg Arg Ala Val Met Gly Lys Leu Met Ala Ile Val Ile Leu
 65 70 75 80
 Ala Pro Ala Ala Phe Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala
 85 90 95
 Pro Gln Ala Pro Glu Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala
 100 105 110
 Val Val Ile Asn Gly Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln
 115 120 125
 His Gly Gly Ser Leu Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp
 130 135 140
 Val Leu Ile Asn Ile Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp
 145 150 155 160
 Thr Thr Ser Gly Trp Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu
 165 170 175
 Leu Ala Leu His Ala Ala His Glu Val Trp Glu Val Ser Glu Glu Glu
 180 185 190
 Arg Leu Ala Ser Lys Ala Leu Ala Gly Glu Ala Ile Asp
 195 200 205

<210> 375
 <211> 1458
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1435)
 <223> RXA01303

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[illegible]

Pro Trp Thr Ile Leu Ala Ala Val Leu Ser Phe Leu Phe Leu Lys Asp
 215 220 225

gtc cca gtc acc gca aat ttc cgg caa cag atc gat atc ttt ggc aac 835
 Val Pro Val Thr Ala Asn Phe Arg Gln Gln Ile Asp Ile Phe Gly Asn
 230 235 240 245

aag aac aca tgg att ttg tcc att atc tac ttg atg aca ttc ggt gcc 883
 Lys Asn Thr Trp Ile Leu Ser Ile Ile Tyr Leu Met Thr Phe Gly Ala
 250 255 260

ttc gcc ggt ttc gcc gcg cag ttc ggt ctg atc atc aac aac aac ttc 931
 Phe Ala Gly Phe Ala Ala Gln Phe Gly Leu Ile Ile Asn Asn Asn Phe
 265 270 275

ggc atc gct tcc ccg atg gca gag act tat cca gct gag atg ctt cac 979
 Gly Ile Ala Ser Pro Met Ala Glu Thr Tyr Pro Ala Glu Met Leu His
 280 285 290

gcc ggt gct acg ttc gcg ttt ctt gga cct ttg att ggt gct ttg gtg 1027
 Ala Gly Ala Thr Phe Ala Phe Leu Gly Pro Leu Ile Gly Ala Leu Val
 295 300 305

cgt gct gca tgg ggt cca ctg tgt gac aga ttc ggt gga gct atc tgg 1075
 Arg Ala Ala Trp Gly Pro Leu Cys Asp Arg Phe Gly Gly Ala Ile Trp
 310 315 320 325

acc ttt gtc ggt ggc atc gga atg act atc gcc act gca gct gcc gca 1123
 Thr Phe Val Gly Gly Ile Gly Met Thr Ile Ala Thr Ala Ala Ala
 330 335 340

atc ttc cta agc aga gcg gag aca cct gat gat ttc tgg cca ttc ctg 1171
 Ile Phe Leu Ser Arg Ala Glu Thr Pro Asp Asp Phe Trp Pro Phe Leu
 345 350 355

tgg tcc atg ctt gcc ctg ttc ttc ttc acc ggt ctg ggc aat gct ggc 1219
 Trp Ser Met Leu Ala Leu Phe Phe Phe Thr Gly Leu Gly Asn Ala Gly
 360 365 370

acc ttc aaa caa atg ccc atg att ttg cct aaa cgc caa gca ggt ggc 1267
 Thr Phe Lys Gln Met Pro Met Ile Leu Pro Lys Arg Gln Ala Gly Gly
 375 380 385

gtg atc ggc tgg acc ggt gcc att ggt gcc ttc ggc ccc ttc att gtc 1315
 Val Ile Gly Trp Thr Gly Ala Ile Gly Ala Phe Gly Pro Phe Ile Val
 390 395 400 405

ggt gtc ttg ctc tcc ttc act cca act gtc gcg ttc ttc tgg ggc tgc 1363
 Gly Val Leu Leu Ser Phe Thr Pro Thr Val Ala Phe Phe Trp Gly Cys
 410 415 420

gtg gtg ttc ttc atc atc gcc acc gct ttg acc tgg atc tac tac gcc 1411
 Val Val Phe Phe Ile Ile Ala Thr Ala Leu Thr Trp Ile Tyr Tyr Ala
 425 430 435

cgc ccg aac gct cca ttc ccg gga taaaccgaaa ggccaatcca tga 1458
 Arg Pro Asn Ala Pro Phe Pro Gly
 440 445

<210> 376

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<211> 445
<212> PRT
<213> Corynebacterium glutamicum
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Ile	Thr	Thr	Phe	Ser	Met	Ile	Ile	Gly	Phe	Cys	Val	Trp	Tyr	Leu	Val	
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Ser	Ala	Ile	Ala	Pro	Leu	Leu	Asn	Arg	Ile	Gly	Phe	Asp	Leu	Ser	Ala	
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Gly	Gln	Leu	Tyr	Trp	Leu	Ala	Ser	Ile	Pro	Gly	Leu	Ala	Gly	Gly	Leu	
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Leu	Ala	Ala	Leu	Thr	Gly	Ile	Gly	Gly	Gly	Val	Phe	Ser	Gly	Tyr	Met	
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Pro	Ser	Thr	Gly	Tyr	Phe	Phe	Pro	Lys	Ala	Lys	Ser	Gly	Thr	Ala	Leu	
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Gly	Ile	Gln	Ala	Gly	Ile	Gly	Asn	Leu	Gly	Val	Ser	Ile	Ile	Gln	Phe	
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Met	Gly	Pro	Trp	Val	Met	Gly	Phe	Gly	Leu	Leu	Gly	Ile	Gly	Phe	Leu	
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Thr	Pro	Gln	Arg	Thr	Ile	Glu	Gly	Thr	Thr	Val	Phe	Val	His	Asn	Ala	
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	210					215					220					
Leu	Phe	Leu	Lys	Asp	Val	Pro	Val	Thr	Ala	Asn	Phe	Arg	Gln	Gln	Ile	
225					230					235					240	
Asp	Ile	Phe	Gly	Asn	Lys	Asn	Thr	Trp	Ile	Leu	Ser	Ile	Ile	Tyr	Leu	
				245					250					255		
Met	Thr	Phe	Gly	Ala	Phe	Ala	Gly	Phe	Ala	Ala	Gln	Phe	Gly	Leu	Ile	
		260					265						270			
Ile	Asn	Asn	Asn	Phe	Gly	Ile	Ala	Ser	Pro	Met	Ala	Glu	Thr	Tyr	Pro	
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Ala	Glu	Met	Leu	His	Ala	Gly	Ala	Thr	Phe	Ala	Phe	Leu	Gly	Pro	Leu	
	290					295					300					

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305 310 315 320

Gly Gly Ala Ile Trp Thr Phe Val Gly Gly Ile Gly Met Thr Ile Ala
325 330 335

Thr Ala Ala Ala Ala Ile Phe Leu Ser Arg Ala Glu Thr Pro Asp Asp
340 345 350

Phe Trp Pro Phe Leu Trp Ser Met Leu Ala Leu Phe Phe Phe Thr Gly
355 360 365

Leu Gly Asn Ala Gly Thr Phe Lys Gln Met Pro Met Ile Leu Pro Lys
370 375 380

Arg Gln Ala Gly Gly Val Ile Gly Trp Thr Gly Ala Ile Gly Ala Phe
385 390 395 400

Gly Pro Phe Ile Val Gly Val Leu Leu Ser Phe Thr Pro Thr Val Ala
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Phe Phe Trp Gly Cys Val Val Phe Phe Ile Ile Ala Thr Ala Leu Thr
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<222> (101)..(715)

<223> RXA02079

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Met Ser Glu Ala Phe
1 5

gat gca acc aaa gtg cgc aaa gct gtg ctc acc gtc gcg ctg ctt aac 163
Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr Val Ala Leu Leu Asn
10 15 20

ttc gct tat ttc ttt gta gaa ttc ttt att gca tta agc gca ggc tcc 211
Phe Ala Tyr Phe Phe Val Glu Phe Phe Ile Ala Leu Ser Ala Gly Ser
25 30 35

gtt tct cta ctg gct gac agt gtc gat ttt ctt gaa gac acc tcc atc 259
Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu Glu Asp Thr Ser Ile
40 45 50

aac ctg ctc att ttc att gcc cta gga tgg ccg ttg gcg agg cgc gca 307
Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro Leu Ala Arg Arg Ala
55 60 65

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gtg atg ggc aaa ctt atg gcg att gtg att ctt gca cct gct gct ttt 355
Val Met Gly Lys Leu Met Ala Ile Val Ile Leu Ala Pro Ala Ala Phe
70 75 80 85

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Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala Pro Gln Ala Pro Glu
90 95 100

gtg ttt ccg atc atc gtc gct tct ctg ggc gcc gtc gtg atc aac ggc 451
Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala Val Val Ile Asn Gly
105 110 115

gcg agt gcc atc att att tct cga gtg cga caa cat ggt ggc tcg ctt 499
Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln His Gly Gly Ser Leu
120 125 130

ggc caa gct gcc ttc cta tcc gcc cga aat gac gtc ctg atc aac att 547
Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp Val Leu Ile Asn Ile
135 140 145

gcc atc atc atg atg gcc tta att acc gca tgg acg acg tct gga tgg 595
Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp Thr Thr Ser Gly Trp
150 155 160

cca gat ttg atc cta ggt tgt ttc atc att ctg ctc gca ctg cac gcc 643
Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu Leu Ala Leu His Ala
170 175 180

gct cac gag gtg tgg gaa gtc agt gag gaa gaa cgc ctc gcc tcc aaa 691
Ala His Glu Val Trp Glu Val Ser Glu Glu Glu Arg Leu Ala Ser Lys
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gcc ctt gct ggg gaa gcc atc gat taggggagca gtatgagctt ttc 738
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<212> PRT

<213> Corynebacterium glutamicum

<400> 378

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20 25 30

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Leu Ser Ala Gly Ser Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu
35 40 45

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Glu Asp Thr Ser Ile Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro
50 55 60

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Leu Ala Arg Arg Ala Val Met Gly Lys Leu Met Ala Ile Val Ile Leu
65 70 75 80

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Ala Pro Ala Ala Phe Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala
85 90 95

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Pro Gln Ala Pro Glu Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala
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Val Val Ile Asn Gly Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln
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His Gly Gly Ser Leu Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp
130 135 140

Val Leu Ile Asn Ile Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp
145 150 155 160

Thr Thr Ser Gly Trp Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu
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<223> RXN00832

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Met Pro Phe Ser Trp
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cta aaa cca att gat tat gcc cgc atc ttt gtc ggc tgg gca tcg att 163
Leu Lys Pro Ile Asp Tyr Ala Arg Ile Phe Val Gly Trp Ala Ser Ile
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Phe Ile Ile Pro Leu Ile Thr Leu Pro Ser Ile Ile Glu Leu Ala Leu
25 30 35

atc gtg gca gtc atc cta ttc tgc gca ttt ggc gtg gtg aag atg gcg 259
Ile Val Ala Val Ile Leu Phe Cys Ala Phe Gly Val Val Lys Met Ala
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Glu Arg Leu Ala His Ile Leu Gly Asp Pro Phe Gly Ser Leu Ile Leu
55 60 65

acc ttg tcg atc gtg atc att gaa gtg att ttg atc tgt gcg gtg atg 355
Thr Leu Ser Ile Val Ile Ile Glu Val Ile Leu Ile Cys Ala Val Met
70 75 80 85

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Gly	Gly	Leu	Arg	His	Gly	Ser	Met	Pro	His	Asn	Gly	Val	Gly	Thr	Pro		
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acc	tac	ttg	gtg	ctg	atc	gca	act	ttt	tcc	gta	atc	gcc	ttt	gcg	gtt	547	
Thr	Tyr	Leu	Val	Leu	Ile	Ala	Thr	Phe	Ser	Val	Ile	Ala	Phe	Ala	Val		
	135					140					145						
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Pro	Ala	Phe	Arg	Gly	Glu	Tyr	Ser	Thr	Gly	Gln	Ala	Leu	Val	Ile	Ser		
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Thr	Leu	Thr	Ala	Val	Val	Tyr	Gly	Phe	Phe	Leu	Phe	Arg	Gln	Met	Gly		
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gcc	caa	gct	ggt	gaa	ttt	caa	gag	gtc	gag	gtc	gca	gaa	aag	gca	gac	691	
Ala	Gln	Ala	Gly	Glu	Phe	Gln	Glu	Val	Glu	Val	Ala	Glu	Lys	Ala	Asp		
		185						190					195				
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Asp	Ala	Ala	Lys	Trp	Glu	Val	Pro	Phe	Arg	Gly	Leu	Ile	Leu	Ile	Ile		
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Thr	Val	Leu	Pro	Ile	Val	Leu	Leu	Ser	His	Asp	Met	Ala	Thr	Val	Met		
	215					220					225						
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Ile	Ile	Ala	Thr	Ile	Val	Phe	Leu	Pro	Glu	Thr	Ile	Thr	Ser	Leu	Lys		
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Ala	Ala	Trp	Thr	Gly	Glu	Ile	Gln	Arg	Val	Ser	Asn	Leu	Ala	His	Gly		
		265						270					275				
gcc	caa	gta	tca	acg	gtg	ggg	ctg	aca	atc	cca	gct	gtt	cta	gtg	atc	979	
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Gly	Val	Ile	Thr	Gly	Gln	Asp	Val	Val	Leu	Gly	Glu	Thr	Pro	Ile	Asn		
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Ser	Lys	Lys	Val	Ser	Ala	Val	His	Gly	Ser	Val	Leu	Leu	Met	Leu	Phe		

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 gaa 1173
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 Ile Glu Leu Ala Leu Ile Val Ala Val Ile Leu Phe Cys Ala Phe Gly
 35 40 45
 Val Val Lys Met Ala Glu Arg Leu Ala His Ile Leu Gly Asp Pro Phe
 50 55 60
 Gly Ser Leu Ile Leu Thr Leu Ser Ile Val Ile Ile Glu Val Ile Leu
 65 70 75 80
 Ile Cys Ala Val Met Leu Gly Pro Ala Asp Ser Thr Thr Ala Gly Arg
 85 90 95
 Asp Ser Val Met Ala Val Ser Met Ile Ile Met Gly Leu Val Val Gly
 100 105 110
 Leu Cys Leu Leu Ile Gly Gly Leu Arg His Gly Ser Met Pro His Asn
 115 120 125
 Gly Val Gly Thr Pro Thr Tyr Leu Val Leu Ile Ala Thr Phe Ser Val
 130 135 140
 Ile Ala Phe Ala Val Pro Ala Phe Arg Gly Glu Tyr Ser Thr Gly Gln
 145 150 155 160
 Ala Leu Val Ile Ser Thr Leu Thr Ala Val Val Tyr Gly Phe Phe Leu
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 Phe Arg Gln Met Gly Ala Gln Ala Gly Glu Phe Gln Glu Val Glu Val
 180 185 190
 Ala Glu Lys Ala Asp Asp Ala Ala Lys Trp Glu Val Pro Phe Arg Gly
 195 200 205
 Leu Ile Leu Ile Ile Thr Val Leu Pro Ile Val Leu Leu Ser His Asp
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<222> (1)..(555)
<223> FRXA00832
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Ala	Gln	Ala	Gly	Glu	Phe	Gln	Glu	Val	Glu	Val	Ala	Glu	Lys	Ala	Asp		
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gac	gca	gca	aaa	tgg	gag	gtc	cca	ttt	aga	ggc	tta	atc	ttg	att	atc		144
Asp	Ala	Ala	Lys	Trp	Glu	Val	Pro	Phe	Arg	Gly	Leu	Ile	Leu	Ile	Ile		
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Thr	Val	Leu	Pro	Ile	Val	Leu	Leu	Ser	His	Asp	Met	Ala	Thr	Val	Met		
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Asp	Glu	Val	Leu	Ala	Ser	Leu	Gly	Ala	Pro	Val	Ala	Met	Ala	Gly	Leu		
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att	att	gcc	acc	att	gtc	ttc	ttg	cca	gag	acc	atc	acc	tcc	ttg	aaa		288
Ile	Ile	Ala	Thr	Ile	Val	Phe	Leu	Pro	Glu	Thr	Ile	Thr	Ser	Leu	Lys		
				85					90					95			
gct	gcg	tgg	aca	gga	gag	att	cag	cga	gta	agc	aac	ctc	gcg	cat	gga		336
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gcc	caa	gta	tca	acg	gtg	ggg	ctg	aca	atc	cca	gct	gtt	cta	gtg	atc		384

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 130 135 140

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 Leu Leu Leu Leu Gly Thr Thr Ile Ala Val Thr Ala Ile Ala Phe Ser
 145 150 155 160

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 Ser Lys Lys Val Ser Ala Val His Gly Ser Val Leu Leu Met Leu Phe
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gaa 578

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 35 40 45

Thr Val Leu Pro Ile Val Leu Leu Ser His Asp Met Ala Thr Val Met
 50 55 60

Asp Glu Val Leu Ala Ser Leu Gly Ala Pro Val Ala Met Ala Gly Leu
 65 70 75 80

Ile Ile Ala Thr Ile Val Phe Leu Pro Glu Thr Ile Thr Ser Leu Lys
 85 90 95

Ala Ala Trp Thr Gly Glu Ile Gln Arg Val Ser Asn Leu Ala His Gly
 100 105 110

Ala Gln Val Ser Thr Val Gly Leu Thr Ile Pro Ala Val Leu Val Ile
 115 120 125

Gly Val Ile Thr Gly Gln Asp Val Val Leu Gly Glu Thr Pro Ile Asn
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 165 170 175

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Val Asp Lys Ala Val 5																
aac act gct atc tct gac gcc aaa aca gcg gcg ctc aag gca ggt gtt 163																
Asn Thr Ala Ile Ser Asp Ala Lys Thr Ala Ala Leu Lys Ala Gly Val 20																
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Gly Leu Asn Arg Ala Thr Ala Ser Glu Glu Glu Glu Asp Leu Ser Ser 35																
agc att aag gtt tct ttg gcc ttt gag ctc gag ggg tta agc aat gca 259																
Ser Ile Lys Val Ser Leu Ala Phe Glu Leu Glu Gly Leu Ser Asn Ala 50																
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Pro Ser Leu Met Val Val Glu Lys Ala Leu Glu Lys Ile Pro Gly Val 65																
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Ser Ala Asp Leu Ile Tyr Pro Ser Gln Thr Ala Trp Ile Thr Ala Thr 85																
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Asp Arg Val His Pro Glu Thr Leu Ile Glu Val Phe Glu Gln Phe Gly 100																
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Ile Lys Ala His Leu Ser Asn Ser Ser Leu Leu Arg Arg His Gln Gln 115																
ctc agc gcg gaa gta aat agg gaa gca cgc ctt gat cgt tac cgc tcc 499																
Leu Ser Ala Glu Val Asn Arg Glu Ala Arg Leu Asp Arg Tyr Arg Ser 130																
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Arg Met Asp Ala Lys Arg Ile Ser Pro Arg Val Arg Arg His Asn Arg 145																
caa gaa atg gta cat gcg gta cgc gct cgt gaa agt ggt tgg att aaa 595																
Gln Glu Met Val His Ala Val Arg Ala Arg Glu Ser Gly Trp Ile Lys 165																

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gtg Val	ctg Leu	ttc Phe	acc Thr 185	gcc Ala	cgc Arg	gca Ala	ctg Leu	att Ile 190	aca Thr	cct Pro	aag Lys	cgt Arg	ttg Leu 195	tgg Trp	gtg Val	691
tcg Ser	ttg Leu	ccg Pro 200	ttt Phe	gcg Ala	ctc Leu	atc Ile	gta Val 205	ttg Leu	gcg Ala	tta Leu	tcg Ser 210	ttg Leu	aat Asn	cct Pro	tcg Ser	739
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gct Ala	gct Ala	gca Ala	tac Tyr 265	gcg Ala	tgg Trp	tct Ser	atc Ile	gcc Ala 270	atg Met	ctg Leu	ttg Leu	ttt Phe	gaa Glu 275	acc Thr	cca Pro	931
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ggc Gly	acg Thr 295	ttg Leu	acc Thr	caa Gln	aac Asn	gag Glu 300	att Ile	tat Tyr	ttt Phe	gat Asp	gtg Val 305	gcc Ala	tgc Cys	gga Gly	atc Ile	1027
acc Thr 310	gtg Val	ttg Leu	ctt Leu	ctt Leu	gcc Ala 315	gga Gly	cgg Arg	ctg Leu	ctg Leu	aca Thr 320	agg Arg	cgt Arg	cga Arg	agc Ser	caa Gln 325	1075
tcc Ser	agt Ser	ttg Leu	tta Leu	gcg Ala 330	gaa Glu	ctt Leu	ggg Gly	cgc Arg	ctc Leu 335	caa Gln	atc Ile	gat Asp	cca Pro	cag Gln 340	cgc Arg	1123
att Ile	gtc Val	act Thr 345	gtg Val	gtg Val	cgt Arg	aaa Lys	cac His	cga Arg 350	ttg Leu	aag Lys	cgc Arg	gta Val 355	gtc Val	cag Gln	gaa Glu	1171
ctg Leu	aac Asn 360	att Ile	cca Pro	gtg Val	cag Gln	gaa Glu	gtc Val 365	cgt Arg	gtc Val	aat Asn	gac Asp 370	gat Asp	gtg Val	aaa Lys	gtt Val	1219
cca Pro	cct Pro 375	aat Asn	acc Thr	acg Thr	atc Ile	cct Pro 380	gtg Val	gat Asp	ggc Gly	act Thr 385	gtc Val	atc Ile	ggg Gly	ggc Gly	ggg Gly	1267
tcg Ser 390	cgg Arg	atc Ile	gca Ala	gct Ala	agc Ser 395	atc Ile	atc Ile	atg Met	gga Gly 400	caa Gln	gac Asp	cag Gln	cgt Arg	gat Asp	gta Val 405	1315
aaa	gta	aat	gac	aaa	gtt	ttc	gcc	ggc	agc	ctc	aac	ctc	gaa	tcc	gaa	1363

Lys Val Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu
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 Val His Arg Trp Val Lys Glu Ala Thr Leu Lys Glu Asn Arg His Asn
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 agg gca gcg atc cgt tcg gcc ggt aac ctt gtg ccc atc acg ttc acc 1507
 Arg Ala Ala Ile Arg Ser Ala Gly Asn Leu Val Pro Ile Thr Phe Thr
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 Leu Ala Val Val Asp Phe Cys Leu Trp Ala Leu Ile Ser Gly Asn Ile
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 aac gct gca ttt acc act acc ttg gct gtc ctt gcg tgc gtg gct ccg 1603
 Asn Ala Ala Phe Thr Thr Thr Leu Ala Val Leu Ala Cys Val Ala Pro
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 gtg gcc tta gcg ttg tct gct cca ctt gcc acg agg aat tcc atc gaa 1651
 Val Ala Leu Ala Leu Ser Ala Pro Leu Ala Thr Arg Asn Ser Ile Glu
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 Val Leu Asp Asp Val Asp Thr Ala Val Phe Asn Arg Val Gly Thr Leu
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 Asp Pro Glu Leu Val Leu Arg Val Ala Gly Ala Leu Ala Met Glu Ser
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 His His Ala Ile Ser Lys Ala Leu Val Lys Ala Ser Arg Glu Ala Arg
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 Asp Thr Gly Ala Gly Gly Glu Asp Val Pro His Trp Ile Glu Val Gly
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 aac gtg gaa atc acc gaa gcc ggc tca ttc caa gca acc atc gag ctg 1987
 Asn Val Glu Ile Thr Glu Ala Gly Ser Phe Gln Ala Thr Ile Glu Leu
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 cca ctg atc aaa cca tct ggc gaa aaa atc atg cgc acc aca gaa gca 2035
 Pro Leu Ile Lys Pro Ser Gly Glu Lys Ile Met Arg Thr Thr Glu Ala
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cga tgg aaa ggc aaa gac cgc gga gtt atc act cta agt gac cac gtg 2179
Arg Trp Lys Gly Lys Asp Arg Gly Val Ile Thr Leu Ser Asp His Val
                680                685                690

aga tca gat tcc tcc gat gcg att att gcg att gaa gaa caa ggc atc 2227
Arg Ser Asp Ser Ser Asp Ala Ile Ile Ala Ile Glu Glu Gln Gly Ile
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gag acc atg atg ctt tca cgt gat act tac ccg gtg gca cgt cga tac 2275
Glu Thr Met Met Leu Ser Arg Asp Thr Tyr Pro Val Ala Arg Arg Tyr
710                715                720                725

gca gac agc tta ggc atc acc cac gtc ttg gcc ggc atc gcg ccg ggc 2323
Ala Asp Ser Leu Gly Ile Thr His Val Leu Ala Gly Ile Ala Pro Gly
                730                735                740

aag aaa gcc cag gtc gtc cgt gca gtc cac acc cgc gga tcc act gtc 2371
Lys Lys Ala Gln Val Val Arg Ala Val His Thr Arg Gly Ser Thr Val
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gcg atg atc ggc gat gaa tca gta atg gac tgt ttg aaa gtc gct gac 2419
Ala Met Ile Gly Asp Glu Ser Val Met Asp Cys Leu Lys Val Ala Asp
                760                765                770

gtg ggt gta ctg atg ggc gtc gat cgt ccc tca gat ctg cgt gat gat 2467
Val Gly Val Leu Met Gly Val Asp Arg Pro Ser Asp Leu Arg Asp Asp
775                780                785

tcc gat gac ccg gca gct gac gtt gtg gtc atg cgc gaa gag gtc atg 2515
Ser Asp Asp Pro Ala Ala Asp Val Val Val Met Arg Glu Glu Val Met
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agc gtg ccg acg ctg ttt aaa ctg gct cga cgc tac gcc aag ttg gtc 2563
Ser Val Pro Thr Leu Phe Lys Leu Ala Arg Arg Tyr Ala Lys Leu Val
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Asn Gly Asn Ile Ala Leu Ala Trp Ile Tyr Asn Gly Val Ala Met Val
                825                830                835

ctt gca gtg tct ggc ttg ctg cat cca atg gct gcg acc gtg gct atg 2659
Leu Ala Val Ser Gly Leu Leu His Pro Met Ala Ala Thr Val Ala Met
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Tyr
870

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<213> Corynebacterium glutamicum

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35 40 45

Gly Leu Ser Asn Ala Pro Ser Leu Met Val Val Glu Lys Ala Leu Glu
50 55 60

Lys Ile Pro Gly Val Ser Ala Asp Leu Ile Tyr Pro Ser Gln Thr Ala
65 70 75 80

Trp Ile Thr Ala Thr Asp Arg Val His Pro Glu Thr Leu Ile Glu Val
85 90 95

Phe Glu Gln Phe Gly Ile Lys Ala His Leu Ser Asn Ser Ser Leu Leu
 100 105 110

Arg Arg His Gln Gln Leu Ser Ala Glu Val Asn Arg Glu Ala Arg Leu
115 120 125

Asp Arg Tyr Arg Ser Arg Met Asp Ala Lys Arg Ile Ser Pro Arg Val
130 135 140

Arg Arg His Asn Arg Gln Glu Met Val His Ala Val Arg Ala Arg Glu
145 150 155 160

Ser Gly Trp Ile Lys Arg Arg Asn His Thr Thr Ser Gln His Glu Asp
165 170 175

Pro Met Ser Gly Asp Val Leu Phe Thr Ala Arg Ala Leu Ile Thr Pro
180 185 190

Lys Arg Leu Trp Val Ser Leu Pro Phe Ala Leu Ile Val Leu Ala Leu
195 200 205

Ser Leu Asn Pro Ser Trp Gln Phe Asp Tyr Trp Gln Trp Leu Ser Ala
210 215 220

Val Leu Ala Ile Pro Val Val Val Trp Gly Ala Trp Pro Phe His Arg
225 230 235 240

Ala Ala Ala Gly Gly Ile Arg Arg Gly Ile Ser Ala Leu Asp Ala Thr
245 250 255

Ser Ser Ile Ala Ile Ala Ala Ala Tyr Ala Trp Ser Ile Ala Met Leu
260 265 270

Leu Phe Glu Thr Pro Gly Gly Lys Ser Trp Arg Ser Tyr Pro Ser Trp
275 280 285

Phe Ala Phe Asp His Gly Thr Leu Thr Gln Asn Glu Ile Tyr Phe Asp
290 295 300

Variable	Mean	Standard Deviation	Minimum	Maximum	Skewness	Kurtosis	Jarque-Bera	Probability > Chi-Square
Age	34.50	10.50	20	65	-0.10	3.00	0.95	0.62
Gender	0.50	0.50	0	1	0.00	3.00	0.95	0.62
Marital Status	0.70	0.46	0	1	0.00	3.00	0.95	0.62
Education	12.50	1.50	9	16	-0.10	3.00	0.95	0.62
Income	15.00	5.00	10	30	-0.10	3.00	0.95	0.62
Assets	25.00	10.00	10	40	-0.10	3.00	0.95	0.62
Liabilities	10.00	5.00	5	20	-0.10	3.00	0.95	0.62
Net Worth	15.00	5.00	10	30	-0.10	3.00	0.95	0.62
Debt Ratio	0.40	0.10	0.30	0.50	-0.10	3.00	0.95	0.62
Equity Ratio	0.60	0.10	0.50	0.70	-0.10	3.00	0.95	0.62
Capital Ratio	0.70	0.10	0.60	0.80	-0.10	3.00	0.95	0.62
Loan Ratio	0.30	0.10	0.20	0.40	-0.10	3.00	0.95	0.62
Asset Ratio	0.50	0.10	0.40	0.60	-0.10	3.00	0.95	0.62
Liability Ratio	0.40	0.10	0.30	0.50	-0.10	3.00	0.95	0.62
Equity Ratio	0.60	0.10	0.50	0.70	-0.10	3.00	0.95	0.62
Capital Ratio	0.70	0.10	0.60	0.80	-0.10	3.00	0.95	0.62
Loan Ratio	0.30	0.10	0.20	0.40	-0.10	3.00	0.95	0.62
Asset Ratio	0.50	0.10	0.40	0.60	-0.10	3.00	0.95	0.62
Liability Ratio	0.40	0.10	0.30	0.50	-0.10	3.00	0.95	0.62
Equity Ratio	0.60	0.10	0.50	0.70	-0.10	3.00	0.95	0.62
Capital Ratio	0.70	0.10	0.60	0.80	-0.10	3.00	0.95	0.62
Loan Ratio	0.30	0.10	0.20	0.40	-0.10	3.00	0.95	0.62
Asset Ratio	0.50	0.10	0.40	0.60	-0.10	3.00	0.95	0.62
Liability Ratio	0.40	0.10	0.30	0.50	-0.10	3.00	0.95	0.62
Equity Ratio	0.60	0.10	0.50	0.70	-0.10	3.00	0.95	0.62
Capital Ratio	0.70	0.10	0.60	0.80	-0.10	3.00	0.95	0.62
Loan Ratio	0.30	0.10	0.20	0.40	-0.10	3.00	0.95	0.62
Asset Ratio	0.50	0.10	0.40	0.60	-0.10	3.00	0.95	0.62
Liability Ratio	0.40	0.10	0.30	0.50	-0.10	3.00	0.95	0.62
Equity Ratio	0.60	0.10	0.50	0.70	-0.10	3.00	0.95	0.62
Capital Ratio	0.70	0.10	0.60	0.80	-0.10	3.00	0.95	0.62
Loan Ratio	0.30	0.10	0.20	0.40	-0.10	3.00	0.95	0.62
Asset Ratio	0.50	0.10	0.40	0.60	-0.10	3.00	0.95	0.62
Liability Ratio	0.40	0.10	0.30	0.50	-0.10	3.00	0.95	0.62
Equity Ratio	0.60	0.10	0.50	0.70	-0.10	3.00	0.95	0.62
Capital Ratio	0.70	0.10	0.60	0.80	-0.10	3.00	0.95	0.62
Loan Ratio	0.30	0.10	0.20	0.40	-0.10	3.00	0.95	0.62
Asset Ratio	0.50	0.10	0.40	0.60	-0.10	3.00	0.95	0.62
Liability Ratio	0.40	0.10	0.30	0.50	-0.10	3.00	0.95	0.62
Equity Ratio	0.60	0.10	0.50	0.70	-0.10	3.00	0.95	0.62
Capital Ratio	0.70	0.10	0.60	0.80	-0.10	3.00	0.95	0.62
Loan Ratio	0.30	0.10	0.20	0.40	-0.10	3.00	0.95	0.62
Asset Ratio	0.50	0.1						

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Arg	Arg	Arg	Ser	Gln 325	Ser	Ser	Leu	Leu	Ala 330	Glu	Leu	Gly	Arg	Leu 335	Gln
Ile	Asp	Pro	Gln 340	Arg	Ile	Val	Thr	Val 345	Val	Arg	Lys	His	Arg 350	Leu	Lys
Arg	Val	Val 355	Gln	Glu	Leu	Asn	Ile 360	Pro	Val	Gln	Glu	Val 365	Arg	Val	Asn
Asp 370	Asp	Val	Lys	Val	Pro	Pro 375	Asn	Thr	Thr	Ile	Pro 380	Val	Asp	Gly	Thr
Val 385	Ile	Gly	Gly	Gly	Ser 390	Arg	Ile	Ala	Ala	Ser 395	Ile	Ile	Met	Gly	Gln 400
Asp	Gln	Arg	Asp	Val 405	Lys	Val	Asn	Asp	Lys 410	Val	Phe	Ala	Gly	Ser 415	Leu
Asn	Leu	Glu	Ser 420	Glu	Ile	Lys	Val	Arg 425	Val	Ile	Arg	Thr	Gly 430	His	Arg
Thr	Arg	Ile 435	Ala	Ala	Val	His	Arg 440	Trp	Val	Lys	Glu	Ala 445	Thr	Leu	Lys
Glu 450	Asn	Arg	His	Asn	Arg	Ala 455	Ala	Ile	Arg	Ser	Ala 460	Gly	Asn	Leu	Val
Pro 465	Ile	Thr	Phe	Thr	Leu 470	Ala	Val	Val	Asp	Phe 475	Cys	Leu	Trp	Ala	Leu 480
Ile	Ser	Gly	Asn	Ile 485	Asn	Ala	Ala	Phe	Thr 490	Thr	Thr	Leu	Ala	Val 495	Leu
Ala	Cys	Val 500	Ala	Pro	Val	Ala	Leu	Ala 505	Leu	Ser	Ala	Pro	Leu 510	Ala	Thr
Arg	Asn	Ser 515	Ile	Glu	Ala	Ala	Ala 520	Arg	His	Gly	Ile	Leu 525	Val	Arg	Ser
Gly 530	Glu	Ile	Phe	Arg	Val	Leu 535	Asp	Asp	Val	Asp	Thr 540	Ala	Val	Phe	Asn
Arg 545	Val	Gly	Thr	Leu	Thr 550	Asp	Gly	Glu	Met	Thr 555	Val	Glu	Thr	Val	Thr 560
Ala	Asp	Lys	Gly	Glu 565	Asp	Pro	Glu	Leu	Val 570	Leu	Arg	Val	Ala	Gly 575	Ala
Leu	Ala	Met 580	Glu	Ser	His	His	Ala	Ile 585	Ser	Lys	Ala	Leu	Val 590	Lys	Ala
Ser	Arg	Glu 595	Ala	Arg	Asp	Thr	Gly 600	Ala	Gly	Gly	Glu	Asp 605	Val	Pro	His
Trp 610	Ile	Glu	Val	Gly	Asn 615	Val	Glu	Ile	Thr	Glu	Ala 620	Gly	Ser	Phe	Gln
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 Arg Thr Thr Glu Ala Leu Leu Trp Arg Pro Arg Ser Met Thr Glu Val
 645 650 655
 Arg Glu His Leu Ser Pro Arg Leu Val Ala Ala Ala Thr Ser Gly Gly
 660 665 670
 Ala Pro Leu Ile Val Arg Trp Lys Gly Lys Asp Arg Gly Val Ile Thr
 675 680 685
 Leu Ser Asp His Val Arg Ser Asp Ser Ser Asp Ala Ile Ile Ala Ile
 690 695 700
 Glu Glu Gln Gly Ile Glu Thr Met Met Leu Ser Arg Asp Thr Tyr Pro
 705 710 715 720
 Val Ala Arg Arg Tyr Ala Asp Ser Leu Gly Ile Thr His Val Leu Ala
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 Gly Ile Ala Pro Gly Lys Lys Ala Gln Val Val Arg Ala Val His Thr
 740 745 750
 Arg Gly Ser Thr Val Ala Met Ile Gly Asp Glu Ser Val Met Asp Cys
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 770 775 780
 Asp Leu Arg Asp Asp Ser Asp Asp Pro Ala Ala Asp Val Val Val Met
 785 790 795 800
 Arg Glu Glu Val Met Ser Val Pro Thr Leu Phe Lys Leu Ala Arg Arg
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 Tyr Ala Lys Leu Val Asn Gly Asn Ile Ala Leu Ala Trp Ile Tyr Asn
 820 825 830
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Leu Thr Gln Asn Glu Ile Tyr Phe Asp Val Ala Cys Gly Ile Thr Val	20	25	30	
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Leu Leu Leu Ala Gly Arg Leu Leu Thr Arg Arg Arg Ser Gln Ser Ser	35	40	45	
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Leu Leu Ala Glu Leu Gly Arg Leu Gln Ile Asp Pro Gln Arg Ile Val	50	55	60	
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Thr Val Val Arg Lys His Arg Leu Lys Arg Val Val Gln Glu Leu Asn	65	70	75	80
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Ile Pro Val Gln Glu Val Arg Val Asn Asp Asp Val Lys Val Pro Pro	85	90	95	
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Asn Thr Thr Ile Pro Val Asp Gly Thr Val Ile Gly Gly Gly Ser Arg	100	105	110	
atc gca gct agc atc atc atg gga caa gac cag cgt gat gta aaa gta				384
Ile Ala Ala Ser Ile Ile Met Gly Gln Asp Gln Arg Asp Val Lys Val	115	120	125	
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Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu Ile Lys	130	135	140	
gtt cgt gtt att cgc act ggt cac cgc acc cgc atc gcc gcg gta cat				480
Val Arg Val Ile Arg Thr Gly His Arg Thr Arg Ile Ala Ala Val His	145	150	155	160
agg tgg gtt aaa gaa gcg acg ttg aag gaa aac cgc cac aat agg gca				528
Arg Trp Val Lys Glu Ala Thr Leu Lys Glu Asn Arg His Asn Arg Ala	165	170	175	
gcg atc cgt tgc gcc ggt aac ctt gtg ccc atc acg ttc acc ctt gct				576
Ala Ile Arg Ser Ala Gly Asn Leu Val Pro Ile Thr Phe Thr Leu Ala	180	185	190	
gtg gtg gac ttc tgt ctg tgg gca ctg atc tct gga aac atc aac gct				624
Val Val Asp Phe Cys Leu Trp Ala Leu Ile Ser Gly Asn Ile Asn Ala	195	200	205	
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Ala Phe Thr Thr Thr Leu Ala Val Leu Ala Cys Val Ala Pro Val Ala	210	215	220	
tta gcg ttg tct gct cca ctt gcc acg agg aat tcc atc gaa gct gca				720
Leu Ala Leu Ser Ala Pro Leu Ala Thr Arg Asn Ser Ile Glu Ala Ala	225	230	235	240
gca cga cac ggt att ttg gtc cgc tct ggt gaa att ttc cga gtt ctc				768
Ala Arg His Gly Ile Leu Val Arg Ser Gly Glu Ile Phe Arg Val Leu	245	250	255	

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Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	10	16
Income	3500	1500	1000	8000
Health	0.8	0.3	0	1
Smoking	0.2	0.4	0	1
Alcohol	0.1	0.3	0	1
Exercise	0.3	0.5	0	1
Stress	0.6	0.4	0	1
Sleep	0.7	0.3	0	1
Diet	0.5	0.5	0	1
Work	0.8	0.3	0	1
Family	0.6	0.4	0	1
Friends	0.7	0.3	0	1
Hobbies	0.5	0.5	0	1
Travel	0.4	0.5	0	1
Shopping	0.6	0.4	0	1
Reading	0.3	0.5	0	1
Writing	0.2	0.4	0	1
Art	0.1	0.3	0	1
Music	0.2	0.4	0	1
Gardening	0.3	0.5	0	1
Volunteering	0.2	0.4	0	1
Religion	0.5	0.5	0	1
Politics	0.4	0.5	0	1
Environment	0.3	0.5	0	1
Technology	0.6	0.4	0	1
Science	0.2	0.4	0	1
History	0.3	0.5	0	1
Geography	0.2	0.4	0	1
Language	0.1	0.3	0	1
Math	0.2	0.4	0	1
Science	0.3	0.5	0	1
History	0.2	0.4	0	1
Geography	0.1	0.3	0	1
Language	0.2	0.4	0	1
Math	0.1	0.3	0	1
Science	0.2	0.4	0	1
History	0.3	0.5	0	1
Geography	0.2	0.4	0	1
Language	0.1	0.3	0	1
Math	0.2	0.4	0	1
Science	0.3	0.5	0	1
History	0.2	0.4	0	1
Geography	0.1	0.3	0	1
Language	0.2	0.4	0	1
Math	0.1	0.3	0	1
Science	0.2	0.4	0	1
History	0.3	0.5	0	1
Geography	0.2	0.4	0	1
Language	0.1	0.3	0	1
Math	0.2	0.4	0	1
Science	0.3	0.5	0	1
History	0.2	0.4	0	1
Geography	0.1	0.3	0	1
Language	0.2	0.4	0	1
Math	0.1	0.3	0	1
Science	0.2	0.4	0	1
History	0.3	0.5	0	1
Geography	0.2	0.4	0	1
Language	0.1	0.3	0	1
Math	0.2	0.4	0	1
Science	0.3	0.5	0	1
History	0.2	0.4	0	1
Geography	0.1	0.3	0	1
Language	0.2	0.4	0	1
Math	0.1	0.3	0	1
Science	0.2	0.4	0	1
History	0.3	0.5	0	1
Geography	0.2	0.4	0	1
Language	0.1	0.3	0	1
Math	0.2	0.4	0	1
Science	0.3	0.5	0	1
History	0.2	0.4	0	1
Geography	0.1	0.3	0	1
Language	0.2	0.4	0	1
Math	0.1	0.3	0	1
Science	0.2	0.4	0	1
History	0.3	0.5	0	1
Geography	0.2	0.4	0	1
Language	0.1	0.3	0	1
Math	0.2	0.4	0	1
Science	0.3	0.5	0	1
History	0.2	0.4	0	1
Geography	0.1	0.3	0	1
Language	0.2	0.4	0	1

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gta ctg atg ggc gtc gat cgt ccc tca gat ctg cgt gat gat tcc gat 1536
Val Leu Met Gly Val Asp Arg Pro Ser Asp Leu Arg Asp Asp Ser Asp
500 505 510

gac ccg gca gct gac gtt gtg gtc atg cgc gaa gag gtc atg agc gtg 1584
Asp Pro Ala Ala Asp Val Val Val Met Arg Glu Glu Val Met Ser Val
515 520 525

ccg acg ctg ttt aaa ctg gct cga cgc tac gcc aag ttg gtc aat ggc 1632
Pro Thr Leu Phe Lys Leu Ala Arg Arg Tyr Ala Lys Leu Val Asn Gly
530 535 540

aat att gct ctg gcc tgg atc tat aac ggt gtt gcc atg gtg ctt gca 1680
Asn Ile Ala Leu Ala Trp Ile Tyr Asn Gly Val Ala Met Val Leu Ala
545 550 555 560

gtg tct ggc ttg ctg cat cca atg gct gcg acc gtg gct atg ctg gcg 1728
Val Ser Gly Leu Leu His Pro Met Ala Ala Thr Val Ala Met Leu Ala
565 570 575

tct tcg ctg ctt att gaa tgg cgc tcg ggc agg gcg cgc aag tac 1773
Ser Ser Leu Leu Ile Glu Trp Arg Ser Gly Arg Ala Arg Lys Tyr
580 585 590

taaccagcaa ttcccaagcc caa 1796

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<210> 386

<211> 591

<212> PRT

<213> Corynebacterium glutamicum

<400> 386

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Lys Ser Trp Arg Ser Tyr Pro Ser Trp Phe Ala Phe Asp His Gly Thr
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Leu Thr Gln Asn Glu Ile Tyr Phe Asp Val Ala Cys Gly Ile Thr Val
20 25 30

```

```

Leu Leu Leu Ala Gly Arg Leu Leu Thr Arg Arg Arg Ser Gln Ser Ser
35 40 45

```

```

Leu Leu Ala Glu Leu Gly Arg Leu Gln Ile Asp Pro Gln Arg Ile Val
50 55 60

```

```

Thr Val Val Arg Lys His Arg Leu Lys Arg Val Val Gln Glu Leu Asn
65 70 75 80

```

```

Ile Pro Val Gln Glu Val Arg Val Asn Asp Asp Val Lys Val Pro Pro
85 90 95

```

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Asn Thr Thr Ile Pro Val Asp Gly Thr Val Ile Gly Gly Gly Ser Arg
100 105 110

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```

Ile Ala Ala Ser Ile Ile Met Gly Gln Asp Gln Arg Asp Val Lys Val
115 120 125

```

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Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu Ile Lys
130 135 140

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Val Arg Val Ile Arg Thr Gly His Arg Thr Arg Ile Ala Ala Val His

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145		150		155		160
Arg Trp Val Lys	Glu Ala Thr Leu Lys	Glu Asn Arg His Asn Arg Ala				
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	180	185			190	
Val Val Asp Phe Cys Leu Trp Ala Leu Ile Ser Gly Asn Ile Asn Ala						
	195	200			205	
Ala Phe Thr Thr Thr Leu Ala Val Leu Ala Cys Val Ala Pro Val Ala						
	210	215			220	
Leu Ala Leu Ser Ala Pro Leu Ala Thr Arg Asn Ser Ile Glu Ala Ala						
	225	230			235	240
Ala Arg His Gly Ile Leu Val Arg Ser Gly Glu Ile Phe Arg Val Leu						
	245	250			255	
Asp Asp Val Asp Thr Ala Val Phe Asn Arg Val Gly Thr Leu Thr Asp						
	260	265			270	
Gly Glu Met Thr Val Glu Thr Val Thr Ala Asp Lys Gly Glu Asp Pro						
	275	280			285	
Glu Leu Val Leu Arg Val Ala Gly Ala Leu Ala Met Glu Ser His His						
	290	295			300	
Ala Ile Ser Lys Ala Leu Val Lys Ala Ser Arg Glu Ala Arg Asp Thr						
	305	310			315	320
Gly Ala Gly Gly Glu Asp Val Pro His Trp Ile Glu Val Gly Asn Val						
	325	330			335	
Glu Ile Thr Glu Ala Gly Ser Phe Gln Ala Thr Ile Glu Leu Pro Leu						
	340	345			350	
Ile Lys Pro Ser Gly Glu Lys Ile Met Arg Thr Thr Glu Ala Leu Leu						
	355	360			365	
Trp Arg Pro Arg Ser Met Thr Glu Val Arg Glu His Leu Ser Pro Arg						
	370	375			380	
Leu Val Ala Ala Ala Thr Ser Gly Gly Ala Pro Leu Ile Val Arg Trp						
	385	390			395	400
Lys Gly Lys Asp Arg Gly Val Ile Thr Leu Ser Asp His Val Arg Ser						
	405	410			415	
Asp Ser Ser Asp Ala Ile Ile Ala Ile Glu Glu Gln Gly Ile Glu Thr						
	420	425			430	
Met Met Leu Ser Arg Asp Thr Tyr Pro Val Ala Arg Arg Tyr Ala Asp						
	435	440			445	
Ser Leu Gly Ile Thr His Val Leu Ala Gly Ile Ala Pro Gly Lys Lys						
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Ala Gln Val Val Arg Ala Val His Thr Arg Gly Ser Thr Val Ala Met						
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$\langle 210 \rangle$	388
$\langle 211 \rangle$	68

<212> PRT

<213> Corynebacterium glutamicum

<400> 388

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Val Ala Ser Val Glu Asp Glu Ile Gly Ile Val Ala Gly Thr Gln Gly
 20 25 30

Val Asp Ile Asp Ile Glu Thr Gly Arg Val Thr Val Thr Gly Glu Gly
 35 40 45

Phe Thr Asp Glu Glu Ile Ile Glu Ala Val Ala Asn Ala Gly Tyr Lys
 50 55 60

Val Ser Gly Arg
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<210> 389

<211> 1925

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1902)

<223> RXN01338

<400> 389

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ggc atc atc act gtc gca gcc ctt gtt gcc atc gca ata cat ctc att 96
 Gly Ile Ile Thr Val Ala Ala Leu Val Ala Ile Ala Ile His Leu Ile
 20 25 30

tta tgg ctg gct cta gat cta gat ggc ctt gct aaa aac tgg cct tta 144
 Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn Trp Pro Leu
 35 40 45

ata gcc atc gtt atc gta ggt ggc att ccg ttg atg tgg gat gtg ctg 192
 Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp Asp Val Leu
 50 55 60

aaa tca gcc att aaa act cgc ggt ggc gcg gat act tta gca gca gtc 240
 Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu Ala Ala Val
 65 70 75 80

tcc atc att act tct gtg ttg tta ggg gag tgg ttg gtt gcc gcg atc 288
 Ser Ile Ile Thr Ser Val Leu Leu Gly Glu Trp Leu Val Ala Ala Ile
 85 90 95

atc gtg ctc atg ctc tct ggt ggt gaa gcg cta gaa gag gca gca tca 336
 Ile Val Leu Met Leu Ser Gly Gly Glu Ala Leu Glu Glu Ala Ala Ser
 100 105 110

cgg cga gcc agt ggc acc ttg gac gca ctt gcc cgg cgc gca cca agt 384
 Arg Arg Ala Ser Gly Thr Leu Asp Ala Leu Ala Arg Arg Ala Pro Ser

115					120					125						
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Thr	Ala	His	Arg	Leu	Leu	Gly	Ala	Thr	Ile	Leu	Asp	Gly	Thr	Glu	Glu	
130					135					140						
atc	gcc	gtg	gaa	gag	atc	acg	ggt	ggt	gat	tta	gtg	gcg	gtg	ctc	ccg	480
Ile	Ala	Val	Glu	Glu	Ile	Thr	Val	Gly	Asp	Leu	Val	Ala	Val	Leu	Pro	
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cat	gaa	ctt	tgt	ccc	gtg	gat	ggt	gaa	atc	gtg	gca	ggc	cac	ggc	acc	528
His	Glu	Leu	Cys	Pro	Val	Asp	Gly	Glu	Ile	Val	Ala	Gly	His	Gly	Thr	
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Met	Asp	Glu	Ser	Tyr	Leu	Thr	Gly	Glu	Pro	Tyr	Val	Val	Ser	Lys	Ser	
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aaa	ggt	tcg	caa	gca	atg	tcg	ggt	gca	gtc	aat	ggt	gat	act	ccg	ctg	624
Lys	Gly	Ser	Gln	Ala	Met	Ser	Gly	Ala	Val	Asn	Gly	Asp	Thr	Pro	Leu	
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Thr	Ile	Val	Ala	Thr	Lys	Leu	Ala	His	Asp	Ser	Arg	Tyr	Ala	Gln	Ile	
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Val	Gly	Val	Leu	His	Glu	Ala	Glu	Asn	Asn	Arg	Pro	Glu	Met	Arg	Arg	
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Met	Ala	Asp	Arg	Leu	Gly	Ala	Trp	Tyr	Thr	Val	Ile	Ala	Leu	Ala	Leu	
245					250					255						
ggt	ggt	ctt	ggc	tgg	att	gtc	tcc	ggc	gac	cca	gtg	agg	ttc	ttg	gct	816
Gly	Gly	Leu	Gly	Trp	Ile	Val	Ser	Gly	Asp	Pro	Val	Arg	Phe	Leu	Ala	
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gtt	gtc	gtt	gtc	gcc	acc	cca	tgt	cca	ttg	ctc	att	gca	gtg	cca	gtg	864
Val	Val	Val	Val	Ala	Thr	Pro	Cys	Pro	Leu	Leu	Ile	Ala	Val	Pro	Val	
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gcg	atc	atc	ggt	gcg	att	tct	ctt	gcg	gct	cgt	cgg	ggc	atc	atc	gtg	912
Ala	Ile	Ile	Gly	Ala	Ile	Ser	Leu	Ala	Ala	Arg	Arg	Gly	Ile	Ile	Val	
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Lys	Asn	Pro	Gly	Met	Leu	Glu	Asn	Ala	Ser	Gly	Val	Lys	Thr	Val	Met	
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ttc	gat	aag	act	gga	acg	ctc	acc	tat	ggc	agg	cca	gtg	att	act	gat	1008
Phe	Asp	Lys	Thr	Gly	Thr	Leu	Thr	Tyr	Gly	Arg	Pro	Val	Ile	Thr	Asp	
325					330					335						
atc	cac	act	gct	ccc	gga	gtt	gag	gaa	gat	aca	gtc	cta	gct	ttg	gct	1056
Ile	His	Thr	Ala	Pro	Gly	Val	Glu	Glu	Asp	Thr	Val	Leu	Ala	Leu	Ala	
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gct	tca	gta	gag	cgc	tac	tcc	aga	cac	ccg	ttg	gct	gac	gcg	att	cgt	1104
Ala	Ser	Val	Glu	Arg	Tyr	Ser	Arg	His	Pro	Leu	Ala	Asp	Ala	Ile	Arg	
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Glu Gly Ala Lys Ala Arg Glu Leu His Leu Pro Asp Val Val Glu Val	
370 375 380	
tcg gaa cgt cca gga cag gga cta acc ggc acg gtg ggc gag cac ctg	1200
Ser Glu Arg Pro Gly Gln Gly Leu Thr Gly Thr Val Gly Glu His Leu	
385 390 395 400	
gtt cga ata acc aat agg cgc agc aca cta gaa att gat cca gac agc	1248
Val Arg Ile Thr Asn Arg Arg Ser Thr Leu Glu Ile Asp Pro Asp Ser	
405 410 415	
aag aac tac att ccg gtg aca agt tcc ggc atg gaa tct gtg gtg ctt	1296
Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser Val Val Leu	
420 425 430	
gtt gat gat aaa tat gca gca ctc att cgc ctc cgg gat gaa cct cgt	1344
Val Asp Asp Lys Tyr Ala Ala Leu Ile Arg Leu Arg Asp Glu Pro Arg	
435 440 445	
gca tct gcc agt gag ttc atc gcg cac ttg ccc aag aag cac aaa gtg	1392
Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys His Lys Val	
450 455 460	
gac aag ctc atg att atc tct ggt gat cgc gca tct gag gtt cgt tac	1440
Asp Lys Leu Met Ile Ile Ser Gly Asp Arg Ala Ser Glu Val Arg Tyr	
465 470 475 480	
ctt gcg gac aag gtt ggc att gat gag gta cac gca gag gcc tca ccg	1488
Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu Ala Ser Pro	
485 490 495	
gaa gac aag ctg aac att gtt aat cgg cat aat gag cac ggc gcc acc	1536
Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His Gly Ala Thr	
500 505 510	
atg ttc tta ggt gat gga atc aac gat gcg cca gcc atg gcc gtt gcc	1584
Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met Ala Val Ala	
515 520 525	
acc gtt ggt gtc gcg atg gga gca gac tcc gat gtc acg tcc gaa gca	1632
Thr Val Gly Val Ala Met Gly Ala Asp Ser Asp Val Thr Ser Glu Ala	
530 535 540	
gca gat gct gtg att ttg gat tct tcc ctg gaa cgt ctc gac gat ctg	1680
Ala Asp Ala Val Ile Leu Asp Ser Ser Leu Glu Arg Leu Asp Asp Leu	
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ctc cac atc agt gca cgg atg cgt cga ata gcg ttg caa tct gcg ggc	1728
Leu His Ile Ser Ala Arg Met Arg Arg Ile Ala Leu Gln Ser Ala Gly	
565 570 575	
ggt ggc atg gcg ttg agt gtc ata gga atg atc ctc gcg gta ttt gga	1776
Gly Gly Met Ala Leu Ser Val Ile Gly Met Ile Leu Ala Val Phe Gly	
580 585 590	
ttc ttg acg cca ctg atg ggt gcg atc ttc caa gag gtc att gac gtg	1824
Phe Leu Thr Pro Leu Met Gly Ala Ile Phe Gln Glu Val Ile Asp Val	
595 600 605	

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ctg gct atc ctc aat tcc gct cgg gtc gca ctg cca cgc gga gcg att 1872
 Leu Ala Ile Leu Asn Ser Ala Arg Val Ala Leu Pro Arg Gly Ala Ile
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agt gat ttt gat acg caa gaa aaa gtt tct tagcagggta acctaaatgt 1922
 Ser Asp Phe Asp Thr Gln Glu Lys Val Ser
 625 630

cgt 1925

<210> 390

<211> 634

<212> PRT

<213> Corynebacterium glutamicum

<400> 390

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Gly Ile Ile Thr Val Ala Ala Leu Val Ala Ile Ala Ile His Leu Ile
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Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn Trp Pro Leu
 35 40 45

Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp Asp Val Leu
 50 55 60

Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu Ala Ala Val
 65 70 75 80

Ser Ile Ile Thr Ser Val Leu Leu Gly Glu Trp Leu Val Ala Ala Ile
 85 90 95

Ile Val Leu Met Leu Ser Gly Gly Glu Ala Leu Glu Glu Ala Ala Ser
 100 105 110

Arg Arg Ala Ser Gly Thr Leu Asp Ala Leu Ala Arg Arg Ala Pro Ser
 115 120 125

Thr Ala His Arg Leu Leu Gly Ala Thr Ile Leu Asp Gly Thr Glu Glu
 130 135 140

Ile Ala Val Glu Glu Ile Thr Val Gly Asp Leu Val Ala Val Leu Pro
 145 150 155 160

His Glu Leu Cys Pro Val Asp Gly Glu Ile Val Ala Gly His Gly Thr
 165 170 175

Met Asp Glu Ser Tyr Leu Thr Gly Glu Pro Tyr Val Val Ser Lys Ser
 180 185 190

Lys Gly Ser Gln Ala Met Ser Gly Ala Val Asn Gly Asp Thr Pro Leu
 195 200 205

Thr Ile Val Ala Thr Lys Leu Ala His Asp Ser Arg Tyr Ala Gln Ile
 210 215 220

Val Gly Val Leu His Glu Ala Glu Asn Asn Arg Pro Glu Met Arg Arg
 225 230 235 240

Met	Ala	Asp	Arg	Leu 245	Gly	Ala	Trp	Tyr	Thr	Val	Ile	Ala	Leu	Ala	Leu
Gly	Gly	Leu	Gly 260	Trp	Ile	Val	Ser	Gly 265	Asp	Pro	Val	Arg	Phe	Leu	Ala
Val	Val	Val 275	Val	Ala	Thr	Pro	Cys 280	Pro	Leu	Leu	Ile	Ala 285	Val	Pro	Val
Ala	Ile 290	Ile	Gly	Ala	Ile	Ser 295	Leu	Ala	Ala	Arg	Arg 300	Gly	Ile	Ile	Val
Lys 305	Asn	Pro	Gly	Met	Leu 310	Glu	Asn	Ala	Ser	Gly 315	Val	Lys	Thr	Val	Met
Phe	Asp	Lys	Thr 325	Gly	Thr	Leu	Thr	Tyr	Gly 330	Arg	Pro	Val	Ile	Thr 335	Asp
Ile	His	Thr	Ala 340	Pro	Gly	Val	Glu	Glu 345	Asp	Thr	Val	Leu	Ala 350	Leu	Ala
Ala	Ser	Val 355	Glu	Arg	Tyr	Ser	Arg 360	His	Pro	Leu	Ala	Asp 365	Ala	Ile	Arg
Glu	Gly 370	Ala	Lys	Ala	Arg	Glu 375	Leu	His	Leu	Pro	Asp 380	Val	Val	Glu	Val
Ser 385	Glu	Arg	Pro	Gly	Gln 390	Gly	Leu	Thr	Gly	Thr 395	Val	Gly	Glu	His	Leu
Val	Arg	Ile	Thr	Asn 405	Arg	Arg	Ser	Thr	Leu 410	Glu	Ile	Asp	Pro	Asp 415	Ser
Lys	Asn	Tyr 420	Ile	Pro	Val	Thr	Ser	Ser 425	Gly	Met	Glu	Ser	Val 430	Val	Leu
Val	Asp	Asp 435	Lys	Tyr	Ala	Ala	Leu 440	Ile	Arg	Leu	Arg	Asp 445	Glu	Pro	Arg
Ala	Ser 450	Ala	Ser	Glu	Phe	Ile 455	Ala	His	Leu	Pro	Lys 460	Lys	His	Lys	Val
Asp 465	Lys	Leu	Met	Ile	Ile 470	Ser	Gly	Asp	Arg	Ala 475	Ser	Glu	Val	Arg	Tyr 480
Leu	Ala	Asp	Lys	Val 485	Gly	Ile	Asp	Glu	Val 490	His	Ala	Glu	Ala	Ser 495	Pro
Glu	Asp	Lys 500	Leu	Asn	Ile	Val	Asn	Arg 505	His	Asn	Glu	His	Gly 510	Ala	Thr
Met	Phe 515	Leu	Gly	Asp	Gly	Ile	Asn 520	Asp	Ala	Pro	Ala	Met 525	Ala	Val	Ala
Thr	Val 530	Gly	Val	Ala	Met	Gly 535	Ala	Asp	Ser	Asp	Val 540	Thr	Ser	Glu	Ala
Ala 545	Asp	Ala	Val	Ile	Leu 550	Asp	Ser	Ser	Leu	Glu 555	Arg	Leu	Asp	Asp	Leu 560

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<210> 391
<211> 2001
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1978)
<223> FRXA01338
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Met Leu Phe Ile Arg																	
1 5																	
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Ser Phe Asp Gly Ile Ile Thr Val Ala Ala Leu Val Ala Ile Ala Ile																	
10 15 20																	
cat ctc att tta tgg ctg gct cta gat cta gat ggc ctt gct aaa aac																	211
His Leu Ile Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn																	
25 30 35																	
tgg cct tta ata gcc atc gtt atc gta ggt ggc att ccg ttg atg tgg																	259
Trp Pro Leu Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp																	
40 45 50																	
gat gtg ctg aaa tca gcc att aaa act cgc ggt ggc gcg gat act tta																	307
Asp Val Leu Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu																	
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Ala Ala Val Ser Ile Ile Thr Ser Val Leu Leu Gly Glu Trp Leu Val																	
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Ala Ala Ser Arg Arg Ala Ser Gly Thr Leu Asp Ala Leu Ala Arg Arg																	
105 110 115																	

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gag	cac	ctg	gtt	cga	ata	acc	aat	agg	cgc	agc	aca	cta	gaa	att	gat	1315	
Glu	His	Leu	Val	Arg	Ile	Thr	Asn	Arg	Arg	Ser	Thr	Leu	Glu	Ile	Asp		
		390			395					400					405		
cca	gac	agc	aag	aac	tac	att	ccg	gtg	aca	agt	tcc	ggc	atg	gaa	tct	1363	
Pro	Asp	Ser	Lys	Asn	Tyr	Ile	Pro	Val	Thr	Ser	Ser	Gly	Met	Glu	Ser		
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Val	Val	Leu	Val	Asp	Asp	Lys	Tyr	Ala	Ala	Leu	Ile	Arg	Leu	Arg	Asp		
			425					430					435				
gaa	cct	cgt	gca	tct	gcc	agt	gag	ttc	atc	gcg	cac	ttg	ccc	aag	aag	1459	
Glu	Pro	Arg	Ala	Ser	Ala	Ser	Glu	Phe	Ile	Ala	His	Leu	Pro	Lys	Lys		
		440					445					450					
cac	aaa	gtg	gac	aag	ctc	atg	att	atc	tct	ggt	gat	cgc	gca	tct	gag	1507	
His	Lys	Val	Asp	Lys	Leu	Met	Ile	Ile	Ser	Gly	Asp	Arg	Ala	Ser	Glu		
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gtt	cgt	tac	ctt	gcg	gac	aag	gtt	ggc	att	gat	gag	gta	cac	gca	gag	1555	
Val	Arg	Tyr	Leu	Ala	Asp	Lys	Val	Gly	Ile	Asp	Glu	Val	His	Ala	Glu		
		470			475					480					485		
gcc	tca	ccg	gaa	gac	aag	ctg	aac	att	gtt	aat	cgg	cat	aat	gag	cac	1603	
Ala	Ser	Pro	Glu	Asp	Lys	Leu	Asn	Ile	Val	Asn	Arg	His	Asn	Glu	His		
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ggc	gcc	acc	atg	ttc	tta	ggt	gat	gga	atc	aac	gat	gcg	cca	gcc	atg	1651	
Gly	Ala	Thr	Met	Phe	Leu	Gly	Asp	Gly	Ile	Asn	Asp	Ala	Pro	Ala	Met		
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Ser	Glu	Ala	Ala	Asp	Ala	Val	Ile	Leu	Asp	Ser	Ser	Leu	Glu	Arg	Leu		
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gac	gat	ctg	ctc	cac	atc	agt	gca	cgg	atg	cgt	cga	ata	gcg	ttg	caa	1795	
Asp	Asp	Leu	Leu	His	Ile	Ser	Ala	Arg	Met	Arg	Arg	Ile	Ala	Leu	Gln		
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acc	cgc	aat	gag	atg	aca	gtc	cgc	gca	atc	gcc	acc	ggt	acg	agt	ctt	1171
Thr	Arg	Asn	Glu	Met	Thr	Val</										

[illegible]

Variable	Mean	SD	Min	Max	Median	Q1	Q3	Mode	Skewness	Kurtosis	Normality
Age	35.2	12.5	18	65	32	28	38	35	0.15	2.8	0.95
Gender	1.2	0.4	1	2	1	1	1	1	-0.1	3.2	0.98
Education	12.5	2.1	8	16	12	11	13	12	0.2	2.5	0.92
Income	1500	500	500	3000	1200	800	1800	1000	0.3	3.5	0.90
Marital Status	1.5	0.5	1	2	1	1	1	1	-0.1	3.1	0.97
Occupation	2.5	1.2	1	4	2	1	3	2	0.2	2.9	0.94
Religion	1.8	0.6	1	3	1	1	1	1	-0.1	3.3	0.96
Health Status	1.2	0.4	1	2	1	1	1	1	-0.1	3.2	0.98
Stress Level	3.5	1.5	1	5	3	2	4	3	0.1	2.7	0.96
Life Satisfaction	4.2	1.0	2	5	4	3	5	4	-0.1	2.9	0.94
Work-Life Balance	3.8	1.2	2	5	4	3	5	4	-0.1	2.8	0.95
Family Support	4.5	0.8	3	5	4	4	5	4	-0.1	2.6	0.97
Community Involvement	2.8	1.1	1	4	3	2	4	3	0.1	2.9	0.93
Personal Growth	3.2	1.3	1	5	3	2	4	3	0.1	2.8	0.94
Overall Well-being	4.0	1.0	2	5	4	3	5	4	-0.1	2.7	0.96

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Gln Val Asn Asp Pro Met Ile Tyr Val Leu Ile Ala Ala Ala Val Leu
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Thr Ala Phe Leu Gly His Trp Thr Asp Thr Ile Val Ile Gly Ala Val
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Val Ile Ile Asn Met Met Val Gly Phe Ile Gln Glu Gly Lys Ala Ala
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Arg Met Leu Ala Ala Thr Asn Leu His Ile Glu Glu Ser Ala Leu Thr
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Gly Glu Ala Glu Ala Val Val Lys Gly Thr Asp Pro Val Glu Ala Asp
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Ala Gly Ile Gly Asp Arg Thr Ser Met Ala Phe Ser Gly Thr Leu Val
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Leu Thr Gly Ser Gly Thr Gly Val Val Thr Ala Thr Gly Ala Gly Thr
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Glu Ile Gly His Ile Thr Thr Met Leu Ala Asp Val Asp Ser Val Asp
 225 230 235 240

Thr Pro Leu Thr Arg Ser Met Lys Lys Phe Ser Ser Ala Leu Ala Ile

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Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	35.5	10.5	20	65	0.1	3.0	0.95
Gender	1.5	0.5	1	2	0.0	3.0	0.95
Marital Status	1.5	0.5	1	2	0.0	3.0	0.95
Education	12.5	2.5	9	16	0.1	3.0	0.95
Income	1500	500	500	3000	0.2	3.0	0.95
Health	1.5	0.5	1	2	0.0	3.0	0.95
Stress	2.5	1.0	1	4	0.1	3.0	0.95
Depression	1.5	0.5	1	2	0.0	3.0	0.95
Life Satisfaction	3.5	1.0	1	5	0.1	3.0	0.95
Work Satisfaction	2.5	1.0	1	4	0.1	3.0	0.95
Family Satisfaction	3.0	1.0	1	4	0.1	3.0	0.95
Community Satisfaction	2.0	1.0	1	4	0.1	3.0	0.95
Overall Satisfaction	2.5	1.0	1	4	0.1	3.0	0.95

Variable	Mean	SD	Min	Max
Age	38.5	12.5	25	65
Gender	Male	Female		
Marital Status	Married	Single		
Education	High School	College		
Occupation	Manager	Worker		
Income	\$30,000	\$40,000		
Health Status	Good	Fair		
Stress Level	Low	High		
Life Satisfaction	High	Low		
Work-Life Balance	Good	Poor		
Family Support	Strong	Weak		
Community Involvement	Active	Passive		
Religious Beliefs	Religious	Secular		
Political Views	Conservative	Liberal		
Environmental Concern	High	Low		
Technology Use	Frequent	Infrequent		
Travel Frequency	Often	Rarely		
Volunteering	Yes	No		
Charitable Giving	Yes	No		
Political Participation	Yes	No		
Community Service	Yes	No		
Neighborhood Watch	Yes	No		
Local Government Engagement	Yes	No		
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Survey Participation	Yes	No		

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gca gtg gtg gga ctt atc acc tgg gac gta gaa cta gca ctg acg ctc 787
 Ala Val Val Gly Leu Ile Thr Trp Asp Val Glu Leu Ala Leu Thr Leu
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tta gtg atc ggc tgc ccc ggc gcg ttg gtt atc tcc atc ccg gtg tcc 835
 Leu Val Ile Gly Cys Pro Gly Ala Leu Val Ile Ser Ile Pro Val Ser
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atc gtc gca ggc atc ggc cgt gct gca cgc gat ggc gtg ctg atc aag 883
 Ile Val Ala Gly Ile Gly Arg Ala Ala Arg Asp Gly Val Leu Ile Lys
 250 255 260

ggt gga gaa tac cta gaa acc gcc gcg aaa gtc gac gtc gtt gtc gtg 931
 Gly Gly Glu Tyr Leu Glu Thr Ala Ala Lys Val Asp Val Val Val Val
 265 270 275

gac aaa act gga acg ctg acc acc ggc cgc cca gaa ctc aca gac gta 979
 Asp Lys Thr Gly Thr Leu Thr Thr Gly Arg Pro Glu Leu Thr Asp Val
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gaa gtc atc gag ccc gcc tac agc cag ggc gag gtg ctg gag ctc gcc 1027
 Glu Val Ile Glu Pro Ala Tyr Ser Gln Gly Glu Val Leu Glu Leu Ala
 295 300 305

gcg cgc gcc gag acg gct tca gaa cat ccg ctt gcc gac gcc atc atc 1075
 Ala Arg Ala Glu Thr Ala Ser Glu His Pro Leu Ala Asp Ala Ile Ile
 310 315 320 325

cgt ggt gcc cag gat cgg ggg ctg tcc aca aca ttg gtg gaa gca gct 1123
 Arg Gly Ala Gln Asp Arg Gly Leu Ser Thr Thr Leu Val Glu Ala Ala
 330 335 340

gaa aac atc acc ggc cga ggc att atc gca aat gtt gat gga cag gca 1171
 Glu Asn Ile Thr Gly Arg Gly Ile Ile Ala Asn Val Asp Gly Gln Ala
 345 350 355

gtt gct gtt gga tct gct gag tta ctt gat cat gaa cca gac tcg acc 1219
 Val Ala Val Gly Ser Ala Glu Leu Leu Asp His Glu Pro Asp Ser Thr
 360 365 370

agg atc ctg gag cta aat gcc gaa gga aag acc gcg atg ttt gtc gga 1267
 Arg Ile Leu Glu Leu Asn Ala Glu Gly Lys Thr Ala Met Phe Val Gly
 375 380 385

gtg aac gga cac gcc att gga atc gtg gcc gtc gcc gac gcc gtt cgt 1315
 Val Asn Gly His Ala Ile Gly Ile Val Ala Val Ala Asp Ala Val Arg
 390 395 400 405

tca gat tct gcc tca gca atc gaa tcg ctg cat aag gcg ggc att caa 1363
 Ser Asp Ser Ala Ser Ala Ile Glu Ser Leu His Lys Ala Gly Ile Gln
 410 415 420

BGI-131CP - 4-10-2010

gtt gtc atg gcg act ggc gac gct cac cgc gtt gca caa aac gtg gcc 1411
 Val Val Met Ala Thr Gly Asp Ala His Arg Val Ala Gln Asn Val Ala
 425 430 435
 tcc aag ctg gga gtg gat gaa gtc tac tca gag cta ctc cct gaa cag 1459
 Ser Lys Leu Gly Val Asp Glu Val Tyr Ser Glu Leu Leu Pro Glu Gln
 440 445 450
 aaa tta gaa ctg gtg cgt gat ctg caa gct gcc ggc aaa acg gtc gcg 1507
 Lys Leu Glu Leu Val Arg Asp Leu Gln Ala Ala Gly Lys Thr Val Ala
 455 460 465
 atg gtg ggt gac gga gtc aac gac acc cca gca ttg gca gct gct gat 1555
 Met Val Gly Asp Gly Val Asn Asp Thr Pro Ala Leu Ala Ala Ala Asp
 470 475 480 485
 atc gga gta gcg atg ggc gtg gca ggt tcc cct gca gcc att gaa acc 1603
 Ile Gly Val Ala Met Gly Val Ala Gly Ser Pro Ala Ala Ile Glu Thr
 490 495 500
 gct gat atc gca ctc atg gcg gat cgt ctc cca cgg ctg gca cat gca 1651
 Ala Asp Ile Ala Leu Met Ala Asp Arg Leu Pro Arg Leu Ala His Ala
 505 510 515
 gtg acc ttg gca aaa cgc acc gta aga acc atg cgc atc aat att ctg 1699
 Val Thr Leu Ala Lys Arg Thr Val Arg Thr Met Arg Ile Asn Ile Leu
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 Ile Ala Leu Ala Thr Val Met Val Leu Leu Ala Gly Val Leu Phe Gly
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 Gly Val Thr Met Ser Val Gly Met Leu Val His Glu Ala Ser Val Leu
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 ctt gtt atc agc atc gcc atg ctg ttg ctg cgt cca aca ctt aaa gaa 1843
 Leu Val Ile Ser Ile Ala Met Leu Leu Arg Pro Thr Leu Lys Glu
 570 575 580
 gat gct gcg caa gca agt gat att aaa cgc tcg gaa ata caa cag atc 1891
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<210> 398

<211> 598

<212> PRT

<213> Corynebacterium glutamicum

<400> 398

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Pro Ile Ala Gln Ser Ala Tyr Gln Ala Leu Arg Ile Arg Met Val Ser
 20 25 30

BGI-131CP - 1998-01-01

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Ile Asp Leu Leu Val Val Val Ala Ala Val Gly Ala Met Phe Ile Asn
      35                      40                      45

Asn Tyr Trp Glu Ser Ala Ala Val Thr Phe Leu Phe Ala Leu Gly Lys
      50                      55                      60

Ala Leu Glu Arg Ala Thr Met Asn Arg Thr Arg Lys Ala Leu Ser Asp
      65                      70                      75                      80

Leu Val Asp Ala Ala Pro Glu Thr Ala Thr Arg Leu Asn Ala Asp Asp
                      85                      90                      95

Ser Thr Glu Val Val Glu Leu Trp Glu Leu Glu Pro Gly Asp Ile Val
      100                      105                      110

Leu Val Arg Asn Gly Glu Gln Ile Pro Val Asp Gly Asn Val Ile Ala
      115                      120                      125

Gly Val Gly Gly Ile Asp Glu Ser Asn Ile Thr Gly Glu Ser Met Pro
      130                      135                      140

Ala Glu Lys Gly Gln Gly Ser Asp Val Tyr Ala Gly Thr Trp Leu Arg
      145                      150                      155                      160

Ser Gly Val Leu Arg Val Glu Ala Thr Gly Ile Gly Ser Asp Ser Thr
      165                      170                      175

Leu Ala Lys Ile Ile His Arg Val Glu Asp Ala Gln Asp Asp Lys Ala
      180                      185                      190

Arg Thr Gln Thr Phe Leu Glu Lys Phe Ser Lys Trp Tyr Thr Pro Gly
      195                      200                      205

Val Met Ile Ala Ala Ala Val Val Gly Leu Ile Thr Trp Asp Val Glu
      210                      215                      220

Leu Ala Leu Thr Leu Leu Val Ile Gly Cys Pro Gly Ala Leu Val Ile
      225                      230                      235                      240

Ser Ile Pro Val Ser Ile Val Ala Gly Ile Gly Arg Ala Ala Arg Asp
      245                      250                      255

Gly Val Leu Ile Lys Gly Gly Glu Tyr Leu Glu Thr Ala Ala Lys Val
      260                      265                      270

Asp Val Val Val Val Asp Lys Thr Gly Thr Leu Thr Thr Gly Arg Pro
      275                      280                      285

Glu Leu Thr Asp Val Glu Val Ile Glu Pro Ala Tyr Ser Gln Gly Glu
      290                      295                      300

Val Leu Glu Leu Ala Ala Arg Ala Glu Thr Ala Ser Glu His Pro Leu
      305                      310                      315                      320

Ala Asp Ala Ile Ile Arg Gly Ala Gln Asp Arg Gly Leu Ser Thr Thr
      325                      330                      335

Leu Val Glu Ala Ala Glu Asn Ile Thr Gly Arg Gly Ile Ile Ala Asn
      340                      345                      350

Val Asp Gly Gln Ala Val Ala Val Gly Ser Ala Glu Leu Leu Asp His

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355 360 365
 Glu Pro Asp Ser Thr Arg Ile Leu Glu Leu Asn Ala Glu Gly Lys Thr
 370 375 380
 Ala Met Phe Val Gly Val Asn Gly His Ala Ile Gly Ile Val Ala Val
 385 390 395 400
 Ala Asp Ala Val Arg Ser Asp Ser Ala Ser Ala Ile Glu Ser Leu His
 405 410 415
 Lys Ala Gly Ile Gln Val Val Met Ala Thr Gly Asp Ala His Arg Val
 420 425 430
 Ala Gln Asn Val Ala Ser Lys Leu Gly Val Asp Glu Val Tyr Ser Glu
 435 440 445
 Leu Leu Pro Glu Gln Lys Leu Glu Leu Val Arg Asp Leu Gln Ala Ala
 450 455 460
 Gly Lys Thr Val Ala Met Val Gly Asp Gly Val Asn Asp Thr Pro Ala
 465 470 475 480
 Leu Ala Ala Ala Asp Ile Gly Val Ala Met Gly Val Ala Gly Ser Pro
 485 490 495
 Ala Ala Ile Glu Thr Ala Asp Ile Ala Leu Met Ala Asp Arg Leu Pro
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 Arg Leu Ala His Ala Val Thr Leu Ala Lys Arg Thr Val Arg Thr Met
 515 520 525
 Arg Ile Asn Ile Leu Ile Ala Leu Ala Thr Val Met Val Leu Leu Ala
 530 535 540
 Gly Val Leu Phe Gly Gly Val Thr Met Ser Val Gly Met Leu Val His
 545 550 555 560
 Glu Ala Ser Val Leu Leu Val Ile Ser Ile Ala Met Leu Leu Leu Arg
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<211> 762

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(739)

<223> FRXA00980

<400> 399

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$\langle 210 \rangle$	400
$\langle 211 \rangle$	213

Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	35.2	12.5	18	65	0.15	3.2	0.98
Gender	0.52	0.50	0	1	-0.05	3.0	0.99
Marital Status	0.68	0.47	0	1	0.10	3.1	0.99
Education	12.5	2.1	8	16	0.20	3.3	0.97
Income	15000	8000	5000	35000	0.30	3.4	0.96
Occupation	1.2	0.8	0	2	0.10	3.1	0.99
Health Status	0.75	0.43	0	1	0.05	3.0	0.99
Stress Level	2.5	1.2	1	4	0.15	3.2	0.98
Life Satisfaction	3.8	1.5	1	5	0.20	3.3	0.97
Resilience	2.2	1.0	1	4	0.10	3.1	0.99
Optimism	3.5	1.3	1	5	0.15	3.2	0.98
Emotional Stability	2.8	1.1	1	4	0.10	3.1	0.99
Self-Esteem	3.2	1.2	1	5	0.15	3.2	0.98
Life Purpose	2.5	1.0	1	4	0.10	3.1	0.99
Meaning in Life	3.0	1.1	1	4	0.15	3.2	0.98
Existential Well-being	2.8	1.0	1	4	0.10	3.1	0.99
Overall Well-being	3.5	1.2	1	5	0.15	3.2	0.98

<213> Corynebacterium glutamicum

Met Phe Val Gly Val Asn Gly His Ala Ile Gly Ile Val Ala Val Ala
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Asp Ala Val Arg Ser Asp Ser Ala Ser Ala Ile Glu Ser Leu His Lys
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Ala Gly Ile Gln Val Val Met Ala Thr Gly Asp Ala His Arg Val Ala
35 40 45

Gln Asn Val Ala Ser Lys Leu Gly Val Asp Glu Val Tyr Ser Glu Leu
50 55 60

Leu Pro Glu Gln Lys Leu Glu Leu Val Arg Asp Leu Gln Ala Ala Gly
65 70 75 80

Lys Thr Val Ala Met Val Gly Asp Gly Val Asn Asp Thr Pro Ala Leu
85 90 95

Ala Ala Ala Asp Ile Gly Val Ala Met Gly Val Ala Gly Ser Pro Ala
100 105 110

Ala Ile Glu Thr Ala Asp Ile Ala Leu Met Ala Asp Arg Leu Pro Arg
115 120 125

Leu Ala His Ala Val Thr Leu Ala Lys Arg Thr Val Arg Thr Met Arg
130 135 140

Ile Asn Ile Leu Ile Ala Leu Ala Thr Val Met Val Leu Leu Ala Gly
145 150 155 160

Val Leu Phe Gly Gly Val Thr Met Ser Val Gly Met Leu Val His Glu
165 170 175

Ala Ser Val Leu Leu Val Ile Ser Ile Ala Met Leu Leu Leu Arg Pro
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Thr Leu Lys Glu Asp Ala Ala Gln Ala Ser Asp Ile Lys Arg Ser Glu
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Ile Gln Gln Ile Ala
210

<213> Corynebacterium glutamicum

<223> RXN02348

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ctc Leu	act Thr	ctc Leu	ggg Gly 25	gcc Ala	cta Leu	ggg Gly	gtt Val	gtg Val 30	ttc Phe	ggc Gly	gac Asp	atc Ile	ggc Gly 35	acc Thr	agc Ser	211
ccc Pro	ctg Leu	tac Tyr 40	tca Ser	ctt Leu	cac His	act Thr	gca Ala 45	ttc Phe	agc Ser	atg Met	cag Gln 50	cac His	aac Asn	aaa Lys	gtc Val	259
gaa Glu	gtc Val 55	act Thr	cag Gln	gaa Glu	aat Asn	gtg Val 60	tac Tyr	ggc Gly	atc Ile	atc Ile	tcc Ser 65	atg Met	gtg Val	ttg Leu	tgg Trp	307
acc Thr 70	atc Ile	act Thr	ttg Leu	atc Ile	gtc Val 75	acc Thr	gtc Val	aaa Lys	tac Tyr 80	gtc Val	atg Met	ctg Leu	gtc Val	acc Thr 85	cga Arg	355
gct Ala	gac Asp	aac Asn	caa Gln 90	gga Gly	caa Gln	ggg Gly	ggc Gly	atc Ile 95	ctg Leu	gcg Ala	ctc Leu	ggt Val	gct Ala 100	ttg Leu	ctg Leu	403
aaa Lys	aac Asn	cgt Arg 105	ggg Gly	cac His	tgg Trp	gga Gly	aaa Lys 110	ttc Phe	gtg Val	gca Ala	gta Val	gcc Ala	ggc Gly 115	atg Met	ttg Leu	451
ggc Gly	gcc Ala	gca Ala 120	ttg Leu	ttt Phe	tat Tyr	ggc Gly	gat Asp 125	gtg Val	gtg Val	atc Ile	acc Thr 130	ccg Pro	gcg Ala	atc Ile	tot Ser	499
gtt Val	ctc Leu 135	agc Ser	gca Ala	aca Thr	gaa Glu	ggc Gly 140	ttg Leu	acg Thr	gtt Val	atc Ile	tcc Ser 145	cca Pro	agc Ser	ttt Phe	gag Glu	547
cgc Arg 150	ttc Phe	att Ile	ctg Leu	ccc Pro	gta Val 155	tct Ser	ctc Leu	gca Ala	gtt Val 160	ctg Leu	atc Ile	gct Ala	att Ile	ttt Phe 165	gca Ala	595
atc Ile	caa Gln	ccg Pro	ctc Leu	ggg Gly 170	aca Thr	gaa Glu	aaa Lys	gtc Val 175	ggc Gly	aaa Lys	gcc Ala	ttc Phe	ggc Gly 180	ccc Pro	atc Ile	643
atg Met	ttg Leu	ctg Leu	tgg Trp 185	ttt Phe	gtc Val	acc Thr	ctt Leu	gca Ala 190	gga Gly	ttg Leu	gga Gly	att Ile	ccg Pro 195	caa Gln	atc Ile	691
atc Ile	ggg Gly	cac His 200	cca Pro	gaa Glu	atc Ile	ttg Leu	cag Gln 205	agc Ser	ttg Leu	tct Ser	cca Pro	cat His 210	tgg Trp	gcc Ala	ctg Leu	739
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gtt Val	gtc Val	ctg Leu	aca Thr	gta Val	acg Thr	ggg Gly	gcg Ala	gaa Glu	gcg Ala	ctc Leu	tac Tyr	gct Ala	gat Asp	atg Met	ggc Gly	835

230						235						240						245	
cat His	ttt Phe	ggg Gly	gcg Ala	agg Arg 250	cca Pro	atc Ile	aga Arg	gtg Val	gcg Ala 255	tgg Trp	ttt Phe	tgc Cys	gtc Val 260	gtc Val	atg Met	883			
cct Pro	gct Ala	tta Leu 265	atc Ile	ttg Leu 265	acg Thr	tat Tyr	ttg Leu	ggg Gly 270	cag Gln	ggc Gly	gcc Ala	ttg Leu 275	gtg Val	atc Ile	aac Asn	931			
cag Gln	cct Pro	gaa Glu 280	gcg Ala	gtg Val	cgc Arg	aac Asn 285	ccc Pro	atg Met	ttt Phe	tat Tyr	ctc Leu	gcg Ala 290	ccg Pro	gaa Glu	ggc Gly	979			
ctg Leu 295	cgg Arg	att Ile	ccg Pro	ttg Leu	gtt Val	att Ile 300	ttg Leu	gcg Ala	acc Thr	atc Ile	gct Ala 305	acg Thr	gtg Val	atc Ile	gca Ala	1027			
tcg Ser 310	cag Gln	gcc Ala	gtg Val	att Ile	tct Ser 315	ggc Gly	gcg Ala	tat Tyr	tca Ser	ttg Leu 320	acc Thr	aag Lys	cag Gln	gcc Ala	gtg Val 325	1075			
aat Asn	ttg Leu	aaa Lys	ctg Leu 330	ctg Leu	cca Pro	cgc Arg	atg Met	gtg Val	atc Ile 335	cgg Arg	cat His	acc Thr	tcc Ser	cgc Arg 340	aaa Lys	1123			
gag Glu	gaa Glu	ggc Gly	cag Gln 345	atc Ile	tat Tyr	atg Met	cca Pro	ctg Leu 350	gtt Val	aat Asn	gga Gly	ttg Leu	ctg Leu 355	ttt Phe	gta Val	1171			
tcc Ser	gtg Val	atg Met 360	gtt Val	gtg Val	gtg Val	ctg Leu	gta Val 365	ttc Phe	cga Arg	tcc Ser	tct Ser	gaa Glu 370	agc Ser	ctc Leu	gcc Ala	1219			
agc Ser 375	gcg Ala	tac Tyr	gga Gly	ctt Leu	gca Ala	gtg Val 380	acc Thr	gga Gly	acc Thr	ttg Leu	gtg Val 385	ctg Leu	gtc Val	agc Ser	gtc Val	1267			
ctg Leu 390	tat Tyr	ctg Leu	atc Ile	tat Tyr	gtt Val 395	cac His	acc Thr	aca Thr	tgg Trp	tgg Trp	aaa Lys	aca Thr	gcg Ala	ctg Leu	ttc Phe 405	1315			
att Ile	gtg Val	ctc Leu	atc Ile	ggc Gly 410	att Ile	cca Pro	gaa Glu	gta Val	ctt Leu 415	cta Leu	ttc Phe	gcc Ala	tgc Ser	aac Asn 420	acc Thr	1363			
acg Thr	aaa Lys	att Ile	cac His 425	gac Asp	ggc Gly	ggc Gly	tgg Trp	ctt Leu 430	cca Pro	cta Leu	ctt Leu	att Ile	gcg Ala 435	gcc Ala	gtg Val	1411			
ctc Leu	atc Ile	gtg Val 440	gtg Val	atg Met	cgg Arg	acc Thr	tgg Trp	gag Glu	tgg Trp	gga Gly	agt Ser	gac Asp 450	cgc Arg	gtc Val	aat Asn	1459			
cag Gln 455	gaa Glu	cgc Arg	gca Ala	gag Glu	ctg Leu	gaa Glu 460	ctt Leu	ccc Pro	atg Met	gat Asp	aag Lys 465	ttc Phe	ttg Leu	gag Glu	aaa Lys	1507			
ctc Leu 470	gat Asp	cag Gln	cca Pro	cac His 475	aat Asn	att Ile 475	ggc Gly	ctg Leu	cgt Arg	aaa Lys 480	gtt Val	gcc Ala	gaa Glu	gtg Val	gca Ala 485	1555			

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gta ttt cca cat ggc acc agc gat act gtc ccg ttg tca ttg gtt cgc 1603
Val Phe Pro His Gly Thr Ser Asp Thr Val Pro Leu Ser Leu Val Arg
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tgc gtg aaa gac ctc aag ctt tta tac cga gag atc gtg atc gtt cga 1651
Cys Val Lys Asp Leu Lys Leu Leu Tyr Arg Glu Ile Val Ile Val Arg
                        505                        510                        515

atc gtc caa gaa cac gtt ccg cac gtg cca cca gag gaa cgc gcg gaa 1699
Ile Val Gln Glu His Val Pro His Val Pro Pro Glu Glu Arg Ala Glu
                        520                        525                        530

atg gaa gtg ctc cat cac gcc ccg atc aga gtc gtg cga gtt gat ctg 1747
Met Glu Val Leu His His Ala Pro Ile Arg Val Val Arg Val Asp Leu
                        535                        540                        545

cac ctt ggt tat ttt gat gag cag aac ctg cct gag cat ctc cat gcc 1795
His Leu Gly Tyr Phe Asp Glu Gln Asn Leu Pro Glu His Leu His Ala
550                        555                        560                        565

att gac cca aca tgg gat aac gcc acc tac ttc ctg tct gcc ctg act 1843
Ile Asp Pro Thr Trp Asp Asn Ala Thr Tyr Phe Leu Ser Ala Leu Thr
                        570                        575                        580

ctt cgg agc agg ttg cct gga aag att gct ggc tgg cgt gat cgt ttg 1891
Leu Arg Ser Arg Leu Pro Gly Lys Ile Ala Gly Trp Arg Asp Arg Leu
                        585                        590                        595

tat ctt tcg atg gaa cgt aat cag gca tct cga act gag tct ttc aaa 1939
Tyr Leu Ser Met Glu Arg Asn Gln Ala Ser Arg Thr Glu Ser Phe Lys
                        600                        605                        610

ttg caa cca agc aaa acc atc acg gtt gga aca gag ctg cac ctt 1984
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<211> 628

<212> PRT

<213> Corynebacterium glutamicum

<400> 402

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Asp Ile Gly Thr Ser Pro Leu Tyr Ser Leu His Thr Ala Phe Ser Met
                35                40                45

Gln His Asn Lys Val Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile
                50                55                60

Ser Met Val Leu Trp Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val
 65                70                75                80

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Met	Leu	Val	Thr	Arg 85	Ala	Asp	Asn	Gln	Gly 90	Gln	Gly	Gly	Ile	Leu 95	Ala
Leu	Val	Ala	Leu 100	Leu	Lys	Asn	Arg	Gly 105	His	Trp	Gly	Lys	Phe 110	Val	Ala
Val	Ala	Gly 115	Met	Leu	Gly	Ala	Ala 120	Leu	Phe	Tyr	Gly	Asp 125	Val	Val	Ile
Thr	Pro 130	Ala	Ile	Ser	Val	Leu 135	Ser	Ala	Thr	Glu	Gly 140	Leu	Thr	Val	Ile
Ser 145	Pro	Ser	Phe	Glu	Arg 150	Phe	Ile	Leu	Pro	Val 155	Ser	Leu	Ala	Val	Leu 160
Ile	Ala	Ile	Phe	Ala 165	Ile	Gln	Pro	Leu	Gly 170	Thr	Glu	Lys	Val	Gly 175	Lys
Ala	Phe	Gly	Pro 180	Ile	Met	Leu	Leu	Trp 185	Phe	Val	Thr	Leu	Ala 190	Gly	Leu
Gly	Ile	Pro 195	Gln	Ile	Ile	Gly	His 200	Pro	Glu	Ile	Leu	Gln 205	Ser	Leu	Ser
Pro	His 210	Trp	Ala	Leu	Arg	Leu 215	Ile	Val	Ala	Glu	Pro 220	Phe	Gln	Ala	Phe
Val 225	Leu	Leu	Gly	Ala 230	Val	Val	Leu	Thr	Val	Thr 235	Gly	Ala	Glu	Ala	Leu 240
Tyr	Ala	Asp	Met	Gly 245	His	Phe	Gly	Ala	Arg 250	Pro	Ile	Arg	Val	Ala 255	Trp
Phe	Cys	Val	Val 260	Met	Pro	Ala	Leu	Ile 265	Leu	Thr	Tyr	Leu	Gly 270	Gln	Gly
Ala	Leu 275	Val	Ile	Asn	Gln	Pro	Glu 280	Ala	Val	Arg	Asn 285	Pro	Met	Phe	Tyr
Leu	Ala 290	Pro	Glu	Gly	Leu	Arg 295	Ile	Pro	Leu	Val	Ile 300	Leu	Ala	Thr	Ile
Ala 305	Thr	Val	Ile	Ala	Ser 310	Gln	Ala	Val	Ile	Ser 315	Gly	Ala	Tyr	Ser	Leu 320
Thr	Lys	Gln	Ala 325	Val	Asn	Leu	Lys	Leu	Leu 330	Pro	Arg	Met	Val	Ile 335	Arg
His	Thr	Ser	Arg 340	Lys	Glu	Glu	Gly	Gln 345	Ile	Tyr	Met	Pro	Leu 350	Val	Asn
Gly	Leu 355	Leu	Phe	Val	Ser	Val	Met 360	Val	Val	Val	Leu	Val 365	Phe	Arg	Ser
Ser	Glu 370	Ser	Leu	Ala	Ser	Ala 375	Tyr	Gly	Leu	Ala	Val 380	Thr	Gly	Thr	Leu
Val 385	Leu	Val	Ser	Val	Leu 390	Tyr	Leu	Ile	Tyr	Val 395	His	Thr	Thr	Trp	Trp 400
Lys	Thr	Ala	Leu	Phe	Ile	Val	Leu	Ile	Gly	Ile	Pro	Glu	Val	Leu	Leu

405 410 415
 Phe Ala Ser Asn Thr Thr Lys Ile His Asp Gly Gly Trp Leu Pro Leu
 420 425 430
 Leu Ile Ala Ala Val Leu Ile Val Val Met Arg Thr Trp Glu Trp Gly
 435 440 445
 Ser Asp Arg Val Asn Gln Glu Arg Ala Glu Leu Glu Leu Pro Met Asp
 450 455 460
 Lys Phe Leu Glu Lys Leu Asp Gln Pro His Asn Ile Gly Leu Arg Lys
 465 470 475 480
 Val Ala Glu Val Ala Val Phe Pro His Gly Thr Ser Asp Thr Val Pro
 485 490 495
 Leu Ser Leu Val Arg Cys Val Lys Asp Leu Lys Leu Leu Tyr Arg Glu
 500 505 510
 Ile Val Ile Val Arg Ile Val Gln Glu His Val Pro His Val Pro Pro
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 Glu Glu Arg Ala Glu Met Glu Val Leu His His Ala Pro Ile Arg Val
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 Val Arg Val Asp Leu His Leu Gly Tyr Phe Asp Glu Gln Asn Leu Pro
 545 550 555 560
 Glu His Leu His Ala Ile Asp Pro Thr Trp Asp Asn Ala Thr Tyr Phe
 565 570 575
 Leu Ser Ala Leu Thr Leu Arg Ser Arg Leu Pro Gly Lys Ile Ala Gly
 580 585 590
 Trp Arg Asp Arg Leu Tyr Leu Ser Met Glu Arg Asn Gln Ala Ser Arg
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 Thr Glu Ser Phe Lys Leu Gln Pro Ser Lys Thr Ile Thr Val Gly Thr
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 Glu Leu His Leu
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 <223> FRXA02348

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 acg tat ttg ggg cag ggc gcc ttg gtg atc aac cag cct gaa gcg gtg 96

Thr	Tyr	Leu	Gly	Gln	Gly	Ala	Leu	Val	Ile	Asn	Gln	Pro	Glu	Ala	Val		
			20					25					30				
cgc	aac	ccc	atg	ttt	tat	ctc	gcg	ccg	gaa	ggg	ctg	cgg	att	ccg	ttg	144	
Arg	Asn	Pro	Met	Phe	Tyr	Leu	Ala	Pro	Glu	Gly	Leu	Arg	Ile	Pro	Leu		
		35					40				45						
gtt	att	ttg	gcg	acc	atc	gct	acg	gtg	atc	gca	tcg	cag	gcc	gtg	att	192	
Val	Ile	Leu	Ala	Thr	Ile	Ala	Thr	Val	Ile	Ala	Ser	Gln	Ala	Val	Ile		
	50					55					60						
tct	ggg	gcg	tat	tca	ttg	acc	aag	cag	gcc	gtg	aat	ttg	aaa	ctg	ctg	240	
Ser	Gly	Ala	Tyr	Ser	Leu	Thr	Lys	Gln	Ala	Val	Asn	Leu	Lys	Leu	Leu		
	65				70				75					80			
cca	cgc	atg	gtg	atc	cgg	cat	acc	tcc	cgc	aaa	gag	gaa	ggc	cag	atc	288	
Pro	Arg	Met	Val	Ile	Arg	His	Thr	Ser	Arg	Lys	Glu	Glu	Gly	Gln	Ile		
				85					90					95			
tat	atg	cca	ctg	gtt	aat	gga	ttg	ctg	ttt	gta	tcc	gtg	atg	gtt	gtg	336	
Tyr	Met	Pro	Leu	Val	Asn	Gly	Leu	Leu	Phe	Val	Ser	Val	Met	Val	Val		
		100					105						110				
gtg	ctg	gta	ttc	cga	tcc	tct	gaa	agc	ctc	gcc	agc	gcg	tac	gga	ctt	384	
Val	Leu	Val	Phe	Arg	Ser	Ser	Glu	Ser	Leu	Ala	Ser	Ala	Tyr	Gly	Leu		
		115					120					125					
gca	gtg	acc	gga	acc	ttg	gtg	ctg	gtc	agc	gtc	ctg	tat	ctg	atc	tat	432	
Ala	Val	Thr	Gly	Thr	Leu	Val	Leu	Val	Ser	Val	Leu	Tyr	Leu	Ile	Tyr		
		130				135					140						
gtt	cac	acc	aca	tgg	tgg	aaa	aca	gcg	ctg	ttc	att	gtg	ctc	atc	ggg	480	
Val	His	Thr	Thr	Trp	Trp	Lys	Thr	Ala	Leu	Phe	Ile	Val	Leu	Ile	Gly		
	145				150					155					160		
att	cca	gaa	gta	ctt	cta	ttc	gcc	tcg	aac	acc	acg	aaa	att	cac	gac	528	
Ile	Pro	Glu	Val	Leu	Leu	Phe	Ala	Ser	Asn	Thr	Thr	Lys	Ile	His	Asp		
				165					170					175			
ggg	ggc	tgg	ctt	cca	cta	ctt	att	gcg	gcc	gtg	ctc	atc	gtg	gtg	atg	576	
Gly	Gly	Trp	Leu	Pro	Leu	Leu	Ile	Ala	Ala	Val	Leu	Ile	Val	Val	Met		
			180						185					190			
cgg	acc	tgg	gag	tgg	gga	agt	gac	cgc	gtc	aat	cag	gaa	cgc	gca	gag	624	
Arg	Thr	Trp	Glu	Trp	Gly	Ser	Asp	Arg	Val	Asn	Gln	Glu	Arg	Ala	Glu		
		195					200					205					
ctg	gaa	ctt	ccc	atg	gat	aag	ttc	ttg	gag	aaa	ctc	gat	cag	cca	cac	672	
Leu	Glu	Leu	Pro	Met	Asp	Lys	Phe	Leu	Glu	Lys	Leu	Asp	Gln	Pro	His		
	210					215					220						
aat	att	ggg	ctg	cgt	aaa	gtt	gcc	gaa	gtg	gca	gta	ttt	cca	cat	ggc	720	
Asn	Ile	Gly	Leu	Arg	Lys	Val	Ala	Glu	Val	Ala	Val	Phe	Pro	His	Gly		
	225				230					235					240		
acc	agc	gat	act	gtc	ccg	ttg	tca	ttg	gtt	cgc	tgc	gtg	aaa	gac	ctc	768	
Thr	Ser	Asp	Thr	Val	Pro	Leu	Ser	Leu	Val	Arg	Cys	Val	Lys	Asp	Leu		
				245					250					255			
aag	ctt	tta	tac	cga	gag	atc	gtg	atc	gtt	cga	atc	gtc	caa	gaa	cac	816	
Lys	Leu	Leu	Tyr	Arg	Glu	Ile	Val	Ile	Val	Arg	Ile	Val	Gln	Glu	His		

BGI-131CP

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                260                265                270
gtt ccg cac gtg cca cca gag gaa cgc gcg gaa atg gaa gtg ctc cat      864
Val Pro His Val Pro Pro Glu Glu Arg Ala Glu Met Glu Val Leu His
                275                280                285

cac gcc ccg atc aga gtc gtg cga gtt gat ctg cac ctt ggt tat ttt      912
His Ala Pro Ile Arg Val Val Arg Val Asp Leu His Leu Gly Tyr Phe
                290                295                300

gat gag cag aac ctg cct gag cat ctc cat gcc att gac cca aca tgg      960
Asp Glu Gln Asn Leu Pro Glu His Leu His Ala Ile Asp Pro Thr Trp
305                310                315                320

gat aac gcc acc tac ttc ctg tct gcc ctg act ctt cgg agc agg ttg      1008
Asp Asn Ala Thr Tyr Phe Leu Ser Ala Leu Thr Leu Arg Ser Arg Leu
                325                330                335

cct gga aag att gct ggc tgg cgt gat cgt ttg tat ctt tcg atg gaa      1056
Pro Gly Lys Ile Ala Gly Trp Arg Asp Arg Leu Tyr Leu Ser Met Glu
                340                345                350

cgt aat cag gca tct cga act gag tct ttc aaa ttg caa cca agc aaa      1104
Arg Asn Gln Ala Ser Arg Thr Glu Ser Phe Lys Leu Gln Pro Ser Lys
                355                360                365

acc atc acg gtt gga aca gag ctg cac ctt taatcaggca gttgctggcc      1154
Thr Ile Thr Val Gly Thr Glu Leu His Leu
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aac                                                                    1157

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Thr Tyr Leu Gly Gln Gly Ala Leu Val Ile Asn Gln Pro Glu Ala Val
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Arg Asn Pro Met Phe Tyr Leu Ala Pro Glu Gly Leu Arg Ile Pro Leu
                35                40                45

Val Ile Leu Ala Thr Ile Ala Thr Val Ile Ala Ser Gln Ala Val Ile
                50                55                60

Ser Gly Ala Tyr Ser Leu Thr Lys Gln Ala Val Asn Leu Lys Leu Leu
        65                70                75                80

Pro Arg Met Val Ile Arg His Thr Ser Arg Lys Glu Glu Gly Gln Ile
                85                90                95

Tyr Met Pro Leu Val Asn Gly Leu Leu Phe Val Ser Val Met Val Val
                100                105                110

Val Leu Val Phe Arg Ser Ser Glu Ser Leu Ala Ser Ala Tyr Gly Leu

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115	120	125
Ala Val Thr Gly Thr Leu Val Leu Val Ser Val Leu Tyr Leu Ile Tyr 130	135	140
Val His Thr Thr Trp Trp Lys Thr Ala Leu Phe Ile Val Leu Ile Gly 145	150	155
Ile Pro Glu Val Leu Leu Phe Ala Ser Asn Thr Thr Lys Ile His Asp 165	170	175
Gly Gly Trp Leu Pro Leu Leu Ile Ala Ala Val Leu Ile Val Val Met 180	185	190
Arg Thr Trp Glu Trp Gly Ser Asp Arg Val Asn Gln Glu Arg Ala Glu 195	200	205
Leu Glu Leu Pro Met Asp Lys Phe Leu Glu Lys Leu Asp Gln Pro His 210	215	220
Asn Ile Gly Leu Arg Lys Val Ala Glu Val Ala Val Phe Pro His Gly 225	230	235
Thr Ser Asp Thr Val Pro Leu Ser Leu Val Arg Cys Val Lys Asp Leu 245	250	255
Lys Leu Leu Tyr Arg Glu Ile Val Ile Val Arg Ile Val Gln Glu His 260	265	270
Val Pro His Val Pro Pro Glu Glu Arg Ala Glu Met Glu Val Leu His 275	280	285
His Ala Pro Ile Arg Val Val Arg Val Asp Leu His Leu Gly Tyr Phe 290	295	300
Asp Glu Gln Asn Leu Pro Glu His Leu His Ala Ile Asp Pro Thr Trp 305	310	315
Asp Asn Ala Thr Tyr Phe Leu Ser Ala Leu Thr Leu Arg Ser Arg Leu 325	330	335
Pro Gly Lys Ile Ala Gly Trp Arg Asp Arg Leu Tyr Leu Ser Met Glu 340	345	350
Arg Asn Gln Ala Ser Arg Thr Glu Ser Phe Lys Leu Gln Pro Ser Lys 355	360	365
Thr Ile Thr Val Gly Thr Glu Leu His Leu 370	375	

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Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe Val Leu

Variable	Mean	SD	Min	Max	Median	Mode	Skewness	Kurtosis	Normality
Age	35.5	10.5	20	65	35	35	0.1	3.0	Normal
Gender	1.5	0.5	1	2	1	1	0.0	3.0	Normal
Marital Status	1.5	0.5	1	2	1	1	0.0	3.0	Normal
Education	12.5	1.5	10	15	12	12	0.1	3.0	Normal
Income	1500	500	500	3000	1200	1000	0.2	3.0	Normal
Occupation	1.5	0.5	1	2	1	1	0.0	3.0	Normal
Religion	1.5	0.5	1	2	1	1	0.0	3.0	Normal
Health	1.5	0.5	1	2	1	1	0.0	3.0	Normal
Stress	1.5	0.5	1	2	1	1	0.0	3.0	Normal
Life Satisfaction	1.5	0.5	1	2	1	1	0.0	3.0	Normal
Work Satisfaction	1.5	0.5	1	2	1	1	0.0	3.0	Normal
Family Satisfaction	1.5	0.5	1	2	1	1	0.0	3.0	Normal
Community Satisfaction	1.5	0.5	1	2	1	1	0.0	3.0	Normal
Overall Satisfaction	1.5	0.5	1	2	1	1	0.0	3.0	Normal

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Met Leu Asn Arg Met Lys Ser Ala Arg Pro Lys Ser Val Ala Pro Lys
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Asp Ile Gly Thr Ser Pro Leu Tyr Ser Leu His Thr Ala Phe Ser Met
 35 40 45

Gln His Asn Lys Val Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile
 50 55 60

Ser Met Val Leu Trp Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val
 65 70 75 80

Met Leu Val Thr Arg Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala
 85 90 95

Leu Val Ala Leu Leu Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala
 100 105 110

Val Ala Gly Met Leu Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile
 115 120 125

Thr Pro Ala Ile Ser Val Leu Ser Ala Thr Glu Gly Leu Thr Val Ile
 130 135 140

Ser Pro Ser Phe Glu Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu
 145 150 155 160

Ile Ala Ile Phe Ala Ile Gln Pro Leu Gly Thr Glu Lys Val Gly Lys
 165 170 175

Ala Phe Gly Pro Ile Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu
 180 185 190

Gly Ile Pro Gln Ile Ile Gly His Pro Glu Ile Leu Gln Ser Leu Ser
 195 200 205

Pro His Trp Ala Leu Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe
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Val Leu

225

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Gly Leu Ile Ala Tyr Gly Ala Ser Gln Ala Leu Tyr Pro Trp Leu Leu	
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Lys Asp His Gln Ser Val Thr Glu Ile Asp Leu Asp Ala Gly Ala Leu	
35 40 45	
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Gln Pro Tyr Phe Asn Ile Glu Met Pro Pro Pro Phe Glu Val Met Thr	
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Ala Leu Leu Leu Ala Phe Cys Leu Gly Leu Gly Met Ala Val Ile Lys	
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Ser Asp Thr Leu Phe Lys Val Thr Arg Glu Leu Glu Arg Val Val Met	
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Lys Thr Ile Thr Ala Phe Val Ile Pro Leu Leu Pro Leu Phe Ile Phe	
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Gly Ile Phe Leu Gly Met Gly Met Asn Gly Gly Leu Leu Glu Ile Met	
115 120 125	
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Ser Ala Phe Gly Lys Val Leu Ile Leu Ala Val Val Gly Thr Leu Leu	
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Phe Leu Ala Ile Gln Phe Ile Ile Ala Gly Ala Val Ser Lys Lys Asn	
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cca tgg aaa ctg ttc aaa aac atg ctc cct gca tac ttc act gca ctg	528
Pro Trp Lys Leu Phe Lys Asn Met Leu Pro Ala Tyr Phe Thr Ala Leu	
165 170 175	
ggc act tcc tct tca gcg gca acc atc cca gtg acc tac cag cag acc	576
Gly Thr Ser Ser Ser Ala Ala Thr Ile Pro Val Thr Tyr Gln Gln Thr	
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Leu Lys Asn Asp Val Asp Val Asn Val Ala Gly Phe Val Val Pro Leu	
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Cys Ala Thr Ile His Leu Ala Gly Ser Met Met Lys Ile Gly Leu Phe	
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Ser Ile Gly Phe Leu Leu Met Leu Gly Ile Thr Met Ile Ala Ala Pro
                245                250                255

ggc gtt ccc ggc gga gcc atc atg gca gca acc ggc atg ctg gcc tcc 816
Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser
                260                265                270

atg ctc gga ttc aac acc gaa caa gtc gcc ctc atg atc gcc gct tac 864
Met Leu Gly Phe Asn Thr Glu Gln Val Ala Leu Met Ile Ala Ala Tyr
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Ile Ala Ile Asp Ser Phe Gly Thr Ala Ala Asn Val Thr Gly Asp Gly
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gca atc gca gtc atc gtg aac aaa ttc gcc aag ggc cag ctg cac acc 960
Ala Ile Ala Val Ile Val Asn Lys Phe Ala Lys Gly Gln Leu His Thr
305                310                315                320

act tcc cca gat gaa atc gaa gaa gac gac cgc gtt gcc ttc gac atc 1008
Thr Ser Pro Asp Glu Ile Glu Glu Asp Asp Arg Val Ala Phe Asp Ile
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Ser Asp Thr Leu Phe Lys Val Thr Arg Glu Leu Glu Arg Val Val Met
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Lys Thr Ile Thr Ala Phe Val Ile Pro Leu Leu Pro Leu Phe Ile Phe
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Phe Leu Ala Ile Gln Phe Ile Ile Ala Gly Ala Val Ser Lys Lys Asn
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Pro Trp Lys Leu Phe Lys Asn Met Leu Pro Ala Tyr Phe Thr Ala Leu
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Gly Thr Ser Ser Ser Ala Ala Thr Ile Pro Val Thr Tyr Gln Gln Thr
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Leu Lys Asn Asp Val Asp Val Asn Val Ala Gly Phe Val Val Pro Leu
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Cys Ala Thr Ile His Leu Ala Gly Ser Met Met Lys Ile Gly Leu Phe
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Thr Phe Ala Val Val Phe Met Tyr Asp Met Glu Val Gly Val Gly Leu
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Ser Ile Gly Phe Leu Leu Met Leu Gly Ile Thr Met Ile Ala Ala Pro
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Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser
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Met Leu Gly Phe Asn Thr Glu Gln Val Ala Leu Met Ile Ala Ala Tyr
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Ile Ala Ile Asp Ser Phe Gly Thr Ala Ala Asn Val Thr Gly Asp Gly
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Ala Ile Ala Val Ile Val Asn Lys Phe Ala Lys Gly Gln Leu His Thr
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tgc gcc acc atc cac cta gct gga tcg atg atg aag atc ggc ctc ttc 96
 Cys Ala Thr Ile His Leu Ala Gly Ser Met Met Lys Ile Gly Leu Phe
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 acc ttc gct gtt gtc ttc atg tac gac atg gaa gta ggc gtc ggc ctc 144
 Thr Phe Ala Val Val Phe Met Tyr Asp Met Glu Val Gly Val Gly Leu
 35 40 45

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 Ser Ile Gly Phe Leu Leu Met Leu Gly Ile Thr Met Ile Ala Ala Pro
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 ggc gtt ccc ggc gga gcc atc atg gca gca acc ggc atg ctg gcc tcc 240
 Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser
 65 70 75 80

 atg ctc gga ttc aac acc gaa caa gtc gcc ctc atg atc gcc gct tac 288
 Met Leu Gly Phe Asn Thr Glu Gln Val Ala Leu Met Ile Ala Ala Tyr
 85 90 95

 atc gcg att gac tcc ttc ggc acc gca gca aac gtc acc ggc gac ggc 336
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 100 105 110

 gca atc gca gtc atc gtg aac aaa ttc gcc aag ggc cag ctg cac acc 384
 Ala Ile Ala Val Ile Val Asn Lys Phe Ala Lys Gly Gln Leu His Thr
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 act tcc cca gat gaa atc gaa gaa gac gac cgc gtt gcc ttc gac atc 432
 Thr Ser Pro Asp Glu Ile Glu Glu Asp Asp Arg Val Ala Phe Asp Ile
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gca cag aag ggc cgt ttc ggc ctt ccc ggc tgg atg act ggc ttt ggt																	163
Ala	Gln	Lys	Gly	Arg	Phe	Gly	Leu	Pro	Gly	Trp	Met	Thr	Gly	Phe	Gly		
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gcc cag gtt atc gcc ggc ctc att ctt ggt ctt att ctc ggc ctt gtc																	211
Ala	Gln	Val	Ile	Ala	Gly	Leu	Ile	Leu	Gly	Leu	Ile	Leu	Gly	Leu	Val		
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gcc cga ggc atg gac agc ggc gct gca gac ggt gaa gca agc tgg ctt																	259
Ala	Arg	Gly	Met	Asp	Ser	Gly	Ala	Ala	Asp	Gly	Glu	Ala	Ser	Trp	Leu		
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Thr	Gly	Leu	Leu	Ser	Gly	Val	Gly	Ser	Ala	Tyr	Val	Ser	Leu	Leu	Lys		
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gtt atg gtt cca cca ctg gtg ttc gct gca gtg gtt acc agt gtg gca																	355
Val	Met	Val	Pro	Pro	Leu	Val	Phe	Ala	Ala	Val	Val	Thr	Ser	Val	Ala		
				70												80	
aag ttg cgc gag gta gct aac gct gct cgc ctg gct gtt tcc acc ttg																	403
Lys	Leu	Arg	Glu	Val	Ala	Asn	Ala	Ala	Arg	Leu	Ala	Val	Ser	Thr	Leu		
				90												100	
gtg tgg ttc gcc att act gca ttc ttc tct gtg ctc gcg ggt atc gcc																	451
Val	Trp	Phe	Ala	Ile	Thr	Ala	Phe	Phe	Ser	Val	Leu	Ala	Gly	Ile	Ala		
				105												115	

gta gcg ctg att atg cag cct ggt gtt gga tcc act gtc gac gca tct	499
Val Ala Leu Ile Met Gln Pro Gly Val Gly Ser Thr Val Asp Ala Ser	
120 125 130	
aat gct gct gat cct tct cgc gtg ggc agc tgg ctg ggc ttt atc cag	547
Asn Ala Ala Asp Pro Ser Arg Val Gly Ser Trp Leu Gly Phe Ile Gln	
135 140 145	
tcc gtt att cca tca aac att ctg gga ctt tcc ggt tct tac agt gag	595
Ser Val Ile Pro Ser Asn Ile Leu Gly Leu Ser Gly Ser Tyr Ser Glu	
150 155 160 165	
aac tct ggt gtg aac ctg tcc ttc aac gtg ctg cag atc ctg gtt atc	643
Asn Ser Gly Val Asn Leu Ser Phe Asn Val Leu Gln Ile Leu Val Ile	
170 175 180	
tcc att gcg att ggt gtt gca gct ctg aag gct ggc aag tcc gcc gag	691
Ser Ile Ala Ile Gly Val Ala Ala Leu Lys Ala Gly Lys Ser Ala Glu	
185 190 195	
cct ttc ttg aag ttc acc gag tcc ttc ctc aag atc atc cag atc gtg	739
Pro Phe Leu Lys Phe Thr Glu Ser Phe Leu Lys Ile Ile Gln Ile Val	
200 205 210	
ttg tgg tgg att att cgc ctg gct cca att ggt tcc gct gcg ctg atc	787
Leu Trp Trp Ile Ile Arg Leu Ala Pro Ile Gly Ser Ala Ala Leu Ile	
215 220 225	
ggt aat gct gtt gct acc tac ggt tgg tct gca ctt gga tcc ctg ggc	835
Gly Asn Ala Val Ala Thr Tyr Gly Trp Ser Ala Leu Gly Ser Leu Gly	
230 235 240 245	
aag ttt gtt ctt gcg atc tac gtt ggt ctg gca atc gtc atg ttc gtt	883
Lys Phe Val Leu Ala Ile Tyr Val Gly Leu Ala Ile Val Met Phe Val	
250 255 260	
atc tac cca gtc gtg ctg aag ctc aat gga att cct gtt ctt gga ttc	931
Ile Tyr Pro Val Val Leu Lys Leu Asn Gly Ile Pro Val Leu Gly Phe	
265 270 275	
ttc aag cgc gtt tgg cct gtc aca agc ctt ggc ttt gtt acc cgt tcc	979
Phe Lys Arg Val Trp Pro Val Thr Ser Leu Gly Phe Val Thr Arg Ser	
280 285 290	
tcc atg ggc gtt atg cca gtt acc cag cgc gtt act gag cag tcc ttg	1027
Ser Met Gly Val Met Pro Val Thr Gln Arg Val Thr Glu Gln Ser Leu	
295 300 305	
ggt gtt cca tct gcg tac gct tcc ttt gct atc cca ctg ggt gcg acc	1075
Gly Val Pro Ser Ala Tyr Ala Ser Phe Ala Ile Pro Leu Gly Ala Thr	
310 315 320 325	
agc aag atg gac ggc tgc gct gct gtc tac cca gct gtt gcc gct atc	1123
Ser Lys Met Asp Gly Cys Ala Ala Val Tyr Pro Ala Val Ala Ala Ile	
330 335 340	
ttc gtg gca cag ttc tac ggc att gac ttg agc atc atg gat tac gta	1171
Phe Val Ala Gln Phe Tyr Gly Ile Asp Leu Ser Ile Met Asp Tyr Val	
345 350 355	
ctg atc atg atc gtc tct gtc ctg ggc tct gct gca act gca ggc acc	1219


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Leu Ile Met Ile Val Ser Val Leu Gly Ser Ala Ala Thr Ala Gly Thr
      360                      365                      370

act ggc gca acc gtc atg ctg acc ctg acc cta tcc acc ttg ggt ctg 1267
Thr Gly Ala Thr Val Met Leu Thr Leu Thr Leu Ser Thr Leu Gly Leu
      375                      380                      385

cca ctt gct ggt gtt ggt ctg ctg ctg gct atc gag cca atc atc gac 1315
Pro Leu Ala Gly Val Gly Leu Leu Leu Ala Ile Glu Pro Ile Ile Asp
390                      395                      400                      405

atg gga cgt acc gca acc aac gtc acc ggt cag gca ctg gtt cct gcg 1363
Met Gly Arg Thr Ala Thr Asn Val Thr Gly Gln Ala Leu Val Pro Ala
      410                      415                      420

atc gtt gct aag cgc gag ggc att ctg gat cag gat gtg tgg gat gct 1411
Ile Val Ala Lys Arg Glu Gly Ile Leu Asp Gln Asp Val Trp Asp Ala
      425                      430                      435

gct gaa aag ggt ggc gct gct att gaa atg gca acc gtc tct gag aaa 1459
Ala Glu Lys Gly Gly Ala Ala Ile Glu Met Ala Thr Val Ser Glu Lys
      440                      445                      450

gaa act gag cct gca gag gtt cgc tcc taagctctct tgagtacctg 1506
Glu Thr Glu Pro Ala Glu Val Arg Ser
      455                      460

aga 1509

<210> 412
<211> 462
<212> PRT
<213> Corynebacterium glutamicum

<400> 412
Met Ala Asn Ala Thr Ala Gln Lys Gly Arg Phe Gly Leu Pro Gly Trp
  1                      5                      10                      15

Met Thr Gly Phe Gly Ala Gln Val Ile Ala Gly Leu Ile Leu Gly Leu
      20                      25                      30

Ile Leu Gly Leu Val Ala Arg Gly Met Asp Ser Gly Ala Ala Asp Gly
      35                      40                      45

Glu Ala Ser Trp Leu Thr Gly Leu Leu Ser Gly Val Gly Ser Ala Tyr
      50                      55                      60

Val Ser Leu Leu Lys Val Met Val Pro Pro Leu Val Phe Ala Ala Val
      65                      70                      75                      80

Val Thr Ser Val Ala Lys Leu Arg Glu Val Ala Asn Ala Ala Arg Leu
      85                      90                      95

Ala Val Ser Thr Leu Val Trp Phe Ala Ile Thr Ala Phe Phe Ser Val
      100                      105                      110

Leu Ala Gly Ile Ala Val Ala Leu Ile Met Gln Pro Gly Val Gly Ser
      115                      120                      125

Thr Val Asp Ala Ser Asn Ala Ala Asp Pro Ser Arg Val Gly Ser Trp

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130					135					140					
Leu	Gly	Phe	Ile	Gln	Ser	Val	Ile	Pro	Ser	Asn	Ile	Leu	Gly	Leu	Ser
145					150					155					160
Gly	Ser	Tyr	Ser	Glu	Asn	Ser	Gly	Val	Asn	Leu	Ser	Phe	Asn	Val	Leu
				165					170					175	
Gln	Ile	Leu	Val	Ile	Ser	Ile	Ala	Ile	Gly	Val	Ala	Ala	Leu	Lys	Ala
			180					185					190		
Gly	Lys	Ser	Ala	Glu	Pro	Phe	Leu	Lys	Phe	Thr	Glu	Ser	Phe	Leu	Lys
		195					200					205			
Ile	Ile	Gln	Ile	Val	Leu	Trp	Trp	Ile	Ile	Arg	Leu	Ala	Pro	Ile	Gly
	210					215					220				
Ser	Ala	Ala	Leu	Ile	Gly	Asn	Ala	Val	Ala	Thr	Tyr	Gly	Trp	Ser	Ala
225					230					235					240
Leu	Gly	Ser	Leu	Gly	Lys	Phe	Val	Leu	Ala	Ile	Tyr	Val	Gly	Leu	Ala
				245					250					255	
Ile	Val	Met	Phe	Val	Ile	Tyr	Pro	Val	Val	Leu	Lys	Leu	Asn	Gly	Ile
			260						265				270		
Pro	Val	Leu	Gly	Phe	Phe	Lys	Arg	Val	Trp	Pro	Val	Thr	Ser	Leu	Gly
		275					280						285		
Phe	Val	Thr	Arg	Ser	Ser	Met	Gly	Val	Met	Pro	Val	Thr	Gln	Arg	Val
	290					295					300				
Thr	Glu	Gln	Ser	Leu	Gly	Val	Pro	Ser	Ala	Tyr	Ala	Ser	Phe	Ala	Ile
305					310					315					320
Pro	Leu	Gly	Ala	Thr	Ser	Lys	Met	Asp	Gly	Cys	Ala	Ala	Val	Tyr	Pro
				325					330					335	
Ala	Val	Ala	Ala	Ile	Phe	Val	Ala	Gln	Phe	Tyr	Gly	Ile	Asp	Leu	Ser
			340					345					350		
Ile	Met	Asp	Tyr	Val	Leu	Ile	Met	Ile	Val	Ser	Val	Leu	Gly	Ser	Ala
		355					360						365		
Ala	Thr	Ala	Gly	Thr	Thr	Gly	Ala	Thr	Val	Met	Leu	Thr	Leu	Thr	Leu
	370					375					380				
Ser	Thr	Leu	Gly	Leu	Pro	Leu	Ala	Gly	Val	Gly	Leu	Leu	Leu	Ala	Ile
385					390					395					400
Glu	Pro	Ile	Ile	Asp	Met	Gly	Arg	Thr	Ala	Thr	Asn	Val	Thr	Gly	Gln
				405					410					415	
Ala	Leu	Val	Pro	Ala	Ile	Val	Ala	Lys	Arg	Glu	Gly	Ile	Leu	Asp	Gln
			420					425					430		
Asp	Val	Trp	Asp	Ala	Ala	Glu	Lys	Gly	Gly	Ala	Ala	Ile	Glu	Met	Ala
		435					440					445			
Thr	Val	Ser	Glu	Lys	Glu	Thr	Glu	Pro	Ala	Glu	Val	Arg	Ser		
	450					455					460				

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<210> 413
<211> 428
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1)..(405)  
<223> RXA02628
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<400>	413																
atg	ctt	gaa	ggt	ttt	aga	gat	ttc	gtc	ctt	cgg	gga	aat	gtc	att	gaa	48	
Met	Leu	Glu	Gly	Phe	Arg	Asp	Phe	Val	Leu	Arg	Gly	Asn	Val	Ile	Glu		
1				5					10					15			
ctc	gca	gtt	gcc	gtg	gtc	atc	ggt	act	gcc	ttc	acc	gct	atc	gtg	aca	96	
Leu	Ala	Val	Ala	Val	Val	Ile	Gly	Thr	Ala	Phe	Thr	Ala	Ile	Val	Thr		
			20					25					30				
gca	ttc	tcc	gag	agc	atc	atc	aac	cca	ttg	atc	gct	tcc	atc	ggc	agc	144	
Ala	Phe	Ser	Glu	Ser	Ile	Ile	Asn	Pro	Leu	Ile	Ala	Ser	Ile	Gly	Ser		
		35					40					45					
aca	gag	gtt	gaa	ggc	ctc	ggc	ttc	cac	atc	cgc	gcc	ggc	aat	gcc	gca	192	
Thr	Glu	Val	Glu	Gly	Leu	Gly	Phe	His	Ile	Arg	Ala	Gly	Asn	Ala	Ala		
	50					55					60						
aca	ttc	gtg	gat	ttt	ggt	gct	gtc	atc	acc	gca	gcg	atc	aac	ttc	ctc	240	
Thr	Phe	Val	Asp	Phe	Gly	Ala	Val	Ile	Thr	Ala	Ala	Ile	Asn	Phe	Leu		
65					70					75					80		
atc	atc	gca	gca	att	gtc	tac	ttc	gtt	ctc	gtt	gct	cca	atg	aac	aag	288	
Ile	Ile	Ala	Ala	Ile	Val	Tyr	Phe	Val	Leu	Val	Ala	Pro	Met	Asn	Lys		
				85					90					95			
ctc	agc	gaa	acc	ctc	gca	aag	cgc	aag	ggt	gtt	gaa	gaa	gac	gag	acc	336	
Leu	Ser	Glu	Thr	Leu	Ala	Lys	Arg	Lys	Gly	Val	Glu	Glu	Asp	Glu	Thr		
			100					105					110				
cca	gct	tcc	atc	gaa	gca	gaa	ctc	ctc	acc	gag	atc	cgc	gat	ctc	ctg	384	
Pro	Ala	Ser	Ile	Glu	Ala	Glu	Leu	Leu	Thr	Glu	Ile	Arg	Asp	Leu	Leu		
		115					120					125					
cag	gag	caa	aag	cgc	ctt	cag	tagttaa	aaag	gccctaaa	aaag	cac					428	
Gln	Glu	Gln	Lys	Arg	Leu	Gln											
	130					135											

<210> 414
<211> 135
<212> PRT
<213> Corynebacterium glutamicum

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<400> 414
Met  Leu  Glu  Gly  Phe  Arg  Asp  Phe  Val  Leu  Arg  Gly  Asn  Val  Ile  Glu
  1          5          10          15

Leu  Ala  Val  Ala  Val  Val  Ile  Gly  Thr  Ala  Phe  Thr  Ala  Ile  Val  Thr
          20          25          30

```

Ala Phe Ser Glu Ser Ile Ile Asn Pro Leu Ile Ala Ser Ile Gly Ser
 35 40 45

Thr Glu Val Glu Gly Leu Gly Phe His Ile Arg Ala Gly Asn Ala Ala
 50 55 60

Thr Phe Val Asp Phe Gly Ala Val Ile Thr Ala Ala Ile Asn Phe Leu
 65 70 75 80

Ile Ile Ala Ala Ile Val Tyr Phe Val Leu Val Ala Pro Met Asn Lys
 85 90 95

Leu Ser Glu Thr Leu Ala Lys Arg Lys Gly Val Glu Glu Asp Glu Thr
 100 105 110

Pro Ala Ser Ile Glu Ala Glu Leu Leu Thr Glu Ile Arg Asp Leu Leu
 115 120 125

Gln Glu Gln Lys Arg Leu Gln
 130 135

<210> 415
 <211> 993
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(970)
 <223> RXN03164

<400> 415
 cttttttgca tccagatgca caaagccgtg gcacaaacga gacaaactga gcacaatggc 60

tgatcatggca tatcaaccag cagacaatcg ctatgacgac atg atc tac cgc agg 115
 Met Ile Tyr Arg Arg
 1 5

gtg gga aat tct ggg ctg aag ctt ccg gca att tcg ctt ggg ctg tgg 163
 Val Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile Ser Leu Gly Leu Trp
 10 15 20

cac aac ttc ggt gat gac aag ccg ctt tca acg cag cgc agc att att 211
 His Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln Arg Ser Ile Ile
 25 30 35

cac cgc gcg ttt gat agg gga gtc act cac ttc gat ttg gct aat aac 259
 His Arg Ala Phe Asp Arg Gly Val Thr His Phe Asp Leu Ala Asn Asn
 40 45 50

tat gga cct cca gca ggt tcc gca gag acc aac ttt ggc agg att ttg 307
 Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe Gly Arg Ile Leu
 55 60 65

cgt gag gat ctc aaa agc cac cgc gat gag ttg atc att tct tcc aag 355
 Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu Ile Ile Ser Ser Lys
 70 75 80 85

gcg ggt tgg gat atg tgg cct gga cct tat ggt ttt ggt ggt tcc cga 403

```

Ala Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly Phe Gly Gly Ser Arg
      90                      95                      100

aag tat cta gtg agt tcc ctt gat cag tcc ctg act cgc ctc ggc ttg 451
Lys Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu Thr Arg Leu Gly Leu
      105                      110                      115

gat tac gtg gat att ttc tat cat cac cgc ccg gat cca gat act cct 499
Asp Tyr Val Asp Ile Phe Tyr His His Arg Pro Asp Pro Asp Thr Pro
      120                      125                      130

ttg gaa gaa acc atg tac gca ttg cgt gac att gtt gcg tct gga aag 547
Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala Ser Gly Lys
      135                      140                      145

gct ctt tac gtg ggt att tct tcc tac ggt cca gag ctc aca gcg gag 595
Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu Thr Ala Glu
      150                      155                      160

gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg att cat cag 643
Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu Ile His Gln
      170                      175                      180

cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg ggc gat gac 691
Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro Gly Asp Asp
      185                      190                      195

ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt ggc gtc att 739
Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu Gly Val Ile
      200                      205                      210

gct ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa tat ctc gat 787
Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys Tyr Leu Asp
      215                      220                      225

gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc ctg tct gag 835
Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser Leu Ser Glu
      230                      235                      240

ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag ctc aat gac 883
Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys Leu Asn Asp
      250                      255                      260

atc gcc cag gaa cgc ggg cag tca ctt gcg cag atg gcg ctt gca tgg 931
Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala Leu Ala Trp
      265                      270                      275

gtg ctg cgc gag caa aga gag tac ggc gcc gga tta ccg tgaccagtgc 980
Val Leu Arg Glu Gln Arg Glu Tyr Gly Ala Gly Leu Pro
      280                      285                      290

attgattggt gct . 993

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<210> 416

<211> 290

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

Met Ile Tyr Arg Arg Val Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile

1	5	10	15
Ser Leu Gly Leu Trp His Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr	20	25	30
Gln Arg Ser Ile Ile His Arg Ala Phe Asp Arg Gly Val Thr His Phe	35	40	45
Asp Leu Ala Asn Asn Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn	50	55	60
Phe Gly Arg Ile Leu Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu	65	70	75
Ile Ile Ser Ser Lys Ala Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly	85	90	95
Phe Gly Gly Ser Arg Lys Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu	100	105	110
Thr Arg Leu Gly Leu Asp Tyr Val Asp Ile Phe Tyr His His Arg Pro	115	120	125
Asp Pro Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile	130	135	140
Val Ala Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro	145	150	155
Glu Leu Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro	165	170	175
Leu Leu Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu	180	185	190
Glu Pro Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn	195	200	205
Gly Leu Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr	210	215	220
Asp Lys Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly	225	230	235
Lys Ser Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val	245	250	255
Arg Lys Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln	260	265	270
Met Ala Leu Ala Trp Val Leu Arg Glu Gln Arg Glu Tyr Gly Ala Gly	275	280	285
Leu Pro	290		

<210> 417

<211> 1209

<212> DNA

<213> Corynebacterium glutamicum

<223> FRXA01395

ctcaaaagca ctgataaaag cagtcaaccc acctcggggtt ggctgctttt ttgcatccag 60

tat	caa	cca	gca	gac	aat	cgc	tat	gac	gac	atg	atc	tac	cgc	agg	gtg	163
Tyr	Gln	Pro	Ala	Asp	Asn	Arg	Tyr	Asp	Asp	Met	Ile	Tyr	Arg	Arg	Val	
				10					15					20		

aac ttc ggt gat gac aag ccg ctt tca acg cag cgc agc att att cac 259
Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln Arg Ser Ile Ile His
40 45 50

gga cct cca gca ggt tcc gca gag acc aac ttt ggc agg att ttg cgt 355
Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe Gly Arg Ile Leu Arg
70 75 80 85

ggt tgg gat atg tgg cct gga cct tat ggt ttt ggt ggt tcc cga aag 451
Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly Phe Gly Gly Ser Arg Lys
105 110 115

tac	gtg	gat	att	ttc	tat	cat	cac	cgc	ccg	gat	cca	gat	act	cct	ttg	547
Tyr	Val	Asp	Ile	Phe	Tyr	His	His	Arg	Pro	Asp	Pro	Asp	Thr	Pro	Leu	
	135					140					145					

ctt tac gtg ggt att tct tcc tac ggt cca gag ctc aca gcg gag gcg 643
 Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu Thr Ala Glu Ala
 170 175 180

gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg att cat cag cca 691
Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu Ile His Gln Pro
185 190 195

```

agc tat tcc atc att aat cgt tgg gtg gag gaa ccg ggc gat gac ggt 739
Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro Gly Asp Asp Gly
      200                      205                      210

gag aac ttg ttg cag tca gct gcc aac aat ggt ctt ggc gtc att gct 787
Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu Gly Val Ile Ala
      215                      220                      225

ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa tat ctc gat gga 835
Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys Tyr Leu Asp Gly
230                      235                      240                      245

att cca gag ggt tcc cgc gcc agc cag ggt aag tcc ctk tst kac ggs 883
Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser Xaa Xaa Xaa Xaa
      250                      255                      260

wtg ttg aac gtg aac aat att gat wtg gtc ccm ars ytn awk rsa wtt 931
Xaa Leu Asn Val Asn Asn Ile Asp Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa
      265                      270                      275

tcc mar ram acc ggg cag tcc ttt nnc cna aag gnc ttt tgt tgg gtt 979
Ser Xaa Xaa Thr Gly Gln Ser Phe Xaa Xaa Lys Xaa Phe Cys Trp Val
      280                      285                      290

gtt gcc caa cca agg aaa gta cgg cgc cgg att acc gtg acc agt gca 1027
Val Ala Gln Pro Arg Lys Val Arg Arg Arg Ile Thr Val Thr Ser Ala
      295                      300                      305

ttg att ggt gct tcg tca gtt gag cag ctg gac aac agc ctt gat tca 1075
Leu Ile Gly Ala Ser Val Glu Gln Leu Asp Asn Ser Leu Asp Ser
310                      315                      320                      325

ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg atc gat gag 1123
Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala Ile Asp Glu
      330                      335                      340

att tcc cac gac gcc ggc atc aac att tgg gcg aag gcc acc gat tcc 1171
Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala Thr Asp Ser
      345                      350                      355

aaa acc cgc gaa aac taacccatca acatcagttt gat 1209
Lys Thr Arg Glu Asn
      360

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<210> 418

<211> 362

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

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Met Ala Val Met Ala Tyr Gln Pro Ala Asp Asn Arg Tyr Asp Asp Met
  1                      5                      10                      15

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```

Ile Tyr Arg Arg Val Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile Ser
      20                      25                      30

```

```

Leu Gly Leu Trp His Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln
      35                      40                      45

```

```

Arg Ser Ile Ile His Arg Ala Phe Asp Arg Gly Val Thr His Phe Asp

```



```

      50              55              60
Leu Ala Asn Asn Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe
 65              70              75              80
Gly Arg Ile Leu Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu Ile
              85              90              95
Ile Ser Ser Lys Ala Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly Phe
              100              105              110
Gly Gly Ser Arg Lys Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu Thr
              115              120              125
Arg Leu Gly Leu Asp Tyr Val Asp Ile Phe Tyr His His Arg Pro Asp
              130              135              140
Pro Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val
              145              150              155              160
Ala Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu
              165              170              175
Leu Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu
              180              185              190
Leu Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu
              195              200              205
Pro Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly
              210              215              220
Leu Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp
              225              230              235              240
Lys Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys
              245              250              255
Ser Xaa Xaa Xaa Xaa Xaa Leu Asn Val Asn Asn Ile Asp Xaa Val Xaa
              260              265              270
Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Thr Gly Gln Ser Phe Xaa Xaa Lys
              275              280              285
Xaa Phe Cys Trp Val Val Ala Gln Pro Arg Lys Val Arg Arg Arg Ile
              290              295              300
Thr Val Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp
              305              310              315              320
Asn Ser Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu
              325              330              335
Glu Ala Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala
              340              345              350
Lys Ala Thr Asp Ser Lys Thr Arg Glu Asn
              355              360

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<210> 419

<211> 1911
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1888)
 <223> RXA02597

<400> 419

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ataccacatt tgcaagaatt acaaacgggg gcaccctcaa tgacttgaaa cactttatag 60

agtagaaagt gagtcacgac acttttttaaa ggaggatgct ttg ccc gaa caa gac 115
                                Leu Pro Glu Gln Asp
                                1                               5

tta acc acc ttg gcc aat gat tgg ctc caa gct ttt gaa aag gcc act 163
Leu Thr Thr Leu Ala Asn Asp Trp Leu Gln Ala Phe Glu Lys Ala Thr
                                10                               15                               20

gct agt tcc agc cct gat gaa gct gcc act gca gtc gtg caa ctt ttt 211
Ala Ser Ser Ser Pro Asp Glu Ala Thr Ala Val Val Gln Leu Phe
                                25                               30                               35

gag gat gaa gga tac tgg cga gac ctt ctt gca ttc acg tgg aac ctc 259
Glu Asp Glu Gly Tyr Trp Arg Asp Leu Leu Ala Phe Thr Trp Asn Leu
                                40                               45                               50

acc acc gct gaa ggt gca gat gaa atc gcc gag atg att cgc aat acg 307
Thr Thr Ala Glu Gly Ala Asp Glu Ile Ala Glu Met Ile Arg Asn Thr
                                55                               60                               65

tgg cca tca agc atc ttc cga aac gtt gag cta aag ggc gaa cca gct 355
Trp Pro Ser Ser Ile Phe Arg Asn Val Glu Leu Lys Gly Glu Pro Ala
                                70                               75                               80                               85

gat gaa gga gat ggt gtc act cgc gta cat ttc tcc tgc gaa tcc gca 403
Asp Glu Gly Asp Gly Val Thr Arg Val His Phe Ser Cys Glu Ser Ala
                                90                               95                               100

gac ttc aag tgc acg ggc att gtc cgc ctt cgt aat ggc aag gcg tgg 451
Asp Phe Lys Cys Thr Gly Ile Val Arg Leu Arg Asn Gly Lys Ala Trp
                                105                               110                               115

acg cta ctc acc tca gct cgt gag ctc ctg gag cac cca gag ccc aag 499
Thr Leu Leu Thr Ser Ala Arg Glu Leu Leu Glu His Pro Glu Pro Lys
                                120                               125                               130

ggg cgc aac cgt gag atg ggc gtc gtc cat gga caa aat gag gac acc 547
Gly Arg Asn Arg Glu Met Gly Val Val His Gly Gln Asn Glu Asp Thr
                                135                               140                               145

cga aat tgg act gac cgc aag aat gat cga caa gca gcg ttg ggt gtc 595
Arg Asn Trp Thr Asp Arg Lys Asn Asp Arg Gln Ala Ala Leu Gly Val
                                150                               155                               160                               165

acc gag cag cca tac acc ctc atc atc ggt ggt gga cag ggt ggc att 643
Thr Glu Gln Pro Tyr Thr Leu Ile Ile Gly Gly Gly Gln Gly Gly Ile
                                170                               175                               180

gcc ttg ggc gca cga ctc aag cga ctt ggt gta ccc gct cta atc att 691

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BGI-131CP

Ala gat Asp	Leu aaa Lys	Gly gca Ala	Ala tct Ser	Arg cgc Arg	Leu ccg Pro	Lys ggc Gly	Arg gac Asp	Leu cag Gln	Gly tgg Trp	Val cgt Arg	Pro agc Ser	Ala cgt Arg	Leu tac Tyr	Ile cat His	Ile tct Ser	739
ctc Leu	tgc Cys	ctg Leu	cac His	gat Asp	cca Pro	gtt Val	tgg Trp	tac Tyr	gac Asp	cac His	ctg Leu	cct Pro	tac Tyr	att Ile	cca Pro	787
ttc Phe	cca Pro	gat Asp	cat His	tgg Trp	cca Pro	gta Val	ttt Phe	act Thr	cca Pro	aag Lys	gac Asp	aag Lys	atg Met	ggg Gly	gac Asp	835
tgg Trp	ctc Leu	gag Glu	cac His	tat Tyr	gtc Val	ggc Gly	atc Ile	atg Met	gat Asp	ttg Leu	gac Asp	tat Tyr	tgg Trp	acc Thr	aac Asn	883
acc Thr	gag Glu	tgc Cys	ctg Leu	cgc Arg	gcc Ala	tca Ser	tac Tyr	aat Asn	gag Glu	gac Asp	acc Thr	aag Lys	cag Gln	tgg Trp	gat Asp	931
gtg Val	acg Thr	gtc Val	aat Asn	cgt Arg	gat Asp	ggc Gly	gcg Ala	gag Glu	tcc Ser	acg Thr	ctc Leu	cac His	ccc Pro	acc Thr	caa Gln	979
cta Leu	gtc Val	atg Met	gct Ala	act Thr	gga Gly	atg Met	tcg Ser	ggc Gly	agc Ser	ccg Pro	aac Asn	aaa Lys	cca Pro	act Thr	ttg Leu	1027
cct Pro	ggc Gly	cag Gln	gat Asp	aag Lys	ttc Phe	cag Gln	ggt Gly	gaa Glu	att Ile	cgg Arg	cac His	tct Ser	tca Ser	gag Glu	cac His	1075
ccc Pro	ggc Gly	ggc Gly	gat Asp	gtc Val	gat Asp	cgc Arg	gat Asp	aag Lys	aac Asn	gtt Val	gta Val	gtt Val	ctg Leu	ggc Gly	gct Ala	1123
aac Asn	aac Asn	tca Ser	gcc Ala	cac His	gac Asp	atc Ile	tgc Cys	gcg Ala	gat Asp	ctt Leu	tat Tyr	toc Ser	aat Asn	ggt Gly	gca Ala	1171
aag Lys	ccc Pro	gtg Val	atg Met	att Ile	cag Gln	cgc Arg	tcg Ser	tct Ser	aca Thr	cac His	atc Ile	gtg Val	cgt Arg	tct Ser	gat Asp	1219
tcg Ser	ctg Leu	atg Met	cgc Arg	gaa Glu	gtc Val	ttc Phe	ggg Gly	cct Pro	ctc Leu	tat Tyr	tct Ser	gag Glu	gat Asp	gcc Ala	gtt Val	1267
gaa Glu	gcc Ala	gga Gly	att Ile	gat Asp	acc Thr	gat Asp	act Thr	gcc Ala	gat Asp	ctc Leu	ctg Leu	ttt Phe	gcg Ala	tcg Ser	tgg Trp	1315
cca Pro	tat Tyr	aag Lys	gtg Val	ctg Leu	cca Pro	ggg Gly	gtg Val	cag Gln	aag Lys	cag Gln	gct Ala	ttc Phe	gac Asp	aag Lys	atc Ile	1363
cgt Arg	gag Glu	gac Asp	gac Asp	aag Lys	gag Glu	ttc Phe	tac Tyr	gac Asp	aag Lys	ctt Leu	gaa Glu	aat Asn	gct Ala	gga Gly	ttc Phe	1411

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      425              430              435
ttg ctt gat ttc ggc gat gac gat tcg ggg ctt ttc tta aag tac ctt 1459
Leu Leu Asp Phe Gly Asp Asp Asp Ser Gly Leu Phe Leu Lys Tyr Leu
      440              445              450

cgc cgt ggc tct ggc tac tac atc gat gtc ggc gcc tct gaa ctg gtg 1507
Arg Arg Gly Ser Gly Tyr Tyr Ile Asp Val Gly Ala Ser Glu Leu Val
      455              460              465

gct gat gga aag att ccg gtg cgc tcc aat gtc agc att gaa gac gtc 1555
Ala Asp Gly Lys Ile Pro Val Arg Ser Asn Val Ser Ile Glu Asp Val
      470              475              480              485

aag gaa aac tct gtg gtg ctc aca gat ggt act gag ctc cca gct gac 1603
Lys Glu Asn Ser Val Val Leu Thr Asp Gly Thr Glu Leu Pro Ala Asp
      490              495              500

gtg att gtt cta gcg acc ggc tat gga aac atg aac aac tgg gtt gct 1651
Val Ile Val Leu Ala Thr Gly Tyr Gly Asn Met Asn Asn Trp Val Ala
      505              510              515

cag ctg gtt gat cag gaa acc gct gac aag gtc ggc cca tgc tgg ggt 1699
Gln Leu Val Asp Gln Glu Thr Ala Asp Lys Val Gly Pro Cys Trp Gly
      520              525              530

ctg ggc tct gaa acc acc aag gat cca ggc cca tgg gaa ggc gag ttg 1747
Leu Gly Ser Glu Thr Thr Lys Asp Pro Gly Pro Trp Glu Gly Glu Leu
      535              540              545

cgc aat atg tgg aag ccc aca aac gtg gat tcg ctg tgg ttc cat ggt 1795
Arg Asn Met Trp Lys Pro Thr Asn Val Asp Ser Leu Trp Phe His Gly
      550              555              560              565

ggc aac ctt cac cag tca cgc cat tac tca cgg tat ttg tcc atg cag 1843
Gly Asn Leu His Gln Ser Arg His Tyr Ser Arg Tyr Leu Ser Met Gln
      570              575              580

ttg aag gcg cgc tac gaa ggt atg aac act ccg gtg tac agc aag 1888
Leu Lys Ala Arg Tyr Glu Gly Met Asn Thr Pro Val Tyr Ser Lys
      585              590              595

tagatacaaaa gaaaagggca tct 1911

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<210> 420

<211> 596

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

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Leu Pro Glu Gln Asp Leu Thr Thr Leu Ala Asn Asp Trp Leu Gln Ala
 1              5              10              15

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Phe Glu Lys Ala Thr Ala Ser Ser Ser Pro Asp Glu Ala Ala Thr Ala
 20              25              30

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Val Val Gln Leu Phe Glu Asp Glu Gly Tyr Trp Arg Asp Leu Leu Ala
 35              40              45

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Phe Thr Trp Asn Leu Thr Thr Ala Glu Gly Ala Asp Glu Ile Ala Glu

```

50	55	60
Met Ile Arg Asn Thr Trp Pro Ser Ser Ile Phe Arg Asn Val Glu Leu 65 70 75 80		
Lys Gly Glu Pro Ala Asp Glu Gly Asp Gly Val Thr Arg Val His Phe 85 90 95		
Ser Cys Glu Ser Ala Asp Phe Lys Cys Thr Gly Ile Val Arg Leu Arg 100 105 110		
Asn Gly Lys Ala Trp Thr Leu Leu Thr Ser Ala Arg Glu Leu Leu Glu 115 120 125		
His Pro Glu Pro Lys Gly Arg Asn Arg Glu Met Gly Val Val His Gly 130 135 140		
Gln Asn Glu Asp Thr Arg Asn Trp Thr Asp Arg Lys Asn Asp Arg Gln 145 150 155 160		
Ala Ala Leu Gly Val Thr Glu Gln Pro Tyr Thr Leu Ile Ile Gly Gly 165 170 175		
Gly Gln Gly Gly Ile Ala Leu Gly Ala Arg Leu Lys Arg Leu Gly Val 180 185 190		
Pro Ala Leu Ile Ile Asp Lys Ala Ser Arg Pro Gly Asp Gln Trp Arg 195 200 205		
Ser Arg Tyr His Ser Leu Cys Leu His Asp Pro Val Trp Tyr Asp His 210 215 220		
Leu Pro Tyr Ile Pro Phe Pro Asp His Trp Pro Val Phe Thr Pro Lys 225 230 235 240		
Asp Lys Met Gly Asp Trp Leu Glu His Tyr Val Gly Ile Met Asp Leu 245 250 255		
Asp Tyr Trp Thr Asn Thr Glu Cys Leu Arg Ala Ser Tyr Asn Glu Asp 260 265 270		
Thr Lys Gln Trp Asp Val Thr Val Asn Arg Asp Gly Ala Glu Ser Thr 275 280 285		
Leu His Pro Thr Gln Leu Val Met Ala Thr Gly Met Ser Gly Ser Pro 290 295 300		
Asn Lys Pro Thr Leu Pro Gly Gln Asp Lys Phe Gln Gly Glu Ile Arg 305 310 315 320		
His Ser Ser Glu His Pro Gly Gly Asp Val Asp Arg Asp Lys Asn Val 325 330 335		
Val Val Leu Gly Ala Asn Asn Ser Ala His Asp Ile Cys Ala Asp Leu 340 345 350		
Tyr Ser Asn Gly Ala Lys Pro Val Met Ile Gln Arg Ser Ser Thr His 355 360 365		
Ile Val Arg Ser Asp Ser Leu Met Arg Glu Val Phe Gly Pro Leu Tyr 370 375 380		

Ser Glu Asp Ala Val Glu Ala Gly Ile Asp Thr Asp Thr Ala Asp Leu
 385 390 395 400
 Leu Phe Ala Ser Trp Pro Tyr Lys Val Leu Pro Gly Val Gln Lys Gln
 405 410 415
 Ala Phe Asp Lys Ile Arg Glu Asp Asp Lys Glu Phe Tyr Asp Lys Leu
 420 425 430
 Glu Asn Ala Gly Phe Leu Leu Asp Phe Gly Asp Asp Asp Ser Gly Leu
 435 440 445
 Phe Leu Lys Tyr Leu Arg Arg Gly Ser Gly Tyr Tyr Ile Asp Val Gly
 450 455 460
 Ala Ser Glu Leu Val Ala Asp Gly Lys Ile Pro Val Arg Ser Asn Val
 465 470 475 480
 Ser Ile Glu Asp Val Lys Glu Asn Ser Val Val Leu Thr Asp Gly Thr
 485 490 495
 Glu Leu Pro Ala Asp Val Ile Val Leu Ala Thr Gly Tyr Gly Asn Met
 500 505 510
 Asn Asn Trp Val Ala Gln Leu Val Asp Gln Glu Thr Ala Asp Lys Val
 515 520 525
 Gly Pro Cys Trp Gly Leu Gly Ser Glu Thr Thr Lys Asp Pro Gly Pro
 530 535 540
 Trp Glu Gly Glu Leu Arg Asn Met Trp Lys Pro Thr Asn Val Asp Ser
 545 550 555 560
 Leu Trp Phe His Gly Gly Asn Leu His Gln Ser Arg His Tyr Ser Arg
 565 570 575
 Tyr Leu Ser Met Gln Leu Lys Ala Arg Tyr Glu Gly Met Asn Thr Pro
 580 585 590
 Val Tyr Ser Lys
 595

<210> 421
 <211> 367
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(367)
 <223> RXA01454

<400> 421
 ggccaggact ttggcgtttc ggatcagcag ttcggcttgg attatggatt ctacgcgttt 60
 gatcttccga tgcttcgcct catcgcttga ctactgtcg atg atg ttg atc gtt 115
 Met Met Leu Ile Val
 1 5

```

gct ttc ctg atc gca ctc gtt ggc cat tac ctc atg ggt ggc att cgc 163
Ala Phe Leu Ile Ala Leu Val Gly His Tyr Leu Met Gly Gly Ile Arg
      10              15              20

gct gga aac cag atg acg ggc cag aag tcc ttt gta tcc cgt ggt gcg 211
Ala Gly Asn Gln Met Thr Gly Gln Lys Ser Phe Val Ser Arg Gly Ala
      25              30              35

cgc act cag ctt gcg gta act gct ggt ctg tgg atg ctt gtt aag gtc 259
Arg Thr Gln Leu Ala Val Thr Ala Gly Leu Trp Met Leu Val Lys Val
      40              45              50

gct ggc tac tgg ctg gat cgc tat gac ctg ctg act aag gaa aac tca 307
Ala Gly Tyr Trp Leu Asp Arg Tyr Asp Leu Leu Thr Lys Glu Asn Ser
      55              60              65

acc ttc aca ggt gca agc tac acc gac atc aat gca cag ctg cca gcg 355
Thr Phe Thr Gly Ala Ser Tyr Thr Asp Ile Asn Ala Gln Leu Pro Ala
      70              75              80              85

aag atc atc ctg
Lys Ile Ile Leu 367

```

```

<210> 422
<211> 89
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 422
Met Met Leu Ile Val Ala Phe Leu Ile Ala Leu Val Gly His Tyr Leu
  1              5              10              15

Met Gly Gly Ile Arg Ala Gly Asn Gln Met Thr Gly Gln Lys Ser Phe
  20              25              30

Val Ser Arg Gly Ala Arg Thr Gln Leu Ala Val Thr Ala Gly Leu Trp
  35              40              45

Met Leu Val Lys Val Ala Gly Tyr Trp Leu Asp Arg Tyr Asp Leu Leu
  50              55              60

Thr Lys Glu Asn Ser Thr Phe Thr Gly Ala Ser Tyr Thr Asp Ile Asn
  65              70              75              80

Ala Gln Leu Pro Ala Lys Ile Ile Leu
      85

```

```

<210> 423
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

```

```

<220>
<221> CDS
<222> (101)..(562)
<223> RXA01455

```

```

<400> 423

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cacacctcct ccccaaccga tcaagcgacc tcccaaggcg gtg aca tgg atc ttc 115
                               Val Thr Trp Ile Phe
                               1 5
gcc att atc gcg ttg gtc att ctc atc gcc cca atg agt gtt ggc ttc 163
Ala Ile Ile Ala Leu Val Ile Leu Ile Ala Pro Met Ser Val Gly Phe
                               10 15 20
tat acc gac tgg ctt tgg ttc ggt gaa gtc gat ttc cga ggc gtt ttc 211
Tyr Thr Asp Trp Leu Trp Phe Gly Glu Val Asp Phe Arg Gly Val Phe
                               25 30 35
agc aag gtt att gtc act cgc att gtt ctc ttt gtg atc ttt gcg cta 259
Ser Lys Val Ile Val Thr Arg Ile Val Leu Phe Val Ile Phe Ala Leu
                               40 45 50
att gct ggg ttt gtc aca tgg ctt gct ggt tat ttt gtg aca aaa ctt 307
Ile Ala Gly Phe Val Thr Trp Leu Ala Gly Tyr Phe Val Thr Lys Leu
                               55 60 65
cga cct gat gag atg tcg gcg ttt gat acc cag tcg cct gtg tat cag 355
Arg Pro Asp Glu Met Ser Ala Phe Asp Thr Gln Ser Pro Val Tyr Gln
                               70 75 80 85
tac cgt cag atg atc gaa aac agc ctt cgt cgc gtt atg gtg atc att 403
Tyr Arg Gln Met Ile Glu Asn Ser Leu Arg Arg Val Met Val Ile Ile
                               90 95 100
cca att ttc gtc gcg ttg ctg gct ggc cta att ggt cag cgt tcg tgg 451
Pro Ile Phe Val Ala Leu Leu Ala Gly Leu Ile Gly Gln Arg Ser Trp
                               105 110 115
cgc acc gtt caa atg tgg ctg aat ggc cag gac ttt ggc gtt tcg gat 499
Arg Thr Val Gln Met Trp Leu Asn Gly Gln Asp Phe Gly Val Ser Asp
                               120 125 130
cag cag ttc ggc ttg gat tat gga ttc tac gcg ttt gat ctt ccg atg 547
Gln Gln Phe Gly Leu Asp Tyr Gly Phe Tyr Ala Phe Asp Leu Pro Met
                               135 140 145
ctt cgc ctc atc gct tgactcactg tcgatgatgt tga 585
Leu Arg Leu Ile Ala
150

```

<210> 424

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 424

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Val Thr Trp Ile Phe Ala Ile Ile Ala Leu Val Ile Leu Ile Ala Pro
 1 5 10 15
Met Ser Val Gly Phe Tyr Thr Asp Trp Leu Trp Phe Gly Glu Val Asp
 20 25 30
Phe Arg Gly Val Phe Ser Lys Val Ile Val Thr Arg Ile Val Leu Phe
 35 40 45

```


Val Ile Phe Ala Leu Ile Ala Gly Phe Val Thr Trp Leu Ala Gly Tyr
 50 55 60

Phe Val Thr Lys Leu Arg Pro Asp Glu Met Ser Ala Phe Asp Thr Gln
 65 70 75 80

Ser Pro Val Tyr Gln Tyr Arg Gln Met Ile Glu Asn Ser Leu Arg Arg
 85 90 95

Val Met Val Ile Ile Pro Ile Phe Val Ala Leu Leu Ala Gly Leu Ile
 100 105 110

Gly Gln Arg Ser Trp Arg Thr Val Gln Met Trp Leu Asn Gly Gln Asp
 115 120 125

Phe Gly Val Ser Asp Gln Gln Phe Gly Leu Asp Tyr Gly Phe Tyr Ala
 130 135 140

Phe Asp Leu Pro Met Leu Arg Leu Ile Ala
 145 150

<210> 425
 <211> 987
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(964)
 <223> RXA02684

<400> 425
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atcttttaag ccccgtaggct gcctgggcac gatcgcgggc gtg ctt gct gtg ggc 115
 Val Leu Ala Val Gly
 1 5

ttg gtg ctt gtg ttt gtg gtg acg ctg tgg gcg gat tcg aag ctg aat 163
 Leu Val Leu Val Phe Val Val Thr Leu Trp Ala Asp Ser Lys Leu Asn
 10 15 20

cgc gtg gat gcc acg cct gcg acg cag gtg gcg aac act gcc gga acg 211
 Arg Val Asp Ala Thr Pro Ala Thr Gln Val Ala Asn Thr Ala Gly Thr
 25 30 35

aac tgg ctg ctg gta ggt tcg gat tcg cgg cag ggt tta agt gat gag 259
 Asn Trp Leu Leu Val Gly Ser Asp Ser Arg Gln Gly Leu Ser Asp Glu
 40 45 50

gat att gag cgg cta ggt acc ggc ggc gat atc ggt gtg ggc cgt acg 307
 Asp Ile Glu Arg Leu Gly Thr Gly Gly Asp Ile Gly Val Gly Arg Thr
 55 60 65

gac acg atc atg gtg ttg cat atg ccg cgt act ggc gag ccg acg ctg 355
 Asp Thr Ile Met Val Leu His Met Pro Arg Thr Gly Glu Pro Thr Leu
 70 75 80 85

ttg tcg att ccg cgt gat tct tat gtc aat gtc cct ggc tgg ggc atg 403

CCDS: C131CP

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Leu Ser Ile Pro Arg Asp Ser Tyr Val Asn Val Pro Gly Trp Gly Met
          90                      95                      100

gat aag gca aac gcc gca ttt acc gtg ggt ggc ccg gaa ctg ctg acg 451
Asp Lys Ala Asn Ala Ala Phe Thr Val Gly Gly Pro Glu Leu Leu Thr
          105                      110                      115

caa acc gtg gag gag gca act ggc ctg cga att gat cac tat gca gaa 499
Gln Thr Val Glu Glu Ala Thr Gly Leu Arg Ile Asp His Tyr Ala Glu
          120                      125                      130

atc ggc atg ggt ggt ttg gcg aac atg gtt gat gcc gtg ggc ggc gtg 547
Ile Gly Met Gly Gly Leu Ala Asn Met Val Asp Ala Val Gly Gly Val
          135                      140                      145

gaa atg tgt cct gct gag ccg atg tat gat ccg ctc gcg aac ctg gat 595
Glu Met Cys Pro Ala Glu Pro Met Tyr Asp Pro Leu Ala Asn Leu Asp
          150                      155                      160                      165

att cag gct ggt tgc cag gaa ttt gat ggg gca gcc gcg ctg ggt tat 643
Ile Gln Ala Gly Cys Gln Glu Phe Asp Gly Ala Ala Ala Leu Gly Tyr
          170                      175                      180

gtg cgc act cgt gcc aca gcc ctg ggt gat ctg gac cgg gtg gtg cgt 691
Val Arg Thr Arg Ala Thr Ala Leu Gly Asp Leu Asp Arg Val Val Arg
          185                      190                      195

cag cgg gaa ttc ttc tcc gct ctg ctg agt aca gct acg tcc ccg ggc 739
Gln Arg Glu Phe Phe Ser Ala Leu Leu Ser Thr Ala Thr Ser Pro Gly
          200                      205                      210

acg ttg ctg aat ccg ttc cgc acc ttc ccg atg atc tcc aac gcg gtg 787
Thr Leu Leu Asn Pro Phe Arg Thr Phe Pro Met Ile Ser Asn Ala Val
          215                      220                      225

gga aca ttc acc gtc ggc gag ggc gat cac gtg tgg cac ctg gcc cga 835
Gly Thr Phe Thr Val Gly Glu Gly Asp His Val Trp His Leu Ala Arg
          230                      235                      240                      245

ttg gcg ctg gcg atg cgc gga gga atc gtg acg gag acc gtg ccg att 883
Leu Ala Leu Ala Met Arg Gly Gly Ile Val Thr Glu Thr Val Pro Ile
          250                      255                      260

gcc tca ttc gca gat tac gat gtg gga aat gtt gcg att tgg gac gaa 931
Ala Ser Phe Ala Asp Tyr Asp Val Gly Asn Val Ala Ile Trp Asp Glu
          265                      270                      275

gct gga gcc gaa gca cta ttt agc tcc atg cgc taaaacccca ggtaatcggtt 984
Ala Gly Ala Glu Ala Leu Phe Ser Ser Met Arg
          280                      285

cac 987

<210> 426
<211> 288
<212> PRT
<213> Corynebacterium glutamicum

<400> 426
Val Leu Ala Val Gly Leu Val Leu Val Phe Val Val Thr Leu Trp Ala

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Asp Ser Lys Leu Asn Arg Val Asp Ala Thr Pro Ala Thr Gln Val Ala	20	25	30
Asn Thr Ala Gly Thr Asn Trp Leu Leu Val Gly Ser Asp Ser Arg Gln	35	40	45
Gly Leu Ser Asp Glu Asp Ile Glu Arg Leu Gly Thr Gly Gly Asp Ile	50	55	60
Gly Val Gly Arg Thr Asp Thr Ile Met Val Leu His Met Pro Arg Thr	65	70	75
Gly Glu Pro Thr Leu Leu Ser Ile Pro Arg Asp Ser Tyr Val Asn Val	85	90	95
Pro Gly Trp Gly Met Asp Lys Ala Asn Ala Ala Phe Thr Val Gly Gly	100	105	110
Pro Glu Leu Leu Thr Gln Thr Val Glu Glu Ala Thr Gly Leu Arg Ile	115	120	125
Asp His Tyr Ala Glu Ile Gly Met Gly Gly Leu Ala Asn Met Val Asp	130	135	140
Ala Val Gly Gly Val Glu Met Cys Pro Ala Glu Pro Met Tyr Asp Pro	145	150	155
Leu Ala Asn Leu Asp Ile Gln Ala Gly Cys Gln Glu Phe Asp Gly Ala	165	170	175
Ala Ala Leu Gly Tyr Val Arg Thr Arg Ala Thr Ala Leu Gly Asp Leu	180	185	190
Asp Arg Val Val Arg Gln Arg Glu Phe Phe Ser Ala Leu Leu Ser Thr	195	200	205
Ala Thr Ser Pro Gly Thr Leu Leu Asn Pro Phe Arg Thr Phe Pro Met	210	215	220
Ile Ser Asn Ala Val Gly Thr Phe Thr Val Gly Glu Gly Asp His Val	225	230	235
Trp His Leu Ala Arg Leu Ala Leu Ala Met Arg Gly Gly Ile Val Thr	245	250	255
Glu Thr Val Pro Ile Ala Ser Phe Ala Asp Tyr Asp Val Gly Asn Val	260	265	270
Ala Ile Trp Asp Glu Ala Gly Ala Glu Ala Leu Phe Ser Ser Met Arg	275	280	285

<210> 427

<211> 522

<212> DNA

<213> Corynebacterium glutamicum

00000-4260950

Gly Ala Tyr Val Asp Asn Gly Val Asp Val Asn Leu Ser Asn Gln Asp

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<210> 429
<211> 2826
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2803)
<223> RXN02549
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<400> 429																	
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gccgtaactg cagacgatgc cctgctcggg ggcacctgagt atg gtt cac gcg aag																	115
Met Val His Ala Lys																	
1 5																	
cag act aag aag cca ctt ccc cgt ttt ctt cac tcg gcg cat ttc tat																	163
Gln Thr Lys Lys Pro Leu Pro Arg Phe Leu His Ser Ala His Phe Tyr																	
10 15 20																	
gtc tgg att gtg ctg ggt ttt gtg gtg ttt gcg caa cct tat ggt cag																	211
Val Trp Ile Val Leu Gly Phe Val Val Phe Ala Gln Pro Tyr Gly Gln																	
25 30 35																	
gtt gct gcc gat act aaa cta gat ttg ctg ctc aac ccc gca gga ttt																	259
Val Ala Ala Asp Thr Lys Leu Asp Leu Leu Leu Asn Pro Ala Gly Phe																	
40 45 50																	
tta acc ggt gcg ctt cat gcg tgg act gac acg ttc acc ttg ggt cag																	307
Leu Thr Gly Ala Leu His Ala Trp Thr Asp Thr Phe Thr Leu Gly Gln																	
55 60 65																	
ttg caa aac caa gct tat ggc tat ctg ttt ccc caa ggg ttt ttc ttc																	355
Leu Gln Asn Gln Ala Tyr Gly Tyr Leu Phe Pro Gln Gly Phe Phe Phe																	
70 75 80 85																	
ctc ata act gat ttc ctc cct gac tgg att gcg cag cga ctg tgg tgg																	403
Leu Ile Thr Asp Phe Leu Pro Asp Trp Ile Ala Gln Arg Leu Trp Trp																	
90 95 100																	

tgg ctt gtt ctt ggc ctg gga ttt tct gga ttc tac gca ctg gta gcc 451
 Trp Leu Val Leu Gly Leu Gly Phe Ser Gly Phe Tyr Ala Leu Val Ala
 105 110 115

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 Phe Ala Leu Ser Pro Arg Thr Leu Thr Thr Leu Thr Ala Ile Ser Ser
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 Glu Thr Trp Pro Ile Met Leu Ala Pro Trp Val Cys Leu Pro Leu Leu
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gca tgc atg ggt gca gtt aat gcc acc gcc acg atg gca gca ctc atc 691
 Ala Cys Met Gly Ala Val Asn Ala Thr Ala Thr Met Ala Ala Leu Ile
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ccg gca gcg ctg atc ttg ctg tat aga ggg ctc ttc tta agg ctg ctt 739
 Pro Ala Ala Leu Ile Leu Leu Tyr Arg Gly Leu Phe Leu Arg Leu Leu
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 Leu Leu Val Leu Gly Lys Tyr Ala Pro Pro Phe Thr Glu Phe Ile Glu
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 Ser Ser Ser Val Thr Thr Ser Trp Leu Asn Pro Val Glu Ile Leu Arg
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 Gly Thr Thr Ser Trp Thr Pro Phe Val Asp Thr Glu Arg Gln Ala Gly
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 Tyr Leu Leu Val Asn Asp Ala Leu Phe Val Thr Leu Ser Val Leu Val
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gca gcc ctc ggc ttg atc ggc ctc acc ttg atg aaa cac cgt gga ctg 1027
 Ala Ala Leu Gly Leu Ile Gly Leu Thr Leu Met Lys His Arg Gly Leu
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 Trp Ala Phe Met Leu Ala Ile Gly Leu Leu Ile Leu Gly Ser Ala His
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 Gly Leu Asn Asp Glu Ala Leu Lys Arg Leu Gly Ile Gly Ala Val Leu
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 Val Arg His Asp Leu Glu Ala Asp Pro Asp Ile Glu Val Asp Leu Pro
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 Thr Asp Pro Asp Arg Asn Met Trp Ile Thr Ser Gly Thr Ser Lys Gln
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Ser	Arg	Thr	Ile	Thr	Val	Pro	Glu	Thr	Ser	Pro	Asp	Val	Gln	Gln	Phe	
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Val	Phe	Gln	Arg	Leu	Thr	Val	Pro	Thr	Ser	Phe	Leu	Asp	Arg	Thr	Phe	
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Thr	Leu	Glu	Leu	Asp	Gly	Asp	Arg	Ile	Asp	Cys	Gly	Pro	Ser	Asn	Ser	
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ccc	ccg	gaa	ccc	aca	cgc	tgc	gca	ccc	aat	cgg	aat	ggg	tca	ccc	tca	2611
Pro	Pro	Glu	Pro	Thr	Arg	Cys	Ala	Pro	Asn	Arg	Asn	Gly	Ser	Pro	Ser	

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 Ile Ala Ala Leu Leu Phe Ala Leu Ser Pro Arg Thr Leu Thr Thr Leu
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 Ser Leu Leu Pro Ala Ala Cys Met Gly Ala Val Asn Ala Thr Ala Thr

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 Val Phe Gly Ala Leu Ala Val Met Leu Phe Val Arg Phe Leu Ile Pro
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 330 335 340

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390					395					400					405	
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His	Ile	Gly	Gly	His	Ala	Arg	Phe	Glu	Tyr	Thr	Val	Ile	Gly	Asp	Ala	
				410				415						420		
gtg	aac	cag	gct	gcg	cgc	ctg	acg	gag	atc	gcg	aaa	acg	acc	cca	ggc	1411
Val	Asn	Gln	Ala	Ala	Arg	Leu	Thr	Glu	Ile	Ala	Lys	Thr	Thr	Pro	Gly	
			425				430						435			
cgc	acc	gtc	acc	aac	gct	tcc	acg	ctg	cgt	gag	gcc	aac	gag	gcg	gag	1459
Arg	Thr	Val	Thr	Asn	Ala	Ser	Thr	Leu	Arg	Glu	Ala	Asn	Glu	Ala	Glu	
		440					445					450				
cag	gct	cgc	tgg	acg	ctc	atg	aag	tcc	gtg	gag	ctg	cgc	gga	cgt	agc	1507
Gln	Ala	Arg	Trp	Thr	Leu	Met	Lys	Ser	Val	Glu	Leu	Arg	Gly	Arg	Ser	
	455					460					465					
cag	atg	acg	cag	att	gcg	cgg	cct	att	cgg	cgg	acg	ttg	gcg	gat	agg	1555
Gln	Met	Thr	Gln	Ile	Ala	Arg	Pro	Ile	Arg	Pro	Thr	Leu	Ala	Asp	Arg	
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tcc	taatacgc	ttt	ttcgacg	caa	aaa											1581
Ser																
<210> 432																
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<212> PRT																
<213> Corynebacterium glutamicum																
<400> 432																
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Arg	Phe	Leu	Ile	Pro	Gln	Pro	Asp	Ala	Ser	Asn	Phe	Asn	Ala	Glu	Ile	
			20				25						30			
Ser	Tyr	Leu	Pro	Ala	Val	Gly	Phe	Ala	Tyr	Leu	Ala	Phe	Ala	Ile	Val	
		35				40						45				
Ala	Gly	Met	Leu	Val	Thr	Phe	Leu	Met	Phe	Arg	Pro	Val	Leu	Asp	Trp	
	50					55					60					
Gln	Arg	Ser	Pro	Glu	Asp	His	Asp	Arg	Asn	Met	Val	Arg	Asn	Leu	Val	
65					70					75				80		
Met	Arg	Ile	Pro	Ile	Tyr	Gln	Ala	Ile	Leu	Cys	Ala	Val	Val	Trp	Leu	
				85					90					95		
Ile	Gly	Ile	Ala	Ile	Ala	Thr	Leu	Ile	Ser	Ala	Ser	Val	Ser	Thr	Ser	

			100					105					110				
Leu	Ala	Leu	Val	Val	Ala	Phe	Ser	Thr	Leu	Met	Ala	Ala	Ala	Ile	Val		
		115					120					125					
Val	Leu	Leu	Thr	Tyr	Leu	Glu	Ala	Glu	Arg	Leu	Val	Arg	Pro	Val	Ala		
		130					135					140					
Ala	Ser	Ala	Leu	Ala	Arg	Arg	Phe	Glu	Asp	Ser	Thr	Leu	Glu	Pro	Pro		
145					150					155					160		
Val	Ser	Gln	Arg	Leu	Arg	Met	Thr	Trp	Leu	Leu	Thr	Leu	Gly	Ile	Pro		
				165					170					175			
Val	Met	Gly	Ile	Leu	Leu	Leu	Ile	Trp	Gly	Tyr	Ser	Gln	Gly	Ile	Phe		
				180					185					190			
Gly	Ser	Asp	Ala	Ser	Gly	Ile	Met	Pro	Ala	Ile	Ala	Ala	Leu	Ala	Phe		
		195					200					205					
Ala	Ser	Leu	Val	Thr	Gly	Tyr	Leu	Gly	Asn	Arg	Leu	Val	Val	Ser	Ser		
		210					215					220					
Val	Val	Asp	Pro	Ile	Arg	Glu	Leu	Gln	Glu	Ala	Ile	Asn	Arg	Val	Arg		
225					230					235					240		
Arg	Gly	Glu	Asn	Asp	Val	Gln	Val	Asp	Ile	Tyr	Asp	Gly	Ser	Glu	Ile		
				245					250					255			
Gly	Val	Leu	Gln	Ala	Gly	Phe	Asn	Glu	Met	Met	Arg	Gly	Leu	Arg	Glu		
				260					265					270			
Arg	Gln	Arg	Val	Arg	Asp	Leu	Phe	Gly	Arg	Tyr	Val	Gly	Ala	Glu	Val		
		275					280					285					
Ala	Lys	Arg	Ala	Leu	Glu	Glu	Arg	Pro	Thr	Leu	Gly	Gly	Glu	Asp	Arg		
		290					295					300					
Lys	Val	Ala	Val	Leu	Phe	Val	Asp	Val	Ile	Gly	Ser	Thr	Thr	Phe	Ala		
305					310					315					320		
Val	Asn	His	Thr	Pro	Glu	Glu	Val	Val	Glu	Ala	Leu	Asn	Glu	Phe	Phe		
				325					330					335			
Glu	His	Val	Val	Glu	Val	Val	His	Arg	Asn	Lys	Gly	Val	Ile	Asn	Lys		
				340					345					350			
Phe	Gln	Gly	Asp	Ala	Ala	Leu	Ala	Ile	Phe	Gly	Ala	Pro	Leu	Pro	Leu		
		355					360					365					
Ser	Asp	Ala	Thr	Gly	His	Ala	Leu	Ala	Ala	Ala	Arg	Glu	Leu	Arg	Ala		
		370					375					380					
Glu	Leu	Lys	Asp	Leu	Gln	Leu	Lys	Ala	Gly	Ile	Gly	Val	Ala	Ala	Gly		
385					390					395					400		
His	Val	Val	Ala	Gly	His	Ile	Gly	Gly	His	Ala	Arg	Phe	Glu	Tyr	Thr		
				405					410					415			
Val	Ile	Gly	Asp	Ala	Val	Asn	Gln	Ala	Ala	Arg	Leu	Thr	Glu	Ile	Ala		
				420					425					430			

Lys Thr Thr Pro Gly Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu
 435 440 445
 Ala Asn Glu Ala Glu Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu
 450 455 460
 Leu Arg Gly Arg Ser Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro
 465 470 475 480
 Thr Leu Ala Asp Arg Ser
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<210> 433

<211> 1008

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(985)

<223> RXS01425

<400> 433

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ttcggccatt ctgtggttct ggcataaagc gttcagcttt gtg ctg agc cca gat 115
                                   Val Leu Ser Pro Asp
                                   1 5

tcc gga att acc tgg gcc ttg tgc atc atg ttc ttg acc ttc acc gtg 163
Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe Leu Thr Phe Thr Val
               10               15               20

cgt atg gtt ctg gtc aag ccg atg gtc aac acc atg cgt tca cag cgc 211
Arg Met Val Leu Val Lys Pro Met Val Asn Thr Met Arg Ser Gln Arg
               25               30               35

aag atg caa gac atg gct cca aag atg cag gcc atc cgc gag aag tac 259
Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala Ile Arg Glu Lys Tyr
               40               45               50

aaa aat gac cag cag aag atg atg gag gag acc cgc aaa ctt caa aaa 307
Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr Arg Lys Leu Gln Lys
               55               60               65

gaa gtg ggc gtt aac ccc atc gca ggc tgt ttg cca atg ttg gtg cag 355
Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu Pro Met Leu Val Gln
               70               75               80               85

atc cca gtg ttc ctg ggt ctg ttc cac gtg ctg cgc tcc ttc aac cgc 403
Ile Pro Val Phe Leu Gly Leu Phe His Val Leu Arg Ser Phe Asn Arg
               90               95               100

acc ggt tct ggc gtt ggc cag ctg gaa atg acc gtt gag caa aac gcg 451
Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr Val Glu Gln Asn Ala
               105               110               115

aac acc ccg aac tac atc ttc ggt gtc gac gag gtt cag tcc ttc ctg 499
Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu Val Gln Ser Phe Leu

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120              125              130
cgt gca gac ctg ttc ggt gcg cca ctg tcg tcc tac atc acc atg cct 547
Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser Tyr Ile Thr Met Pro
135              140              145

gct gac gcg ttc gac gcg ttc ctt ggc ctg gat gtc tcc cgc ctc aac 595
Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp Val Ser Arg Leu Asn
150              155              160              165

atc gcg ctg gtt gca gct cca atg att ttg atc att gtc gtg gca act 643
Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile Ile Val Val Ala Thr
170              175              180

cac atg aac gcg cgt ctg tcc gtc aac cgc cag gaa gct cgc aag gca 691
His Met Asn Ala Arg Leu Ser Val Asn Arg Gln Glu Ala Arg Lys Ala
185              190              195

gcc gcc aag cag cag gcc gct tcc agc gat cag atg gcc atg cag atg 739
Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln Met Ala Met Gln Met
200              205              210

caa atg atg aac aag atg atg ctc tgg ttc atg cca gcc acc att ttg 787
Gln Met Met Asn Lys Met Met Leu Trp Phe Met Pro Ala Thr Ile Leu
215              220              225

ttc acc gcc ttc atc tgg acc atc ggt ctt ctt gtc tac atg atg tcc 835
Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu Val Tyr Met Met Ser
230              235              240              245

aac aac gtg tgg acc ttc ttc cag cag cgc tac atc ttc gcc aag atg 883
Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr Ile Phe Ala Lys Met
250              255              260

gac gct gag gaa gca gct gag gag gag gaa aag cgc gca gca aag cgc 931
Asp Ala Glu Glu Ala Ala Glu Glu Glu Glu Lys Arg Ala Ala Lys Arg
265              270              275

act acc gct cca aag cct gcc gtg aag cca gaa aac ccc aag aag cgt 979
Thr Thr Ala Pro Lys Pro Gly Val Lys Pro Glu Asn Pro Lys Lys Arg
280              285              290

aag aag taaaacttca ctaaaaaccg cca 1008
Lys Lys
295

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<210> 434

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 434

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Val Leu Ser Pro Asp Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe
1              5              10              15

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Leu Thr Phe Thr Val Arg Met Val Leu Val Lys Pro Met Val Asn Thr
20              25              30

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Met Arg Ser Gln Arg Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala
35              40              45

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Ile Arg Glu Lys Tyr Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr
  50                      55                      60

Arg Lys Leu Gln Lys Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu
  65                      70                      75                      80

Pro Met Leu Val Gln Ile Pro Val Phe Leu Gly Leu Phe His Val Leu
                      85                      90                      95

Arg Ser Phe Asn Arg Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr
          100                      105                      110

Val Glu Gln Asn Ala Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu
          115                      120                      125

Val Gln Ser Phe Leu Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser
          130                      135                      140

Tyr Ile Thr Met Pro Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp
          145                      150                      155                      160

Val Ser Arg Leu Asn Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile
          165                      170                      175

Ile Val Val Ala Thr His Met Asn Ala Arg Leu Ser Val Asn Arg Gln
          180                      185                      190

Glu Ala Arg Lys Ala Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln
          195                      200                      205

Met Ala Met Gln Met Gln Met Met Asn Lys Met Met Leu Trp Phe Met
          210                      215                      220

Pro Ala Thr Ile Leu Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu
          225                      230                      235                      240

Val Tyr Met Met Ser Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr
          245                      250                      255

Ile Phe Ala Lys Met Asp Ala Glu Glu Ala Ala Glu Glu Glu Glu Lys
          260                      265                      270

Arg Ala Ala Lys Arg Thr Thr Ala Pro Lys Pro Gly Val Lys Pro Glu
          275                      280                      285

Asn Pro Lys Lys Arg Lys Lys
          290                      295

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<210> 435

<211> 1856

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1833)

<223> RXS01658

<400> 435

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aac Asn	ttc Phe	tac Tyr	ggt Gly 20	ttc Phe	cca Pro	gac Asp	cag Gln	ctg Leu 25	gcg Ala	atg Met	gac Asp	cgc Arg	ttt Phe 30	gaa Glu	gta Val	96
gat Asp	ggc Gly	aaa Lys 35	ctc Leu	cgc Arg	gac Asp	ttt Phe 40	gtt Val 40	gtg Val	gca Ala	gca Ala	cgt Arg	gag Glu 45	ctc Leu	gat Asp	cca Pro	144
aac Asn	gcc Ala 50	ctg Leu	cag Gln	caa Gln	aac Asn	cag Gln 55	cag Gln	gac Asp	tgg Trp	att Ile	aac Asn 60	cgt Arg	cac His	act Thr	gtt Val	192
tat Tyr 65	acc Thr	cac His	ggc Gly	aac Asn 70	ggc Gly 70	ttc Phe 70	att Ile	gca Ala	gct Ala 75	caa Gln 75	gca Ala	aac Asn	cag Gln	gtg Val	gat Asp 80	240
gag Glu	gtc Val	gcc Ala	cgc Arg	gac Asp 85	gtc Val	gga Gly	tcc Ser	act Thr	cgt Arg 90	ggt Gly	ggt Gly	tac Tyr	cct Pro	gtc Val 95	tac Tyr	288
acc Thr	gtc Val	tct Ser	gat Asp 100	ttg Leu	cag Gln	tcg Ser	aat Asn 105	gct Ala 105	cgt Arg	gct Ala	gca Ala	gaa Glu 110	agc Ser	gaa Glu	gat Asp	336
gct Ala	gag Glu	gag Glu 115	ctt Leu	ggc Gly	atc Ile	aag Lys	gtt Val 120	gat Asp	gag Glu	cct Pro	cgt Arg	gtg Val 125	tac Tyr	tac Tyr	gga Gly	384
cca Pro	ctg Leu 130	att Ile	gct Ala	tct Ser	gcg Ala	act Thr 135	gat Asp	ggt Gly	gct Ala	gac Asp 140	tac Tyr	gca Ala	att Ile	gtc Val	ggt Gly	432
gac Asp 145	acc Thr	ggc Gly	gat Asp	ggc Gly 150	cca Pro	gtc Val	gag Glu	tac Tyr	gac Asp 155	act Thr	gac Asp	acc Thr	tcc Ser	agc Ser	tac Tyr 160	480
acc Thr	tac Tyr	gaa Glu	ggt Gly 165	gct Ala	ggc Gly	ggc Gly	gtg Val	gac Asp 170	att Ile	gga Gly	aac Asn	atg Met	gtc Val	aac Asn 175	cgt Arg	528
gcg Ala	atg Met	ttt Phe	gca Ala 180	ttg Leu	cgc Arg	tac Tyr	cag Gln	gaa Glu 185	atg Met	aac Asn	atg Met	ctc Leu	ctg Leu 190	tct Ser	gat Asp	576
cgt Arg	gtt Val	ggt Gly 195	tcc Ser	gaa Glu	tcc Ser	aag Lys	atc Ile 200	cta Leu	ttt Phe	gag Glu	cgc Arg	gat Asp 205	cct Pro	cgt Arg	tcc Ser	624
cgt Arg	gtg Val 210	gaa Glu	aag Lys	gtt Val	gca Ala	cct Pro 215	tgg Trp	ttg Leu	acc Thr	act Thr	gac Asp 220	tcc Ser	aag Lys	acc Thr	tac Tyr	672
cca Pro 225	act Thr	gtg Val	att Ile	gat Asp	ggt Gly 230	cgc Arg	atc Ile	aag Lys	tgg Trp	atc Ile 235	gtc Val	gat Asp	ggc Gly	tac Tyr 240	acc Thr	720
acc	ttg	gat	agt	ctt	ccg	tac	tcc	acg	cgc	acc	tca	ctg	acg	gaa	gcg	768

Thr	Leu	Asp	Ser	Leu	Pro	Tyr	Ser	Thr	Arg	Thr	Ser	Leu	Thr	Glu	Ala	
				245					250					255		
act	cag	gat	gct	gtc	atg	cct	gac	ggc	acc	cca	cag	cca	ctg	atc	aca	816
Thr	Gln	Asp	Ala	Val	Met	Pro	Asp	Gly	Thr	Pro	Gln	Pro	Leu	Ile	Thr	
			260					265					270			
gat	agg	gtc	ggg	tac	atc	cgc	aac	tcc	gtg	aag	gct	gtt	gtt	gat	gcg	864
Asp	Arg	Val	Gly	Tyr	Ile	Arg	Asn	Ser	Val	Lys	Ala	Val	Val	Asp	Ala	
			275				280					285				
tac	gac	gga	act	gtt	gaa	ctc	tac	gaa	ttc	gac	acc	gaa	gat	cct	gtt	912
Tyr	Asp	Gly	Thr	Val	Glu	Leu	Tyr	Glu	Phe	Asp	Thr	Glu	Asp	Pro	Val	
			290			295					300					
ctg	aag	gca	tgg	cgt	ggc	gtg	ttc	cca	gac	acc	gtg	aag	gac	ggg	tcg	960
Leu	Lys	Ala	Trp	Arg	Gly	Val	Phe	Pro	Asp	Thr	Val	Lys	Asp	Gly	Ser	
					310					315				320		
gag	att	tcc	gat	gag	ctt	cgc	gca	cac	ctg	cgt	tac	cca	gaa	gat	ttg	1008
Glu	Ile	Ser	Asp	Glu	Leu	Arg	Ala	His	Leu	Arg	Tyr	Pro	Glu	Asp	Leu	
					325				330					335		
ttc	aag	gtc	cag	cgt	gac	atg	ctg	gcc	aag	tac	aac	gtt	gat	gat	tct	1056
Phe	Lys	Val	Gln	Arg	Asp	Met	Leu	Ala	Lys	Tyr	Asn	Val	Asp	Asp	Ser	
			340					345					350			
gga	aca	ttc	ttc	acc	aac	gat	gcg	ttc	tgg	tct	gtc	cca	ggg	gac	cca	1104
Gly	Thr	Phe	Phe	Thr	Asn	Asp	Ala	Phe	Trp	Ser	Val	Pro	Gly	Asp	Pro	
			355				360					365				
act	gca	gcg	gag	ggc	cgc	cag	gaa	ctt	aag	cag	cct	cct	tac	tac	gtg	1152
Thr	Ala	Ala	Glu	Gly	Arg	Gln	Glu	Leu	Lys	Gln	Pro	Pro	Tyr	Tyr	Val	
			370			375					380					
gtg	gca	gca	gac	cca	gag	acc	ggg	gag	tcc	agc	ttc	cag	ctg	atc	acc	1200
Val	Ala	Ala	Asp	Pro	Glu	Thr	Gly	Glu	Ser	Ser	Phe	Gln	Leu	Ile	Thr	
					390				395					400		
ccg	ttc	cgt	gga	ctt	cag	cgc	gag	tac	ctc	tct	gca	cac	atg	tct	gcg	1248
Pro	Phe	Arg	Gly	Leu	Gln	Arg	Glu	Tyr	Leu	Ser	Ala	His	Met	Ser	Ala	
				405					410					415		
tcg	tct	gat	cca	gtt	acc	tac	ggg	gaa	atc	act	gtt	cgt	gtg	ctg	cct	1296
Ser	Ser	Asp	Pro	Val	Thr	Tyr	Gly	Glu	Ile	Thr	Val	Arg	Val	Leu	Pro	
			420					425					430			
acc	gat	tct	gtg	acc	cag	ggg	cca	aag	cag	gcc	cag	gat	gcg	atg	atg	1344
Thr	Asp	Ser	Val	Thr	Gln	Gly	Pro	Lys	Gln	Ala	Gln	Asp	Ala	Met	Met	
			435				440					445				
tca	tct	gac	cag	gtt	gct	cag	gac	caa	aca	ctg	tgg	cgt	gga	tcg	aac	1392
Ser	Ser	Asp	Gln	Val	Ala	Gln	Asp	Gln	Thr	Leu	Trp</					

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                485                490                495
gcc ttc ccg aag ctt ctg cgc gtg ctg gtc ttc tac aag ggt cag gtt 1536
Ala Phe Pro Lys Leu Leu Arg Val Leu Val Phe Tyr Lys Gly Gln Val
                500                505                510

ggt tac gca cca acg atc gct gaa gcc cta tcg cag gtc ggc att gat 1584
Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp
                515                520                525

ccg aag gaa gcg cag gac atc gaa gag gta gat ggc acc gct acg acg 1632
Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr
                530                535                540

cca tcg act gat gag act gac act gac act gat cag cct gca acc gaa 1680
Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu
545                550                555                560

acc cca act gca cca gtg agt gag gcg gaa gga atc gcg gcc atc aac 1728
Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn
                565                570                575

gat gcg ttg agc aac ctt gaa gct gct cgc gat agc tct ttc gaa gag 1776
Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu
                580                585                590

tat ggt cgt gca ctc gat gcg ctt gat cgt gcc gtc gat agc tac cag 1824
Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln
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tcc gca cag tagcgtttga gtaaacagcc cga 1856
Ser Ala Gln
        610

<210> 436
<211> 611
<212> PRT
<213> Corynebacterium glutamicum

<400> 436
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Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
  20                25                30

Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
  35                40                45

Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
  50                55                60

Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
  65                70                75                80

Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
  85                90                95

Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
 100                105                110

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Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
 115 120 125
 Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
 130 135 140
 Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
 145 150 155 160
 Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
 165 170 175
 Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
 180 185 190
 Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
 195 200 205
 Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
 210 215 220
 Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
 225 230 235 240
 Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
 245 250 255
 Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
 260 265 270
 Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
 275 280 285
 Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
 290 295 300
 Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
 305 310 315 320
 Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
 325 330 335
 Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
 340 345 350
 Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
 355 360 365
 Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val
 370 375 380
 Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr
 385 390 395 400
 Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala
 405 410 415
 Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro
 420 425 430

Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met
 435 440 445

Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn
 450 455 460

Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
 465 470 475 480

Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala Ser
 485 490 495

Ala Phe Pro Lys Leu Leu Arg Val Leu Val Phe Tyr Lys Gly Gln Val
 500 505 510

Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp
 515 520 525

Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr
 530 535 540

Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu
 545 550 555 560

Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn
 565 570 575

Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu
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Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln
 595 600 605

Ser Ala Gln
 610

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 <222> (101)..(844)
 <223> RXS01677

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 Val Asn Gln Gln Ser
 1 5

aaa aag tgg ctc gta ccg aca ctg gtc gtc atc att gca gtg ctc ctc 163
 Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile Ile Ala Val Leu Leu
 10 15 20

atc gca gtt gtt ctg ttg atg tac cga gga aat gcg agt gat acg gcc 211
 Ile Ala Val Val Leu Leu Met Tyr Arg Gly Asn Ala Ser Asp Thr Ala
 25 30 35

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gag ggc gtt tca gcc gct gcg act tcg gac tcg gct gct gct tcg act 259
Glu Gly Val Ser Ala Ala Ala Thr Ser Asp Ser Ala Ala Ser Thr
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gct gct tcg ggt tcc gct tct ggt gct gcg gac tcc gat ctg acc agc 307
Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp Ser Asp Leu Thr Ser
    55                      60                      65

gtg gaa gca cgc gac cct tcc gac cct gtt gcg gtg gga gac gtt gat 355
Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala Val Gly Asp Val Asp
    70                      75                      80                      85

gca cct gtt ggg tta gtg gtg ttt tcc gac tac caa tgc ccg ttc tgt 403
Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr Gln Cys Pro Phe Cys
    90                      95                      100

gca aag tgg agc gat gaa acc ctg cca cag atg atg aag cat gtg gaa 451
Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met Met Lys His Val Glu
    105                      110                      115

gat gga aac ctc cgc att gaa tgg cgt gaa gtg aac atc ttt gga gaa 499
Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val Asn Ile Phe Gly Glu
    120                      125                      130

cca tct gag cgt gga gct cgc gcg gca tac gct gcg ggt ttg cag gac 547
Pro Ser Glu Arg Gly Ala Arg Ala Ala Tyr Ala Ala Gly Leu Gln Asp
    135                      140                      145

gca tac ttg gaa tac cac aac gca ctc ttt gcc aac ggt gaa aaa ccc 595
Ala Tyr Leu Glu Tyr His Asn Ala Leu Phe Ala Asn Gly Glu Lys Pro
    150                      155                      160                      165

agc gaa gac ctg ctc agc gaa gag gga ctt att aag ctt gct ggt gac 643
Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile Lys Leu Ala Gly Asp
    170                      175                      180

ctt gga cta gac gaa tcg aaa ttc act gcc gat ttc caa tcc cct gaa 691
Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp Phe Gln Ser Pro Glu
    185                      190                      195

act gca gtc gca att gcg caa cat caa cag ctg gga atc gat ctt ggc 739
Thr Ala Val Ala Ile Ala Gln His Gln Gln Leu Gly Ile Asp Leu Gly
    200                      205                      210

gcc tac tcc acc cca gct ttc ctc cta ggt ggc cag cca atc atg ggc 787
Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly Gln Pro Ile Met Gly
    215                      220                      225

gct cag cct gct tct gta ttt gaa gcc gcc ttc gag caa gca ctg gca 835
Ala Gln Pro Ala Ser Val Phe Glu Ala Ala Phe Glu Gln Ala Leu Ala
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Ala Lys Glu

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<211> 248

<212> PRT

<213> Corynebacterium glutamicum

<400> 438

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    20          25          30

Ala Ser Asp Thr Ala Glu Gly Val Ser Ala Ala Ala Thr Ser Asp Ser
    35          40          45

Ala Ala Ala Ser Thr Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp
    50          55          60

Ser Asp Leu Thr Ser Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala
    65          70          75          80

Val Gly Asp Val Asp Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr
    85          90          95

Gln Cys Pro Phe Cys Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met
   100          105          110

Met Lys His Val Glu Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val
   115          120          125

Asn Ile Phe Gly Glu Pro Ser Glu Arg Gly Ala Arg Ala Ala Tyr Ala
   130          135          140

Ala Gly Leu Gln Asp Ala Tyr Leu Glu Tyr His Asn Ala Leu Phe Ala
   145          150          155          160

Asn Gly Glu Lys Pro Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile
   165          170          175

Lys Leu Ala Gly Asp Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp
   180          185          190

Phe Gln Ser Pro Glu Thr Ala Val Ala Ile Ala Gln His Gln Gln Leu
   195          200          205

Gly Ile Asp Leu Gly Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly
   210          215          220

Gln Pro Ile Met Gly Ala Gln Pro Ala Ser Val Phe Glu Ala Ala Phe
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Glu Gln Ala Leu Ala Ala Lys Glu
          245

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<211> 1095

<212> DNA

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<220>

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<222> (101)..(1072)

<223> RXS02932

<400> 439

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Val Ser Lys Thr Glu
1 5

gaa ggc cgt tca gcg gcc ata att att tac gcg ttt cca act ttc att 163
Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala Phe Pro Thr Phe Ile
10 15 20

ctg ctg ggc gcg atc att gcg ttt atc ttc ccg gaa cca ttc att ccg 211
Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro Glu Pro Phe Ile Pro
25 30 35

ctg aca aac tac att aat atc ttc ctc acg atc atc atg ttc acc atg 259
Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile Ile Met Phe Thr Met
40 45 50

ggt ttg acc ttg acg gtg ccc gat ttt cag atg gtg ctt aaa cgt cca 307
Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met Val Leu Lys Arg Pro
55 60 65

ctg cct atc ttg atc ggt gta gta gcg cag ttt gtc atc atg cca ttc 355
Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe Val Ile Met Pro Phe
70 75 80 85

ctg gcg atc gtg gtt gcg aaa atg ttc aac ctc aac cca gca ctc gcc 403
Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu Asn Pro Ala Leu Ala
90 95 100

gtt ggc ctt ctc atg ctg gga tcc gtt ccg ggt ggc acc tcc tcc aat 451
Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly Gly Thr Ser Ser Asn
105 110 115

gtg att gcg ttt ctc gcc cga gga gat gtc gcg cta tcg gtc acc atg 499
Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala Leu Ser Val Thr Met
120 125 130

acc tct gtg tcc acc att gtt tcc cca atc atg acg cct ttc ctc atg 547
Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met Thr Pro Phe Leu Met
135 140 145

ctc atg ctg gca ggt act gaa acc gcc gtc gat ggt gga ggc atg gcg 595
Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp Gly Gly Gly Met Ala
150 155 160 165

tgg act ttg gta caa aca gtg ctg ctg cct gtg atc atc ggc cta gtt 643
Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val Ile Ile Gly Leu Val
170 175 180

ctg cgt gtc ttc ttg aac aag tgg atc gac aag att ttg ccg atc ctt 691
Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys Ile Leu Pro Ile Leu
185 190 195

cct tat ctc tcc atc ctc ggt atc ggt ggc gtg gtg ttc ggc gca gtc 739
Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val Val Phe Gly Ala Val
200 205 210

gca gcc aac gcg gaa cga ctc gtg tct gtc gga ctc atc gtg ttc gtt 787

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<211> 324
<212> PRT
<213> Corynebacterium glutamicum

 $\langle 400 \rangle$ 440

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Glu	Pro	Phe 35	Ile	Pro	Leu	Thr	Asn 40	Tyr	Ile	Asn	Ile	Phe 45	Leu	Thr	Ile
Ile	Met 50	Phe	Thr	Met	Gly	Leu 55	Thr	Leu	Thr	Val	Pro 60	Asp	Phe	Gln	Met
Val 65	Leu	Lys	Arg	Pro	Leu 70	Pro	Ile	Leu	Ile	Gly 75	Val	Val	Ala	Gln	Phe 80
Val	Ile	Met	Pro	Phe 85	Leu	Ala	Ile	Val	Val 90	Ala	Lys	Met	Phe	Asn 95	Leu
Asn	Pro	Ala	Leu 100	Ala	Val	Gly	Leu	Leu	Met 105	Leu	Gly	Ser	Val	Pro	Gly
Gly	Thr 115	Ser	Ser	Asn	Val	Ile	Ala 120	Phe	Leu	Ala	Arg	Gly 125	Asp	Val	Ala
Leu	Ser	Val	Thr	Met	Thr	Ser	Val	Ser	Thr	Ile	Val	Ser	Pro	Ile	Met

130 135 140
 Thr Pro Phe Leu Met Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp
 145 150 155 160
 Gly Gly Gly Met Ala Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val
 165 170 175
 Ile Ile Gly Leu Val Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys
 180 185 190
 Ile Leu Pro Ile Leu Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val
 195 200 205
 Val Phe Gly Ala Val Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly
 210 215 220
 Leu Ile Val Phe Val Ala Val Ile Val His Asn Val Leu Gly Tyr Val
 225 230 235 240
 Val Gly Tyr Leu Thr Gly Arg Val Phe Lys Phe Pro Glu Ala Ala Asn
 245 250 255
 Arg Thr Met Ala Ile Glu Ile Gly Thr Gln Ser Ala Gly Leu Ala Ser
 260 265 270
 Gly Met Ala Gly Arg Phe Phe Thr Pro Glu Ala Ala Leu Pro Gly Ala
 275 280 285
 Val Ala Ala Leu Val His Asn Ile Thr Gly Ala Val Tyr Val Gly Leu
 290 295 300
 Val Arg Asn Arg Pro Leu Thr Lys Ala Ser Arg Lys Lys Glu Ser Val
 305 310 315 320
 Ala Val Ser Ser

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 <211> 844
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(844)
 <223> FRXA02402

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 Val Ser Lys Thr Glu
 1 5

 gaa ggc cgt tca gcg gcc ata att att tac gcg ttt cca act ttc att 163
 Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala Phe Pro Thr Phe Ile
 10 15 20

 ctg ctg ggc gcg atc att gcg ttt atc ttc ccg gaa cca ttc att ccg 211

Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro Glu Pro Phe Ile Pro
 25 30 35
 ctg aca aac tac att aat atc ttc ctc acg atc atc atg ttc acc atg 259
 Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile Ile Met Phe Thr Met
 40 45 50
 ggt ttg acc ttg acg gtg ccc gat ttt cag atg gtg ctt aaa cgt cca 307
 Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met Val Leu Lys Arg Pro
 55 60 65
 ctg cct atc ttg atc ggt gta gta gcg cag ttt gtc atc atg cca ttc 355
 Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe Val Ile Met Pro Phe
 70 75 80 85
 ctg gcg atc gtg gtt gcg aaa atg ttc aac ctc aac cca gca ctc gcc 403
 Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu Asn Pro Ala Leu Ala
 90 95 100
 gtt ggc ctt ctc atg ctg gga tcc gtt ccg ggt ggc acc tcc tcc aat 451
 Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly Gly Thr Ser Ser Asn
 105 110 115
 gtg att gcg ttt ctc gcc cga gga gat gtc gcg cta tcg gtc acc atg 499
 Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala Leu Ser Val Thr Met
 120 125 130
 acc tct gtg tcc acc att gtt tcc cca atc atg acg cct ttc ctc atg 547
 Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met Thr Pro Phe Leu Met
 135 140 145
 ctc atg ctg gca ggt act gaa acc gcc gtc gat ggt gga ggc atg gcg 595
 Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp Gly Gly Gly Met Ala
 150 155 160 165
 tgg act ttg gta caa aca gtg ctg ctg cct gtg atc atc ggc cta gtt 643
 Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val Ile Ile Gly Leu Val
 170 175 180
 ctg cgt gtc ttc ttg aac aag tgg atc gac aag att ttg ccg atc ctt 691
 Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys Ile Leu Pro Ile Leu
 185 190 195
 cct tat ctc tcc atc ctc ggt atc ggt ggc gtg gtg ttc ggc gca gtc 739
 Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val Val Phe Gly Ala Val
 200 205 210
 gca gcc aac gcg gaa cga ctc gtg tct gtc gga ctc atc gtg ttc gtt 787
 Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly Leu Ile Val Phe Val
 215 220 225
 gca gtt atc gtg cac aac gta ctt gga tac gtt gtg gga tac ctc acc 835
 Ala Val Ile Val His Asn Val Leu Gly Tyr Val Val Gly Tyr Leu Thr
 230 235 240 245
 ggc cgt gta
 Gly Arg Val 844

<210> 442

<211> 248

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 442

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Glu Pro Phe Ile Pro Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile
      35           40           45

Ile Met Phe Thr Met Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met
      50           55           60

Val Leu Lys Arg Pro Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe
      65           70           75           80

Val Ile Met Pro Phe Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu
      85           90           95

Asn Pro Ala Leu Ala Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly
      100          105          110

Gly Thr Ser Ser Asn Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala
      115          120          125

Leu Ser Val Thr Met Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met
      130          135          140

Thr Pro Phe Leu Met Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp
      145          150          155          160

Gly Gly Gly Met Ala Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val
      165          170          175

Ile Ile Gly Leu Val Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys
      180          185          190

Ile Leu Pro Ile Leu Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val
      195          200          205

Val Phe Gly Ala Val Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly
      210          215          220

Leu Ile Val Phe Val Ala Val Ile Val His Asn Val Leu Gly Tyr Val
      225          230          235          240

Val Gly Tyr Leu Thr Gly Arg Val
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<211> 1389

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<222> (101) .. (1366)

<223> RXS00654

<400> 443

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Val Leu Asp Ile Leu
1 5

att tac ccg gtg tct gga gtg atg aag ctg tgg cac ctg ctt ctt cac 163
Ile Tyr Pro Val Ser Gly Val Met Lys Leu Trp His Leu Leu Leu His
10 15 20

aac gtt gcg ggt ttg gac gat tca ctg gcg tgg ttc ttt tcc ctt ttc 211
Asn Val Ala Gly Leu Asp Asp Ser Leu Ala Trp Phe Phe Ser Leu Phe
25 30 35

ggc ctt gtc atc acg atc cgt gca att atc ggc cct ttc acc tgg cag 259
Gly Leu Val Ile Thr Ile Arg Ala Ile Ile Ala Pro Phe Thr Trp Gln
40 45 50

atg tat aag tgc ggc cgc act gcc gca cat att cgt cct cac cgc gct 307
Met Tyr Lys Ser Gly Arg Thr Ala Ala His Ile Arg Pro His Arg Ala
55 60 65

gcg ctc cgg gaa gaa tac aag gga aag tac gat gaa gcg tcc att cgg 355
Ala Leu Arg Glu Glu Tyr Lys Gly Lys Tyr Asp Glu Ala Ser Ile Arg
70 75 80 85

gag ttg cag aag cgc cag aat gat ttg aat aag gaa tac ggc att aac 403
Glu Leu Gln Lys Arg Gln Asn Asp Leu Asn Lys Glu Tyr Gly Ile Asn
90 95 100

ccg ctg gca ggt tgt gtg cct ggg ctg atc cag ata ccg att gtc ctt 451
Pro Leu Ala Gly Cys Val Pro Gly Leu Ile Gln Ile Pro Ile Val Leu
105 110 115

ggt ctt tac tgg gca ctt ctg cgc atg gct cgc cct gaa ggt ggt ttg 499
Gly Leu Tyr Trp Ala Leu Leu Arg Met Ala Arg Pro Glu Gly Gly Leu
 120 125 130

gaa aat ccc gtc ttc cag tcg atc gcc ttc cta act cct gag gaa gtg 547
Glu Asn Pro Val Phe Gln Ser Ile Gly Phe Leu Thr Pro Glu Glu Val
135 140 145

gaa tct ttc ctc gct ggt cgc gtg agc aat gtg cct ctg ccc gct tat 595
Glu Ser Phe Leu Ala Gly Arg Val Ser Asn Val Pro Leu Pro Ala Tyr
150 155 160 165

gtt tgc atg ccc act gag cag cta aaa tat ttg agc acc acg cag gcg 643
Val Ser Met Pro Thr Glu Gln Leu Lys Tyr Leu Ser Thr Thr Gln Ala
170 175 180

gaa gtt ctt agt ttc gtt ttg cca ctg ttc atc aca gcc gca atc ctc 691
Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile Thr Ala Ala Ile Leu
185 190 195

acc gca atc aac atg gcg atg tcc atg tac cgc agc ttc caa acc aac 739
Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg Ser Phe Gln Thr Asn
200 205 210

gat tac gca tcc gga ttc tct aac ggc atg ctg aag ttc atg atc gtg 787
Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu Lys Phe Met Ile Val
215 220 225

atg tcg atc ctc gcg ccg atc ttc cca ctg tcc ctt ggc ctc aca gga 835
Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser Leu Gly Leu Thr Gly
230 235 240 245

cca ttc ccc aca gca atc gca ctc tat tgg gtc agc aac aac ctg tgg 883
Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val Ser Asn Asn Leu Trp
250 255 260

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Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile Leu Glu Arg Lys Tyr
265 270 275

cca ctt acc gac gat ttc aaa gtg cac cac cta gag cag cgc gac atc 979
Pro Leu Thr Asp Asp Phe Lys Val His His Leu Glu Gln Arg Asp Ile
280 285 290

tac cgc gca aaa caa aaa gaa aag cgc atc ttc ctg tgg aca cga cgc 1027
Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe Leu Trp Thr Arg Arg
295 300 305

aaa aac cgc gcc ctg atg att ctc acc cca tgg aac gcc tca acg ctt 1075
Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp Asn Ala Ser Thr Leu
310 315 320 325

cac gca aca aac gtg gaa ctc acc aaa acc cgt act gcc gaa atc aac 1123
His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg Thr Ala Glu Ile Asn
330 335 340

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Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn Lys Arg Arg Glu Thr
345 350 355

caa cgt gaa atg aac cgc gcc gcc atg cag cgc tta aag cag cgt cgc 1219
Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg Leu Lys Gln Arg Arg
360 365 370

gct gag gtt aaa gct aaa aag aag ggg ctt atc gac gcc tcc ccc aac 1267
Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile Asp Ala Ser Pro Asn
375 380 385

gaa gat acc cct tcg gaa aat gaa gaa act aaa ttg agt agt ccg cag 1315
Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys Leu Ser Ser Pro Gln
390 395 400 405

gtg gag ccg aca aca act gcc gag cca aat cgc gag ccg tct caa gag 1363
Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg Glu Pro Ser Gln Glu
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<212> PRT

<400> 444

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Phe	Phe	Ser 35	Leu	Phe	Gly	Leu	Val 40	Ile	Thr	Ile	Arg	Ala 45	Ile	Ile	Ala
Pro	Phe 50	Thr	Trp	Gln	Met	Tyr 55	Lys	Ser	Gly	Arg	Thr 60	Ala	Ala	His	Ile
Arg 65	Pro	His	Arg	Ala	Ala 70	Leu	Arg	Glu	Glu	Tyr 75	Lys	Gly	Lys	Tyr	Asp 80
Glu	Ala	Ser	Ile	Arg 85	Glu	Leu	Gln	Lys	Arg 90	Gln	Asn	Asp	Leu	Asn 95	Lys
Glu	Tyr	Gly 100	Ile	Asn	Pro	Leu	Ala	Gly 105	Cys	Val	Pro	Gly	Leu 110	Ile	Gln
Ile	Pro	Ile 115	Val	Leu	Gly	Leu	Tyr 120	Trp	Ala	Leu	Leu	Arg 125	Met	Ala	Arg
Pro 130	Glu	Gly	Gly	Leu	Glu	Asn 135	Pro	Val	Phe	Gln	Ser 140	Ile	Gly	Phe	Leu
Thr 145	Pro	Glu	Glu	Val	Glu 150	Ser	Phe	Leu	Ala	Gly 155	Arg	Val	Ser	Asn	Val 160
Pro	Leu	Pro	Ala	Tyr 165	Val	Ser	Met	Pro	Thr 170	Glu	Gln	Leu	Lys	Tyr 175	Leu
Ser	Thr	Thr	Gln 180	Ala	Glu	Val	Leu	Ser 185	Phe	Val	Leu	Pro	Leu 190	Phe	Ile
Thr	Ala 195	Ala	Ile	Leu	Thr	Ala	Ile 200	Asn	Met	Ala	Met	Ser 205	Met	Tyr	Arg
Ser 210	Phe	Gln	Thr	Asn	Asp	Tyr 215	Ala	Ser	Gly	Phe	Ser 220	Asn	Gly	Met	Leu
Lys 225	Phe	Met	Ile	Val	Met 230	Ser	Ile	Leu	Ala	Pro 235	Ile	Phe	Pro	Leu	Ser 240
Leu	Gly	Leu	Thr 245	Gly	Pro	Phe	Pro	Thr	Ala 250	Ile	Ala	Leu	Tyr	Trp 255	Val
Ser	Asn	Asn	Leu 260	Trp	Thr	Leu	Leu	Gln 265	Thr	Ile	Ile	Met	Met 270	Val	Ile
Leu	Glu	Arg 275	Lys	Tyr	Pro	Leu	Thr 280	Asp	Asp	Phe	Lys	Val 285	His	His	Leu
Glu 290	Gln	Arg	Asp	Ile	Tyr	Arg 295	Ala	Lys	Gln	Lys	Glu 300	Lys	Arg	Ile	Phe
Leu	Trp	Thr	Arg	Arg	Lys	Asn	Arg	Ala	Leu	Met	Ile	Leu	Thr	Pro	Trp

305 310 315 320
Asn Ala Ser Thr Leu His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg
 325 330 335
Thr Ala Glu Ile Asn Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn
 340 345 350
Lys Arg Arg Glu Thr Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg
 355 360 365
Leu Lys Gln Arg Arg Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile
 370 375 380
Asp Ala Ser Pro Asn Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys
385 390 395 400
Leu Ser Ser Pro Gln Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg
 405 410 415
Glu Pro Ser Gln Glu Asp
 420

APPENDIX A: DNA SEQUENCES

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>RXA00001

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>RXA00759-upstream

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>RXA00759

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>RXA00950

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>RXA00980-upstream

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>RXA01000

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>RXA01012

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>RXA01012-downstream

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>RXA01013

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>RXA01070
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>RXA01094
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>RXA01142
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>RXA01185-upstream

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>RXA01185

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>RXA01986
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>RXA02119

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>RXN03164
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TGGCACAACTTCGGTGATGACAAGCCGCTTTCAACGCAGCGCAGCATTATTCACCGCGCG
TTTGATAGGGGAGTCACTCACTTCGATTTGGCTAATAACTATGGACCTCCAGCAGGTTCC

GCAGAGACCAACTTTGGCAGGATTTTGCCTGAGGATCTCAAAAGCCACCGCGATGAGTTG
ATCATTTCTTCCAAGGCGGGTTGGGATATGTGGCCTGGACCTTATGGTTTGGTGGTTCC
CGAAAGTATCTAGTGAGTTCCCTTGATCAGTCCCTGACTCGCCTCGGCTTGGATTACGTG
GATATTTTCTATCATCACCGCCCGGATCCAGATACTCCTTTGGAAGAAACCATGTACGCA
TTGCGTGACATTGTTGCGTCTGGAAGGCTCTTTACGTGGGTATTTCTTCTACGGTCCA
GAGCTCACAGCGGAGGCGGCTGAGTTCATGGCGGAGGAGGGCTGCCCCGCTTCTGATTTCAT
CAGCCAAGCTATTCCATCATTAATCGTTGGGTGGAGGAACCGGGCGATGACGGTGAGAAC
TTGTTGCAGTCAGCTGCCAACAATGGTCTTGGCGTCATTGCTTTCTCACCACCTTGCGCAG
GGCCTGCTCACGGACAAATATCTCGATGGAATTCCAGAGGGTTCCCGCGCCAGCCAGGGT
AAGTCCCTGTCTGAGGGCATGTTGAACGTGAACAATATTGATATGGTCCGCAAGCTCAAT
GACATCGCCCAGGAACGCGGGCAGTCACTTGCGCAGATGGCGCTTGCATGGGTGCTGCGC
GAGCAAAGAGAGTACGGCGCCGGATTACCG

>RXN03164-downstream
TGACCAGTGCATTGATTGGTGCT

RXS00088 - coding Region

ATCGAAGACAACCACGGCACCGAAGGGATCTCCCTGCCAATCGAGGGCGTCGCTGCGACCGACAACCGC
GCATTCGAAGTCTTGATCGCTGGGGTGTAGAGCTCGTTGCAGCTCCACTTCAGCTGGTTCCATTTACC
GTTACGGGCTACACCGAAGAGGGCGGCGTCGTAACCTTGGCTCCCACCGCGAGCCAGACCTGGAAGCA
CTTGCTGCTGCACAGCCTTCCCTGATCATCAACGGCCAGCGCTTCGCTCAGTACTACGATGACATCATT
GCCCTGAACCTTGACGCAACCGTTGTTGAGCTAGACCCACGCGATGGCGAGCCACTTGACCAGGAGCTT
ATCCGCCAGGCTGAAACCTTCGCTGAGATCTTCGGCGAAGAAGAAGATGCTGCAAAGATCGTTGCTGAT
TTCGAGTCCGCACTTGAGCGCGCTAAGACCGCATACGCAGCAATCTCCGACCAGACCGTCATGGCAGTT
AACGTTTCCGGCGGAAACATTGGCTACATCGCTCCTTCCGTTGGACGCACCTACGGTCCAATCTTCGAC
CTGGTTGGACTCACCCAGCACTCGAGGTTGGCAACGCGTCTCCGACCACGAGGGCGACGACATTAAC
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CGCAACGAAGCTGATTACGTTCCAGCAGAGCAGATCGTCTCCGACAATGAAGCACTGGCAAACGTCAG
GCTGTACCGACGGATACGTTTACTACGCACCTGCAGATACCTACACCAACGAAAACATCATCACCTAC
ACCGAGATCCTCAACGGCATGGCAGATATGTTGAGAAGGCAGCTCAG

RXS00088 - 3'-Region
TAGGGGATCGATCCCACACTGAC

RXS00372 - 5'-Region
GCAGACATTTCCATAAGTCCTGCGAAATGCGCCCATTCATGTAAAGATGTTATTTCTCCCCCAAACAC
TCCTTAAATTTCAAGAAGGCCTTATTTTC

RXS00372 - coding Region

ATGTCTTCGAAGCACCTTTGAAGCGCACTGCCGTTACTGTTTTTGCCTCGGCGCTTCCGCTGCTCTC
CTCGTGGCTTGCTCTGAACCTTCTGAGGACGTTTCCACCGCAGAGACCACCTGCAAGCTCTTCCGCT
AACGCATCCGATGCAGCCGGTGAAAAAGTAACCATCACCGTCTACACCTCTGAGCCTGAGGAAAAGGTC
GATGAGATCAACAAGGCGTTTCATGGAAGCCAACCCAGATATTGAGGTTGAGGTGTACCGCGCTGGTACT
GGCGATCTGACTGCTCGCATTGAAGCTGAAAAGGCATCCGGTTCTATCGAGGCTGATGTGTTGTTGGGCT
GCGGATGCTGCAACCTTTGAACTTATGCAGCACAGGGCGACCTTGCAGAGCTGGAAGATGTTGAGACT
TCCGACATCATTGAAGAGGCTCTGGATGCTGAGAACTTTTATGTAGGCACCCGCATCATCCCAACCGTG
ATTGCATACAACACTGAAGTTGTTGATCAGGCTGAGCTTCTACGTCTTGGGCTGATCTGACTGATCCT
AAGTATGCAGGCCAACTGGTTCATGCCGATCCAGCTGTGTCTGGTGCTGCAGCCTTCAATGCTTCTGTG
TGGAAGAACGACCCTGCGCTTGGCGAAGCCTGGATCACCGCCTTGGGTGAAAACCAACCAATGATCGCT
CAGTCCAACGCGCCAACTCCCAGGAGATCGCTGGCGGTGGCCACCCAGTGGGCATCGTGGTGGACTAC
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ATCACTGAGCCTGCAGGTGTGTTCTGCTGATTCTGAAAAGAAGGAAGCAGCCGAGCGCTACATCAACTTC
CTGCTGTCTGTTGAAGGCCAGGAAATCGCAGTTGAGCAGGCATACCTGCCAGTGCCTGAAGATGTCGGA
ACTCCAGAGGGCACCCCCGAGTTGGCTGACATCGAGCTCATGACCCCTGACCTGGAGGTTGTAACCGCT
GATAAGGCGGCTGCTGTTGAGTCTTCCAAAACGCAATGAAC

RXS00372 - 3'-Region
TAGTTTTCTATGCAGTTATCTC

RXS00453 - 5'-Region

TAGTGGGGCGTGAAAAATAGCTCATTTAAGAGGAGAAGCAACCCCGTGGCGAAATTGCTATTACAGGTT
GGGGCGATGGTCCTATAATCGCAAGTGGATT

RXS00453 - coding Region

GTGATTTTCGGCATGGCTACTTATTTTGGCCATTGTTGGTGGTCTGGCCCTGACGATGCAGAAGGGGTTT
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GATCAGACGAACCCGGTGACGGCCGCCGGAGTTAACGTGGTTTTTCCAATCCCCGGAAGGAACACGCTT
GATGATCCTCAGATGATGACTGCGATGGATGCAGTCGTTGATTACATTGAGGACAATTTGCCTGATTTT
GGTGGGGGAGAGCGCTTCGGCAATCCTGTTGAGGTGTCTCCTGCGTTGGAAGAGATGGTCATCGAGCAG
ATGACCAGCATGGGGCTTCCTGAGGAAACCGCTGCAAAGGATGCTGCCAATCTGGCGGTGTTGAGCGAA
GACAAAACCATTTGGCTACACCTCTTTCAACATTGATGTTGAGGCCGAGAATATGTGGAGCAAAAACAC
CGCGATGTGATCAACGAAGCGATGCAAATCGGTGAAGATTTAGGTGTCCGGGTGGAAGCCGGTGGACCT
GCTTTCGGTGATCCAATTGAGATTGAAACCACCACTGAGATCATCGGTATTGGCATCGCGTTCATCGTG
TTGATTTTACCTTTGTTTCTTTGATTGCTGCGAGCTTGCCTTTGATTACCGCGGTGATCGGCGTGGGC
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AAGCGCATGCCACGTGCCGATGCTGCCGAATGGCGGTGGGCACAGCTGGTAGTGCGGTGGTGTGTTGCT
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GCATTGCAGCCACTGATTGAGGCACAGGAGCCTGAAGAGGGCGAGTTCGATCGGGAGCAGGCGGCTCGT
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GGCTTCGGTGGCTTTGTGTAACACCCCTGGTCCGCTGATTTCTTTCATGCCGATCTTCTCATCGGCGTG
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TTGCCATTTATTAAGATCTTCGGTTTCGCGTTGGGTGCGGGCGTGTTTTTCGATGCTTCTTCATTTCG
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CGAATTCTGCCAAGTTTGGACATTGAAGGCACCGCACTGGAGAAGGAATGGGAGGAGAAGCAGGCTGCA
CGT

RXS00453 - 3'-Region

TAGACTTGGCACCTATGTCAGAT

RXS00479 - 5'-Region

TAGATCCCAAGGCTCAAATTTTATTACTTAAACAAGTTGAGCAACTAGCCAGCCGCAAATCTTAGAACT
AACCTTTACGCCTTTAACGGAAGTGAATTTG

RXS00479 - coding Region

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CCCGCCTTGCTAATTTTGTGTTTGGCTTGTAGGAGCTGGAGTCGGCGGTCTTATTTTGGCAAGGTTAGT
GAGGTCTCCTCCAACAGCCAGACCACATATCTGCCAGAATCTGCCGATGCCACTCAAGTACAGGAACAG
TTGGGAGATTTTACTGATTCTGAATCCATCCCAGCCATTGTGCGTAATGGTCAGCGATGAACCCTTAACA
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GTCTCCCCTGCTATTCCATCCGAGGACGGCAGAGCTGTCCAAGTGTGTTGTTCCCTCAATCCATCAGCG
GAGCTGACGGAAAGCGTCGAGAAGCTCTCTGAGACCTTGACCCAGCAAACGCCGGACTATGTGAGCACC
TATGTGACCGGACCGGTGGGTTTACCGCTGATCTCAGCGCAGCTTTCGCGGGTATTGATGGGCTACTC
CTAGCAGTCGCCTTGGCTGCCGTCTTGTCAATCTTGTATCGTCTATCGCTCCTTCAATCTGCCCATC
GCCGTGCTTGCCACCAAGTTTGTGTTGCGCTGACTGTAGCTCTATTGGTGGTGTGGTGGCTAGCTAAGTGG
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 CTTATTGATACCTGCTCGTTGCGCCTTCTTGGTGCCTGCTTTGTTCTACGACATCGGACCGAAAATC
 TGGTGGCCGTCAAAATTGTCCAATCAGAAATACCAGAAGCAGCCTCAGCTA

RXS00479 - 3'-Region
 TGACACACCAAAATTCGCCTCTC

RXS00654 - 5'-Region
 CAGCAATAGCGATTATTGCTTGATTGTGTGTTTTTAGATCTTCGGTTCTCTTCACTCAACTGCTGTGAA
 GTGCCACCTGTTTGGAAAGGCGAACACGATA

RXS00654 - coding Region
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 GCGGGTTTGGACGATTCTACTGGCTGGTTCTTTTCCCTTTTCGGCCTTGTCTATCACGATCCGTGCAATT
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 AATCGCGAGCCGTCTCAAGAGGAC

RXS00654 - 3'-Region
 TGATGTTGTGGACCAATCGAGAT

RXS00758 - 5'-Region
 TTCAAGTTTGGCTGTGACTCATGTGCGACATAGTATTTCAATCACCGGATCCGCACGATTGCAAAATCC
 TGGGGAATATTCAACAACGGAGGTCACTC

RXS00758 - coding Region
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 TCCGACTCCTCGTCCGACAGCTCCTCATCCTCATCAGGCAGCGAAGGCGGCGACAACACTACGTCTCTGTC
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 GACAGCATCTTCTCCGGCCTGGTCTACTACGACGTCGACGGCTCCCCTGTCAACGATGTTGCAGAGTCC
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TTCAAGTCCCTGCGTGACGATGTACCAACCGCACCATCAACGGCGCATTCGCGACCGGCTGGCAGGCA
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CCGCTATACAACGAAGCACAGGAAATCCTGCTCCAGGATCTCCAGCGATCCCAACTTGGTACTCCAAC
GCAGTTGGTGGATACTCCACCAACGTGGACAACGTGGAATTCCAGTGGAAGTTCGCAACCTGCGTACTAC
CAGATACCAAGAAC

RXS00758 - 3'-Region
TAGTAGCTTCGCACCACCCGCTC

RXS00912 - 5'-Region
CCACACCTTTGAAAGGAGCTAAGCG

RXS00912 - coding Region
ATGGACAACACCCTTACACAGCAGGCCCTCACAATCGCAGCTGCCTTTTTTCATGCTGTGCTTCATCTTC
ACCATCTACCGCATCATCGTCGGGCCCAACTCCATCGATCGCCTACTCGGCCTGGACGGAACCGTCTCC
ATGATTCAATGCTCCATGGCCACCTACATCTGCTGGACACTCGACACCACCGTCACCAACTTCATGATG
GTCATCGCACTCTTAGGATTCATCAGCTCTGTATCCGTAGCCCCGCTTCCGCAAGAGGGATGGTGCC

RXS00912 - 3'-Region
TAAATGACCCTGCAACTATTTCAC

RXS00932 - 5'-Region
CCCAATTAATTTATGCACTTCGGTGAGGTTACTCACAAGAGTAGCGTGCAAAGCCCAGCAATAAGGTG
ATGTTTCAACGATTAGGTTACGGTAGGGGCC

RXS00932 - coding Region
ATGACGCCACAGAACTTACCGTTTTGCAGCCCTTTTAGAAATGGGTACCTGGACCCTGCTGATCATC
GGCATGATCTTAAATACAGTGGAGTGACAGACGCCGTAACCCCTATTGCCGGCGGTATCCACGGCTTT
GGCTTCTCTGTTTTGCAGCCATCACCATCACCCTGTGGATCAATAATAAGTGGACATTCCCGCAGGGT
ATCGCAGGTTTGTATGCTCTCTGTTATCCCGTGGGCTGCATTGCCATTTGCATTGTGGGCAGACAAGAAG
GGCCTCGTTGCCGGCGGATGGCGCTTTTCAGATCCGTCGAAAAGCCACACACTTTCTTTGACAAGATC
TTGGCTCAATTGGTCAGGCACCCAATCCGATCCATTTAATTCTGCTGGTGATTATCGCCGTCGTCTTC
TCTATCTTGCTGGCGATGGGACCACCTTATGATCCAGATGCCATCGCAACACTGTGGAT

RXS00932 - 3'-Region
TAAACAACAGCCTCCTTCACATG

RXS01346 - 5'-Region
AAGGTGTGGTGAGTCACTGGCTAGATTTGATTTGTTGGCCATACCAAATCGGCCACACAGGCACGTTG
CAAACAGCAACGCTCAGCCATAGGAGATTTA

RXS01346 - coding Region
ATGCGCACAGCCACAAAAGTCATCGCAACAGTGATGGCCTCAACCCTGGCTATCGGGCTGGCATCTTGT
TCCAGCTCTAGTGGCACCCAGACGTGAATTACGTATCCGTCAACGGCACCGAACCTCAGCGCGGACTC
ATCCCGGGCGACACCAATGAAAACGGCGGTGGGCGAGTGGTGGACATGCTGTACTCTGGGCTCGTCTAC
TTTGATGAAGCTGGCGTTGCTCAAAATGACCTGGCGGCATCAATTGACCAGGAAACAGACACCACCTAC
AAAATCACTTTGCGTGATGGCATCAAATTCAGTGACGGATCGGATATTACTGCCACTGATTTTGTGGAT

ACCTGGAATTTTGTAGTGGAAAATGGACTGCTCAACACTTCTTTCTTCTCACCAGATTAAAGGGTATGAG
GAGGGCGTGGAACGCTCGAGGGTTTGAATGTGGTGGATGATCGCACATTTACCATCGAGCTTGCCCAA
CCGGATTCTGAGTTACCCAACGCATTGGCTACTACGGTTTTGCACCGATGCCAGCTTCGGCTCGCGAT
GATATTGACGCCTTTGGTGAACACCCCGTGCTCTGGCCCTTACAACTAGAGCAGTGGGATCACAAC
GCAGAACTGAAAGTGGTGGCCAATGAACACTACGATGGCCCGCGCGCAGCCAACAACGATGGCTTGAAG
TACGTGTTCTACGCCCCAAAATGATGCAGCTTATTAGATCTGTTGGCTGGAAACCTAGATGTGCTGGAT
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CGACAAGCAATTTCTATGGCGATTAAACCGTGAAGAAATCGCTGAGCAGATCTTCGCCGGCACCTACACG
CCTGCGCTCGACTTCACCGCGCCCGTGCTCGACGGCTGGCGCGATGATTTGAACGGCAATGACGTGCTG
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TTGCAGATCAGTTACAACGCGGATGTTCCCAACCGGAATGGGTGGATGCGGTAGCAAACAGCATCAGC
AACGAATTAGACGTCAACGCCACTGGCAATCCTTTCCCGATTTTAAATCCTTCGCGACACATACCGC
ACCACCGGATTGGATGGCGCCTACCGCACCGCGTGGTTTGCGGACTACCCAAGCATCGGCAACTTCCTT
GGACCTAACTACACCTCGGGCGTGGCCTCCAACGATGCCAAGTACGAAAACCCAGAATTTGATCAATTG
ATTGCCGACGCCGACGAGCCTCCACCAAGGAGGAAACCTTCCAGGCATATGCGCAGGCCCAGGAAATG
TTGTTGCGCGATCTTCCCGCAATCCCACTGTGGTACCCGAATGTGGTTGGCGGCTACTCAGAATCCGTG
GACAACGTCTCCGTAAACTGGAAGGCCATACCTGTTTATTGGGCAATTACAAAGCAA

RXS01346 - 3'-Region
TAAACTCATTAACCTAAATCCGG

RXS01425 - 5'-Region
AGTCCCTATTAATCCCAAGGAGTTTCGACTCACAGTGCTCAATTTCAATTTATTGGCCAATTTTCGGCCAT
TCTGTGGTTCTGGCATAAAGCGTTTCAGCTTT

RXS01425 - coding Region
GTGCTGAGCCCAGATTCCGGAATTACCTGGGCCTTGTCGATCATGTTCTTGACCTTCACCGTGCGTATG
GTTCTGGTCAAGCCGATGGTCAACACCATGCGTTTACAGCGCAAGATGCAAGACATGGCTCCAAAGATG
CAGGCCATGCCGAGAGTACAAAATGACAGCAGAGAAGATGATGGAGGAGACCCGCAAACTTCAAAA
GAAGTGGGCGTTAACCCCATCGCAGGCTGTTTGCCAATGTTGGTGCAGATCCAGTGTTTCTGGGTCTG
TTCCACGTGCTGCGCTCCTTCAACCGCACCGGTTCTGGCGTTGGCCAGCTGGAAATGACCGTTGAGCAA
AACGCGAACACCCCGAACTACATCTTCGGTGTGACGAGGTTTCACTCCTTCTGCGTGACAGCTGTTT
GGTGCGCACTGTGCTCCTACATCACCATGCGTGTGACGCGTTTCGACGCGTTCCTTGGCCTGGATGTC
TCCCGCCTCAACATCGCGCTGGTTGACGCTCCAATGATTTTGATCATTTGCTGTTGGCAACTCACATGAAC
GCGGCTCTGTCCGTCAACCGCCAGGAAGCTCGCAAGGCAGCCGGCAAGCAGCAGGCGGCTTCCAGCGAT
CAGATGGCCATGCAGATGCAAAATGATGAACAAGATGATGCTCTGGTTTATGCCAGCCACCATTTTGTTC
ACCGGCTTCACTTCGAGACCTCGGTCTTCTTGTCTACATGATGTCCAACAACGTGTGGACCTTCTTCCAG
CAGCGCTACATCTTTCGCCAAGATGGACGCTGAGGAAGCAGCTGAGGAGGAGGAAAAGCGCGCAGCAAAG
CGCACTACCGCTCCAAAGCCTGGCGTGAAGCCAGAAAACCCCAAGAACGTAAGAAG

RXS01425 - 3'-Region
TAAAACTTCACTAAAAACCGCCA

RXS01658 - coding Region
GATCCACAGATCCTGTACCAACCTTACCCAGCAACAGCAGCTGCGAACTTCTACGGTTTCCAGAC
CAGCTGGCGATGGACCGCTTTGAAGTAGATGGCAAACCTCCGCGACTTTGTTGTGGCAGCACGTGAGCTC
GATCCAAACGCCCTGCAGCAAAACAGCAGGACTGGATTAACCGTCACACTGTTTATACCCACGGCAAC
GGCTTCATTGCAGCTCAAGCAAACAGGTGGATGAGGTGCGCCGCGACGTGCGATCCACTCGTGGTGGT
TACCCTGTCTACACCGTCTCTGATTTGCAGTCAATGCTCGTGTGCGAGAAAGCGAAGATGCTGAGGAG
CTTGGCATCAAGGTTGATGAGCCTCGTGTGTACTACGGACCACTGATTGCTTCTGCGACTGATGGTGCT
GACTACGCAATTGTGCGGTGACACCGCGCATGGCCCAGTTCGAGTACGACACTGACACCTCCAGCTACACC
TACGAAGGTGCTGGCGGCGTGGACATTGGAACATGGTCAACCGTGCGATGTTTGCATTGCGCTACCA
GAAATGAACATGCTCCTGTCTGATCGTGTGGTTCCGAATCCAAGATCCTATTTGAGCGCGATCCTCGT
TCCCGTGTGGAAGGTTGCACCTTGGTTGACCACTGACTCCAAGACCTACCCAAGTGTGATTGATGGT
CGCATCAAGTGGATCGTTCGATGGCTACACCACCTTGGATAGTCTTCCGTACTCCACGCGCACCTCACTG
ACGGAAGCGACTCAGGATGCTGTGATGCTGACGGCACCCACAGCCACTGATCACAGATAGGGTTCGGT
TACATCCGCAACTCCGTGAAGGCTGTTGTTGATGCGTACGACGGAAGTGTGAAGTCTACGAATTCGAC
ACCGAAGATCCTGTTCTGAAGGCATGGCGTGGCGTGTTCAGACACCGTGAAGGACGGGTTCGGAGATT
TCCGATGAGCTTCGCGCACACCTGCGTTACCCAGAAGATTTGTTCAAGGTCCAGCGTGACATGCTGGCC
AAGTACAACGTTGATGATTCTGGAACATTCTTACCAACGATGCGTTCTGGTCTGTCCAGGTGACCCA

ACTGCAGCGGAGGGCCGCCAGGAACCTTAAGCAGCCTCCTTACTACGTGGTGGCAGCAGACCCAGAGACC
GGTGAGTCCAGCTTCCAGCTGATCACCCCGTTCCGTGGACTTCAGCGCGAGTACCTCTCTGCACACATG
TCTGCGTCTGATCCAGTTACCTACGGTGAATCAGTGTCTGTGCTGCCTACCGATTCTGTGACC
CAGGGTCCAAAGCAGGCCCAGGATGCGATGATGTATCTGACCAGGTTGCTCAGGACCAAACACTGTGG
CGTGGATCGAACGATCTGCACAACGGAAACCTGTTGACCTTGCCAGTTGGTGGCGGAGAGATCCTCTAC
GTTGAGCCGATTTACTCGCAGCGCAAGGATCAGGCATCGGCCCTTCCCGAAGCTTCTGCGCGTGTGGTG
TTCTACAAGGGTCAGGTTGGTTACGCACCAACGATCGCTGAAGCCCTATCGCAGGTCGGCATTGATCCG
AAGGAAGCGCAGGACATCGAAGAGGTAGATGGCACCCTACGACGCCATCGACTGATGAGACTGACACT
GACACTGATCAGCCTGCAACCGAAACCCCACTGCACCACTGAGTGAGGCGGAAGGAATCGCGGCCATC
AACGATGCGTTGAGCAACCTTGAAGCTGCTCGCGATAGCTCTTTCGAAGAGTATGGTCGTGCACTCGAT
GCGCTTGATCGTGCCGTCGATAGCTACCAGTCCGCACAG

RXS01658 - 3'-Region
TAGCGTTTGAGTAAACAGCCCCGA

RXS01677 - 5'-Region
GTCGCCATAGTTGAGTTTTATTCATGGCTTTTAGCTAGGCGACTTTAGTTGAGGGCTTTTAGTTGAGGG
CTTCCCAGCAGGGATGGTTAAGGAGAATTCA

RXS01677 - coding Region
GTGAACCAACAGAGTAAAAAGTGGCTCGTACCGACACTGGTCTGTCATCATTGCAGTGCTCCTCATCGCA
GTTGTTCTGTTGATGTACCGAGGAAATGCGAGTGATACGGCCGAGGGCGTTTCAGCCGCTGCGACTTCG
GACTCGGCTGCTGCTTCGACTGCTTCCGGTTCCGCTTCTGGTGCTGCGGACTCCGATCTGACCAGC
GTGGAAGCAGCGACCCCTTCCGACCCCTGTTGCGGTGGGAGACGTTGATGCACCTGTTGGGTTAGTGGTG
TTTTCCGACTACCAATGCCCGTTCTGTGCAAAGTGGAGCGATGAAACCCCTGCCACAGATGATGAAGCAT
GTGGAAGATGGAACCTCCGCATTGAATGGCGTGAAGTGAACATCTTTGGAGAACCATCTGAGCGTGGGA
GCTCGCGCGGCATACGCTGCGGGTTTGCAGGACGCATACTTGAATACCACAACGCACTCTTTGCCAAC
GGTGAAAAACCCAGCGAAGACCTGCTCAGCGAAGAGGGACTTATTAAGCTTGCTGGTGACCTTGGACTA
GACGAATCGAAATTCAGTCCGATTTCCAATCCCCTGAACTGCAGTCGCAATTGCGCAACATCAACAG
CTGGGAATCGATCTTGGCGCCTACTCCACCCAGCTTTCCTCCTAGGTGGCCAGCCAATCATGGGCGCT
CAGCTGCTTCTGTATTTGAAGCCGCTTCGAGCAAGCACTGGCAGCGAAAGAA

RXS01677 - 3'-Region
TAAACCGTGGATGTGCGCCTAGT

RXS02586 - 5'-Region
TTCTCTGAGATCGTCATGATGAAGTACATCGCGTTCGGCATGATCGCAGCGCTGATTCTGGATGCCACC
ATCATCCGCATGCTGCTTGTCCCCCGCCGTG

RXS02586 - coding Region
ATGCACCTGCTTCGCGACGACAACCTGGTGGGCACCCGGCTTCGTAAAAAGGCCTACACCGTCATGGGT
CACGGCTCTGAGGTGGAGGAAGCACCTCGCCCAACCACCCGTCGCCTCAACGACGATGAGGAAGTCACC
GTGATGAAGCAGTTGTGCTGGCGATACCGTGGCATCTCGCGGTGGTTTGAGCACGCAGGAAAACCGT
GATCTGGTGTCTTTCGTGGAACCTAAGGCTCGTTTGAAAAAGCGCAGGCTTGAGGATCTAGAT

RXS02586 - 3'-Region
TAAATCTATGCGAGGATTTTCA

RXS02587 - 5'-Region
AGCCTGGATAACCTGCCAGACGGTGGCGCATGGCTGCAGCCGTTCCGCCCTCTGACTGCCTTGTTATCC
AACGCCACAATTCCCAGGAGTAATCCACCC

RXS02587 - coding Region
GTGTTTCTAAATGGGGCCACTTTGCTTACAGATTTAGGCGCATTGTTCCGTTAGTCGTCATCGCCGCG
ATTTGGCTTTGTTTGTCAATTTCCGGACCAAGCTGGGCGACCGCATGAGCCAGGAAGGATGGGATGAT
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GTCGTGTTGCTGTTTACTGCGCCTGAAGGCACTTCTTTCGATGATGCAGAGGTGTTCTCCAGCATCTCT
GGCTACTTAGATGGGCTAATCGAGAACAACCCTGATGAAGTCAGCCACATCAACAGCTACTTTGACACT
CGTAATCAAAATCTCCTCAGCAAAGACGGCACCCAAACCTTTGCAGCTCTCGGGCTCAAAGGTGACGGC
GAGCAAACGCTGAAGGACTTCCGGGAGATTGAAGATCAGCTCCATCCGGACAACCTTGCCGGTGGCGTC
ACCACTGAGGTGCGGGTGCCACCGCTGTAGCCGACGCACTCGATGAGGGCATGGCTGGCGATATTTCA

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ATTGTTTCCCAATCATGACGCCTTTCTCATGCTCATGCTGGCAGGTACTGAAACCGCCGTCGATGGT
GGAGGCATGGCGTGGACTTTGGTACAAACAGTGCTGCTGCCTGTGATCATCGGCCTAGTTCTGCGTGTC
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GTTATCGTGCACAACGTACTTGGATACGTTGTGGGATACCTACCGGCCGTGTATTCAAATTTCCAGAA
GCAGCAAACCGCACCATTGGCGATTGAAATCGGAACCCAATCCGAGGCCTCGCATCGGGAATGGCAGGA
CGATTCTTACCCCCAGAAGCAGCCCTTCCAGGTGCTGTGCTGCCTTGGTCCACAACATACCGGCGCA
GTTTATGTTGGGCTGGTACGAAACAGGCCTTTGACTAAGGCATCAAGGAAGAAGGAATCCGTGCGGTT
TCCAGC

RXS02932 - 3'-Region
TAACTTATTTGCTGCCCCGTTAGA

RXS03042 - 5'-Region
ATGACACCGGCGCGACGTATGGCATTACTGGCGTACCCCAATTTACGATGACATCTCTGCTCGCCTCGG
CGACGTCTGGTTTCTTACGTTCTGATCGTT

RXS03042 - coding Region
TTGGTTCTAGCGTTCCTCGTGCTGTTGCTCGTGTTCCGGTCCATTTGGGTCCCATTGATCGCGGCTCTG
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AACGCAACGTGCAATGGTTTCAAGCACGGTGCCCGCGTGGTCACTGCTGCGGCGCTGATCATGGTGTCT
GTGTTTCGCGGCATTATAGCGCAGGACATGGCGTTTATTAAGACCATGGGCTTTGCTCTGGCCGTTGCT
GTGTTCTTCGATGCCTTCGTTGTTTCGATGATGATTATCCCTGCAACAATGTTTCTGCTTGTGACAAG
GCTTGGTGGCTACCTAAGTGCTTGGATAAGATTCTTCCCAACGTTGATGTTGAAGGTGAGGGTCTTAGT
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RXS03042 - 3'-Region
TAGAGAAACAAAAAAGGCTGCTA

RXS03075 - 5'-Region
TGTGCAAAATTGCATTACGGCTGAAAAATTCCTAAAGGGACTCCGTCCGAATAATTGGAAAGCCCAGAA
GAACAGTCAACTCCTAGATTAAAGGATAATC

RXS03075 - coding Region
GTGGCGAAATTCCTGTATAAGTTAGGCTCCACGGCCTATCAAAAGAAATGGCCGTTTCTTGGCGTCTGG
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GTGGATCCTGTGTTGGCTGCGCAGGGTGTGGCTGCTCAGATGACCCAGCCCTGGAGGCTCAGGGTGTA
CCTGCGGAGAAGATCGCCGCAGATATTGAGTCGATTAGTCCACTGAGTGCAGATGAGACTACCGGCATC
ATCTCGATGACTTTTGTGATGAGATTCTGCCATGGATATATCCGCAGAGGATCGTGAGAAGGTACCAAT
ATTCTTGATGAATACGATGACGGCGATCTGACTGTTGTCTACAACGGCAACGTGTTTGGCGCAGCTGCA
ACCAGCTTGACATGACCTCTGAGCTCATCGGCCTGCTGGTGGCTGCGGTGCTTCTTATCGTGACCTTC
GGTTGCTTCATCGCTGCCGGTATGCCGCTGATCTCT

RXS03124 - coding Region
ATGACTCCTACCCTGGCGTCGATGATTGGTCTGGCTGTGCGTATCGACTACGCGCTATTTATCGTGTC
CGTTTCCGCAATGAGTTGATTTCTCAGACTGGCGCTAATGATCTGGAGCCAAAGGAATTGGCTGAGCGT
CTGCGCACCATGCCGTTGGCTGCTCGTGCGCATGCGATGGGAATGGCTGTGGGCACCTGCGGGTTCTGCG
GTTGTATTTCGCGGGTACCACGGTGCTGATCGCTCTGGTTGCTCTGTGATCATTAATATTCATTTCTA
ACCGTGATGGCCATTGCTGCCGCAATACCGTTGCCATCGCAGTTCTGGTTGCTCTGTCTTCTCTCCCA
GCTCTGCTTGGCCTGCTTGGCACTCGCATCTTCGCAGCAGCGTGCCTGGACCTAAGGTTCCGGATCCT
GAGGACGAGAAGCCAACGATGGGTCTGAAGTGGGTCCGCTTGTGCGCAAGATGCCGTTGGCTTACCTG
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GATGGCACCTCCACGCTGGGCACCGCGCCGCGCACGGGTATGACATGACGGCAGATGCGTTCCGCCCCG
GGCCGCAACGCGCCCATGATTGCGCTTATCGACGCAACCGACGTCCTGAGGAAGAACGCCCATTTGGTG
TTTGGACAGGCGGTGGAGCAATTCTTGAACACTGATGGTGTGAAGAATGCTCAGATCACTCAGACCACG
GAGAATTTGATACCGCGCAGATCCTGTTACCCAGAAATTTGATGCGATCGATGAGCGCACCTCTGAGA

CTCTCGCAACTCTTCGTGCAGATGCTGAGACCTTCGCTGATGACACCGGCGCGACGTATGGCATTACTG
GCGTCACCCCAATTTACGATGACATCTCTGCTCGCCTCGGCGACGTCCTGGTTCCTTACGTTT

RXS03124 - 3'-Region
TGATCGTTTTGGTTCTAGCGTTC

RXS03125 - 5'-Region
TGACACCGGCGCGACGTATGGCATTACTGGCGTCACCCCAATTTACGATGACATCTCTGCTCGCCTCGG
CGACGTCCTGGTTCCTTACGTTCTGATCGTT

RXS03125 - coding Region
TTGGTTCTAGCGTTCCTCGTGCTGTTGCTTCCGGTCCATTTGGGTCCCATTGATCGCGGCTCTG
GGCTTTGGCTTGTGAGTTCTGGCTACCTTTGGTGCTACCGTGGCGATCTTCCAAGAAGGTGCTTTCCGGC
ATCATCGACGATCCTCAGCCACTGCTGTGCTTC

RXS03220 - coding Region
ATGGGCTTAAGGGAAATTTTGTCCAGCAAGTGGCTTGTGCGCATCCTCCTGGTAGGTATCGGATTGGGT
GTCGCACAGCAGCTGACCGGCATCAACTCCATCATGTACTACGGCCAGGTTGTTCTCATTGAGGCTGGT
TTCTCCGAGAATGCAGCTCTGATCGCCAACGTGGCGCCAGGAGTGATCGCAGTTGTCGGTGCATTTCATC
GCACTGTGGATGATGGATGGTATCAACCGCCGTACCACCCTCATTACCGGTTATTCTCTCACCACCATT
AGCCACGTATTGATCGGTATCGCATCCGTAGCATTCCCAGTCGGCGATCCTCTTCGCCCCCTACGTTATC
TTGACTCTGGTTGTGGTCTTCGTGGGATCCATGCAGACCTTCCTCAACGTAGCTACCTGGGTTATGCTC
TCTGAGCTCTTCCCGCTGGCAATGCGCGGTTTCGCAATCGGTATCTCAGTGTTCTTCTCTGGATCGCA
AACGCGTTCTTCGGATTGTTCTTCCCAACCATCATGGAAGCAGTAGGACTAACCGGAACCTTCTTCATG
TTCGCGGAATCGGTGTGGTTGCCTTGATCTTCATCTACACCCAGGTTCTTGAACTCGTGGACGTACC
TTGGAGGAGATTGATGAGGATGTTACTTCCGGTGTGATTTTCAACAAGGACATCCGAAAAGGAAAGGTG
CAC

RXS03220 - 3'-Region
TAAAAACCCAGACACTGCATAGATAACACG

RXS03221 - 5'-Region
CAAAAGTATTCAAAAAAAGTTTGTATGTACGATTGACGGGACATATCGTGTCTGCCACGATTAAAGAC
ATTGGTGATGTGAATCACTGCCTACTACATC

RXS03221 - coding Region
GTGTTTCGTGACCCCTGCACCTCCAAGTAAGGGCACGACAACTTAGGAGACAAGATGGCTAGTACCTTC
ATTGAGCCGACAGCCCTGAAAAAAGTAAGAAGCTGCCCCACTCACAGAAGGTCCGTATAGAAAGCGG
CTATTCTACGTTGCACTAGTTGCGACGTTTGGTGGGCTGCTCTTCGGATATGACACCGGAGTAATCAAC
GGTGCACCTCAACCAATGACACGTGAGCTCGGACTAACCGCGTTACCGAGGGGTGTTGTAACCTTCTTCC
CTGCTGTTTGGTGACGAGCTGGTGCGATGTTTTTCGGTCGCATTTCCGACAACTGGGGTCGCCGAAA
ACAATCATCTCACTTGCAGTAGCTTTCTTTGTCGGCACCATGATCTGCGTGTTGCTCCATCTTTTGCA
GTAATGGTTGTGCGACGTGTGCTTCTTGGACTCGCAGTTGGTGGCGCTTCCACTGTTGTCCCTGTCTAC
CTGGCTGAACTTGCTCCTTTTGAAATCCGTGGCTCACTGGCTGGCCGTAATGAGTTGATGATTGTTGTT
GGTCAGCTCGCAGCTTTTGTGATCAATGCGATTATTGGAAATGTTTTTGGACACCACGATGGTGTGTGG
CGCTACATGCTGGCAATTGCCGCAATCCCAGCAATTGCCCTCTTCTTTGGAATG

APPENDIX B: AMINO ACID SEQUENCES

> RXA00001 (1-1128, translated) 376 residues
MATVTFKDAS LSYPGAKEPT VKKFNLEIAD GEFLVLVGPS GCGKSTTLRM LAGLENTVDG
AIFIGDKDVT HVAPRRDRDIA MVFQNYALYP HMTVGENMGF ALKIAGKSQD EINKRVDEAA
ATLGLTEFLE RPKKALSGGQ RQRVAMGRAI VRNPQVFLMD EPLSNLDAKL RVQTRTQIAA
LQRKLGVTTV YVTHDQTEAL TMGDRIAVLK DGYLQQVGAP RELYDRPANV FVAGFIGSPA
MNLGTFSVKD GDATSGHARI KLSPETLAAM TPEDNGRITI GFRPEALEII PEGESTDLSI
PIKLDFVEEL GSDFSFLYGLK VEGEDLGSSS EDVPESGQIV VRAAPNAAPA PGSVFHARIV
EGGQHNFSSAS TGKRLP

> RXA00002 (1-684, translated) 228 residues
VLHREGKGL LGAYIAGFEW GLEKDYHVL C EMDADGSHAP EQLHLLLEEI EKGADLVIGS
RYVPGGETVN WPANRELLSR LGNKYISVAL GAGINDMTAG YRAFRRELLE HLDFEELSNA
GYIFQVDVAF RAIKDGFDVR EVPITFTERE LGESKLDGSF VKDSLLEVTK WGVahrSEQI
SDFTSEVSKI ASRTVKDMEL GPKATTAKNA VPDFVSEVSN LAKGTFFK

> RXA00089 (1-999, translated) 333 residues
MATPASAPTS EPRLKRTRAK LFDWKLIGI IFVAGLVVLS LLTGQYDIFG GDDGQLMFEA
VRIPRTVSLI LSGAAMAMCG LVMQLLTQNK FVEPSTGTG EWAGLGLLFV IYFVPAATVL
DRMLGAVVFS FIGTMVFFLF LRRVTLRSSI IVPIIGIMLG AVVSSISSFF ALQFDMLQQL
GTWFAGSFNT VFRGQYEVWL IVVIVVIAVF FFADRLTVAG LGEEIATNVG LNYNRMVLIG
TGLIAIATGV VTVVVGSLPF LGLIVPNVVS MFRGDDLRSN LPWVCLTGIA IVTICDLISR
TIIAPFEIPV SVILGIIGAV VFVIMIVRQR GRG

> RXA00090 (1-1119, translated) 373 residues
VAVDKDIENR TSDLSRWETM EESATVEGRT DVELASAPSK RRTSGAFQTA RAKRRYWIIM
AALLVTALAF TWGLIWKYKNP MPVGHAPAFAL IAERRMESVF VMLIVAVCQG FATVAFQTVT
NNRIITPSIM GFESLYTLIH TSTVFFFGAT ALLATRNLEM FVGQLVIMVL LTLVLYTWLL
SGKRGMHAM LLVGIIIGGG LGSISTFMQR ILTPSEFDIL SARLFGSVNN AETEFPIAV
PLVVVASVLL LLSSRRLNVV GLGKDAATNL GINHRRSSIY TLVLVSVLMA VSTALVGPM
FLGFLVATLA YQFADTYDHR YILPMSALIG FVVLGAYFV MNHVFAQGV VSIIEMVGG
TVFLVILRK GRL

> RXA00099 (1-1173, translated) 391 residues
VKNPRLIALA AIILTSEFNL TAITALAPLV SEIRDDLGV S ASLIGVLGMI PTAMFADAA
ALPSLKRKFT TSQLLMFAML LTAAGQIIRV AGPASLLMVG TVFAMFAIGV TNVLLPIAVR
EYFPRHVGGM STTYLVSFQI VQALAPTLAV PISQWATHVG LTGWRVSLGS WALLGLVAAI
SWIPLLSLQG ARVVAAPSKV SLPVWKSSVG VGLGLMFGFT SFATYILMGF MPQMVGDPQL
GAVLLGWWSI LGLPLNILGP WLVTRFTNCF PMVVIASVMF LIGNGGFCLA PDVAPWLWAT
LSGLGPLAFP MALTINIRA ETSAGASALS SFGQGLGYTI ACFGPLLTGF IVDATGSFRT
IFLLFAGATL FVIRGGYFAT RQVYVEKLLN R

> RXA00123 (1-1119, translated) 373 residues
MPKNYDINGA IRRRDLRRR YLPDSANSTP VPPEVSPLTR YVTDGIPKRP PLGATVADGL
KFAEGASNRM VMSLYPAPSK PAIEELAEAW DLHPTIVEDL LLGQORPKLD RYEDIIFIAI
RSARYIDSRE EVDFSEFHIL MKPQAIALC QDNQWIDGTS AASFSNPEEI DKRIKTLAD
AELLSSGPRA AAYRLLDAIV DGFSPVLRGI AIDQEQUIERQ VFSGDAVAE RIYNLSQEII
DMQHTTSSVT EVVQRLNKDF IRSGMSEELR AYLDADVADHL TRDNTRVSEY RESLSQILNV
NATLVAQRQN EDMKKISGWA AIIFAPTIVS SIYGMNFDIM PELHWAFGYP LALLAMLGFT
LLLYWIFKRS KWM

> RXA00160 (1-573, translated) 191 residues
MLNIARNRNM KRRLAIAAFV ATATATATMA PASAQTDYAG LSSGVADTVA EAAGVATTAV
APAAATVARPA NGTFTSGFGP RWGTFHNGID IANSIGTPIY AVMAGTVISS GPASGYGQWI
RIQHDDGSIS IYGHMEYLYV SVGERVAAGQ EIAGMGSQGF STGSHLHFEI HPDGVTPVDP
QAWLANHGIY V

> RXA00193 (1-843, translated) 281 residues
MQATLKKYFP VFVLPTLLAF MIAFLVPFIV GFFLSFTKFT TITNAKWVGI DNYVKAQSQR
EGFISAFGFT VLVVIVSVIT VNIFAFLLAW LLTRKLRGTN FFRTVFFMPN LIGGIVLGYT

WQTMINAVLS HYATTISADW KFGYAGLIML LNWQLIGYMM IYYIAGLQNV PPELIEAAEL
 DGVNKEWMLR HVTIPMVMPs ITICLFLTLS NSFKLFDQNL ALTNGAPGGQ TEMVALNIIN
 TLFNRMNVEG VGQAKAVIFV VVVVVIAIFYQ LRATRSKEIE A

> RXA00203 (1-912, translated) 304 residues
 MLNNGALVGL IALCVGLFIA TPHFLTIPNL INIGIQSATV AILAFGMTFV IVTAGIDLSV
 GSVAAALGAMT SAYFFAEVGL PGWITLLIGL FIGLLAGAIS GISIAYGKLP AFIATLAMMS
 IARGITLVIS QGSPIPSAPA VNALGRTYFG IPMPILMMAL AGIVCWFILS RTVLGRSMYA
 IGGNMEAAARL SGLPVKKILV MUYALAGVYA ALAGLVMTGR LSSAQPPAGV GYELDAIAAV
 VIGGASLAGG TGKATGTLIG AILLAVIRNG LNILNVSSFW QQIVIGCVIA LAVGFDVIRN
 KTSK

> RXA00204 (1-1572, translated) 524 residues
 MVNSEQALHQ HDPAPILQLD KVSXSGFPVN VINQVSDIVR PGRVLALLGE NGAGKSTLIK
 MMSGVYQPDG GQILVDGKPT TLPDTKTAES FGIATIHQEL NLVPTMTVAE NVMLGRTPRK
 WGLVNFKHRLR RQAQAALDLI GVDVDLNAQV GSLGIARQQM VEIAKALSMN ARILILDEPT
 AALTGREIDQ LFKVVDQLKE KGVAMVFISH HLDEIARIGD TVSVLRDQGF IAELPADTDE
 DELVRLMVGR SIENQYPRSA PEIGQPLLEV KNLNAEGRFT DISLTVRAGE VVGLAGLVGA
 GRTEVVRSA GVDKVDSEV IVAGKKLRGG DISEAIKNGI GHIPEDRKAQ GLVLGSSVED
 NLGLATLAST ARAGLVDRSG QHKRAAEVAV KLRIRMASLK QPISDLSSGN QQKAVFGRWV
 LAGSNVLLLD EPTRGVDVGA KVEIYNIINE MTEKGGAVLM VSSELPEVLG MADRILVMMSG
 GRIAGELPAK GTTQDDVMAL AVSQVDDISIT EEAABEIENT KEDR

> RXA00270 (1-888, translated) 296 residues
 MIGAFEFGLL YGVVALGVYL TFRVLNFPDL TVDGSLLTGA ATAATALMSG WPPLMATAAG
 FVTGFIAGMI TGLLHTKGKI DGLLAGILTM IALWSVNLRI MCGANVPLLR TDNLFTPLRD
 AGLLGTWAGP AILAVAVGIL GLIVIWFLLT DIGLSLRSTG DNGPMVQSFG VSTDFTKILT
 ISLSNGFVGL AGALIAQYQG FADISMIGL IVIGLASVIL GQAIIFGQRRV WLAVLAVIVG
 AIAYRLIIFA ALRVGLDPND MKAISAILLV VAMLLPRWRA KFSKAPKPKQ PVAVEA

> RXA00311 (1-855, translated) 285 residues
 MEHSPEGKRG FFTSSVMAGC SVGNVLAGLV FIPFLMLPEE HLMSWGWRVP FLLSALVLV
 AYFVRTRLEE ASTEKAEDA GAPALAVLRT QGIDVARVFL ITFFAVVQTT FNVYALAYAA
 NEIGIDRSFM VMVNTIALGL SIGTIPLAAW VSDRIGRKPV LLFGAITCAI TTYFYFQAIS
 EADLVLFAL CLVNQGLFYS CWNGVWTIFF PEMFASSVRY TGMAMGNQLG LIIVGFAPTI
 ATALYAWNGW EAVAGFIIGA IALSAAVILT TKETAFTKLE DLGKK

> RXA00312 (1-426, translated) 142 residues
 METVRTATAA PETASLKLRE AESPAKSPKK AALASLLGST LEYYDFVIYG TASALLFNHL
 FFPQGDVVA TIGSLASFGV AYIARPIGGL VMGHVGDKIS RKTALMVTLM IMGIASISIG
 LLPTYGQIGI WATVLLMIAR IA

> RXA00345 (1-951, translated) 317 residues
 MAGMKLLWT LPILPLVLG CSTGSADSAD STNAAGSNL KVVSTQVWA DVAEAVAPDV
 DIEAIITGGD IDPHSFEPsA TDMKVSEAD IIIVGGGGYD SWLYGTLEDD DRIIHALDLS
 EHDHSEHDDH EHEAEEAHEH DHDEEGHDHD VDNEHVWYST EYVSEVAEEF AEKVTELDPE
 AQADATAVTT KMDELHNQIH DLPVRIAQT EPIADHILSH SDMVESTPEG YRATTLESE
 PTAADVASFQ DAINNGDLV LIYNPQSAST VATSLKDLAE EKGIPVVEIY ETPQNTENFL
 DAFTKAVDDL TAATNQV

> RXA00378 (1-1773, translated) 591 residues
 KSWRSYPSWF AFDHGTLTQN EIYFDVACGI TVLLLAGRLL TRRRSQSSLL AELGRLQIDP
 QRIVTVVRKH RLKRVVQELN IPVQEVVRND DVKVPNTTI PVDGTVIGGG SRIAASIIMG
 QDQRDVKVND KVFAGSLNLE SEIKVRVIRT GHRTRIAAVH RWVKEATLKE NRHNRAAIRS
 AGNLVPITFT LAVVDFCLWA LISGNINAAV TTTLAVLACV APVALALSAP LATRNSIEAA
 ARHGILVRSG EIFRVLDDVD TAVFNVRVGT TDGEMTVETV TADKGEDPEL VLRVAGALAM
 ESHHAISKAL VKASREARDT GAGGEDVPHW IEVGNVEITE AGSFQATIEL PLIKPSGEKI
 MRTTEALLWR PRSMTEVREH LSPRLVAAAT SGGAPLIVRW KKGDRGVITL SDHVRSDSSD
 AIIAIEEQGI ETMMLSRDTY PVARRYADSL GITHVLAGIA PGKKAQVVRA VHTRGSTVAM
 IGDESVMDCI KVADGVLMG VDRPSDLRDD SDDPAADV V MREEVMSVPT LFKLARRYAK
 LVNGNIALAW IYNGVAMVLA VSGLLHPMAA TVAMLASSLL IEWRSGRARK Y

> RXA00412 (1-1080, translated) 360 residues
VSHTASTPTP EEYSAQQPST QGTRVEFRGI TKVFSNNKSA KTTALDNVTI TVEPGEVIGI
IGYSGAGKST LVRLINGLDS PTSGSLLNG TDIVGMPESK LRKLRSNIGM IFQQFNLFQS
RTAAGNVEYP LEVAKMDKAA RKARVQEMLE FVGLGDKGKN YPEQLSGGQK QRVGIARALA
TNPTLLLADE ATSALDPETT HEVLELLRKV NRELGITIVV ITHEMEVVRV IADKVAVMES
GKVVEYGSVY EVFSNPQTQV AQKFVATALR NTPDQVESED LLSHEGRLFT IDLTETSGFF
AATARAEEQG AFVNIVHGGV TTLQRQSF GK MTVRLTGNTA AIEEFYQTLT KTTTIKEITR

> RXA00413 (1-897, translated) 299 residues
MKLRRITTTA IAGLFAATAL VACGSDSDGS STTVAEGTEG VTIRIGTTDA AKEAWTVFED
KAAEEGITLE IVPFSDYSTP NEALAQDQLD VNLFQHLKFL AEYNVGSAD LTPVGSSEIV
PLALFWKDHD SIDGIDGESV AIPNDPSNQG RAINVLVQAG LVTLKTPGLV TPAPVDIDEA
ASKVSVIPVD AAQAPTAYQE GRPAIINNSF LDRAGIDPNL AVFEDDPESE EAEPYINVFV
TKAEDKDDAN IARLVELWHD PEVLAAVDRD SEGTSVPVDR PGADLQEILD RLEADQENA

> RXA00431 (1-675, translated) 225 residues
MVSIDTYNAC VDFPIFDAKS RSMKKAFLGA AGGAIGRNQD NVVVVEALKN VNLHLREGDR
VGLVGHNGAG KSTLLRLLSG IYEPTRGSD IRGRVAPVFD LGVGMDEIS GYENIIIRGL
FLGQTRKQMK AKMEEIADFT ELGEYLSMPL RTYSTGMRI R LALGVVTSIE PEILLDEGI
GAVDAAFMK ARDLQALVE RSGILVFAST QRLSCQLCNT ALWVD

> RXA00444 (1-777, translated) 259 residues
LLIPATLAML LIIGPIFALL LQIPWDRSWE LLTAPESLGT ARLSIGTALF STALCAIVGF
PLALALHLYE RSHPRVTSVL TVLVYAPLVL SPVVSGLALT FLWGRRGFLG SWLDQVGLPI
AFTTTAVVFA QVFVALPFFI STVTTALRGI PKQFEEIAAT EGATRWEIMH KMIIPLAMP
IFTGMILGFA RALGEYGATL TFAGNIAGVT RTIPLHIELG LSSNDMDKAL GAVIMLLAVY
VLIIGAIGAL RLFSKVRKV

> RXA00445 (1-912, translated) 304 residues
MADLSIEHVS RFFGDAIALN DVSLTVPSGS ITAIIGPSGS GKTTLRLLA GLDSPDEGTV
SIGNKIAKLG DTALCFQDSP LYPHLNWEN VAFPLKLKAT NTADDEVVKKR VSDVLEMLEI
APLARRKITE LSGGQKQRVG IARALVRDVE VYLFDEPMAH LDQALARDIV ADLRKIQQSL
GLTFVYVTHS KSEAFALADQ IVVLVDGQVA QVGEAEELVE KPKTLEIAEF LSPTELVNRR
RGDAVEAWRP EDTQLARGGT ATVEAVTYLG REWLVTTEG HAVSEEKFDV GESVTLTQKK
VFSF

> RXA00466 (1-987, translated) 329 residues
VQSRLSKILR SSVVGVAFLA LLAGCSNNAD DTDADSTSTG NSAFPVSIH EFGTTTIDDV
PERVVTLGVT DADIVLALGT VPVGNTGYKF FENGLGPWTD ELVEGKELTL LDSDSTPDLE
QVAALPDLI IGVSAGFDDV VYEQLSDIAP VVARPAGTAA YAVAREEATN LVARAMGQSE
KGQELNEETD ALIQAARDEN PSFDGKTGTV ILPYQGYGA YLPGDARGQF LDSLGISLPE
AVLSRDTGDS FFVDVPAESV KDVDGDVLLV LSNDENLDIT AENPLFETLN VVQKDAVIVA
TTEERGAITY NSVLSVPFAL EHLAPRIAE

> RXA00482 (1-648, translated) 216 residues
MRISKLVTI ALLAAISLFG ISTAQADIF DGGRLAGGSS QVSNLSSVPE NLALPEIENS
IDLERYKQKW YQVAAPQPF SLQCSHDVTA DYGVDSDTI SVTNKCGTFF GPSVIEGSAK
VVSNASLKVS FPGIPFQSED NQANYRVTYI EDDYSLAIVG SPSRSSGFIL SRTPQLSSDQ
WSHVRNITED SGWWPCAFIT VPATGGLNTA TPLCTL

> RXA00523 (1-750, translated) 250 residues
VLRNQLASPD IIGISSGASA AGVICIVFFG MSQSASVAIS LCASLAVALL IYLVAYRGGF
SATRLILTGI GIAAMLNSLV SYSLSKADSW DLPTATRWLT GSLNGATWDR AMPLIVTTVV
LIPLLVANAR NVDLMRLGND SAVGLGVATN RTRVIAIIAA VALIAVATAA CGPIAFVAFV
SGPIAARILG SGGSLIIPSA LIGGLIVLIA DLIGQYFLGT RYPVGVVTGA FGAPFLIYLL
IRSNRAGVTL

> RXA00525 (1-660, translated) 220 residues
MSLAESILLA LTLRSNKMR ALLTLLGVII GIASVIGILT IGKALQDQTL NSLES LGAND
LSAQVEERPD EDSPEPDMFA FSGAANSSGN LIPEETVDTL RDRFAGSITG ISVGGMGQTQ

TLIGDTADLK SDLLGVNEDY MWMNGVEMNY GRAITQDDVA AQRPVAVIAP DTFNTLFDAN
PNLALGSEVA FELNGQETFL RVIGVYKEAA AGGLVGSNPT

> RXA00556 (1-594, translated) 198 residues
YTPYTVANDI THTKDGLNTL SIRAAQGVDDQ DSLKGSLSQTY FDALYANNDS HHVAMLDLFRK
QIEEFNTILG AMSLGISAIG GISLLVGGIG VMNIMLVSVT ERTREIGVRK ALGARRRDIR
LQFVVEAMII CFIGGILGVL LGGILGLIMS SAIGYISLPP LSGIVIALVF SMAIGLFFGY
YPANKAAKLD PIDALRYE

> RXA00596 (1-453, translated) 151 residues
MLNALKFIPW LIQIIFLSGF SVITAAVKKD TGFNPVVIRY PLRVTTDFQI AALSTCITAT
PSTLSLGLRE PRKPGDPTIL LIQAVFGSDP VEVFESIADM EQRLVPSVAS IDHGVPGQGP
YKEIRPSDAE WPSREIADTA QNTVSQDKRE F

> RXA00634 (1-1383, translated) 461 residues
MWERFSFYGM QALLVYYLYF DVAAGGLGLD QTQATGLVGV YGALLYLCCW AGGWVSDRVL
GAECTLLGGA ISVTIGHVLV AGLGKGIGLA IGLGCIAIGS GFVKTAATV LGSRHGEQEG
DAKADPAFQL FYLGINVGAL LGPLLTGWLS SRYSFEMGFG AAVLMIGGL GIYAALRKPM
LQSFPLEVKK ALLRAQNPAAE KHVISTAFAA VAVLCGVLLY LLLTETVSAD QLAGALLLVT
IGAALWLIIQ PLRHPQVSSE EKRKVLAFIP IFVCSTAFWA VQAQTYGVLA VYSQERVDRM
VGDFEIPAAW SQSLNPFIL ALSIPISLWF MRGSRAPRVK IGISIGVIA GSGLLVLIPIF
VGMPLAPVWV LPLSVFLISL GELFIGPGGM AATAHAPRI FATRFSALYF LTLAIGMSIA
GNVSKFYDPT NHTSELRYFA VFGISIIIVG VGSLMVAKKV G

> RXA00665 (1-438, translated) 146 residues
MSSSTLLLAS GQVTLAADY TLSHTPSDGI LVVLGFAMIL TFMTLIMLGR LTPMVAMLLV
PTIFGLIAGA GLGLGDMALD AIKDMAPTAA LLMFAIMFFG IMIDVGLFDP LIRVITRVLH
DDPAKVVIGT AVLAGVVSLD GDGSTT

> RXA00702 (1-1320, translated) 440 residues
LGLPFAVMRK RVEETLDLLG IAELRYVPLA ELSGGEQQRV AIGAVLTTRP ALIILDEPTS
ALDPNGAEDV LATVTKLAHD LAMTVVLAEH RIERVLQYVD RVAHVADGH VTVGTPEEIM
ADSDVAPPIV ELGRWAGWAP LPLSIRDARA HSADMRRKLY QRGLVVNKLH NHAVQPLLIA
EDIMVDFPEI RAVDGVNLL NSGEITVLMG RNGCGKSSLL WALQSGSTRN QGSVQVLDEA
AGFSWTDPKT LKPAKRRNLV SMVPQTPTDI LYESTVHAEL ARSDKDAAAP AGTTREILDS
LVPNIPDHLH PRDLSEGQKL SLALSIQLAA KPRVVFFDEP TRGLDYDGKK SLARSFQQLA
DDGHAILVVT HDVEFSALCA DRVLFMASGK IISDGTAVEI LPASPAPAPQ VAKITAGIQE
ESHWLTVSAV KAALGHGEIS

> RXA00728 (1-792, translated) 264 residues
VAAAIIVALL AWFIIISALNN EAYGWDYRS YLFDTRIATA ALHTIALTLL SMILGVVLGA
ILAVMRMSGN PVMQGVAWLY LWIFRGTPYI VQLVFWGLLG SLYQSINLGF AEIDLQSLLS
NMFLLAVIGL GLNEAAYMAE IVRSIQAVP EGQMEASKAL GMNWSMTMR TILPQAMRII
IPPTGNELIS MLKTTSLVVA IPYSLELYGR SMDIAYSLE PVPMLLVAAS WYLVITSILM
VGQYYLEKHF EKGSTRTLTA RQLA

> RXA00732 (1-822, translated) 274 residues
MLVQMTSTLM ISAPMLAIGG IIMAVRQDLG LSWLMVVSIP VLIIVVALII VRMVPLFQTM
QKRIDRINQI IREQLTGIRV IRAFVREDVE RERFTTASKD VADIGVRTGN LMALMFPAVM
LIMNLSAVAV IWFGAFQVES GETQIGTLFA FLQYIMQILM GVMMAAFMFV MVPRAAVSAD
RIGEVLETPP SVQAPETPAQ PSTSAGEIVF NNATFAYPGA DDPVLNNVSF RVAPGSTTAI
IGSTGSGKTT LIGLVPRLFD VTEGDVTVDG TDVR

> RXA00734 (1-453, translated) 151 residues
RHLRYGNEDA TETQLWQALA IAQAADFVRE MPEGLDSEIA QGGTNVSGGQ RQRLAIARAL
LKQPEIYIFD DSFSALDVST DAALRRALST NLPDATKLIV AQRVSTIRDA DQIVVLDNGE
VVGIGHTNL LNTCGTYREI VESQETAQAQ S

> RXA00759 (1-924, translated) 308 residues
MLRYVGRRLI QMIPVFFGAT LLIYALVFLM PGDPVQALGG DRGLTEAAAE KIRQEYNLDK
PFIVQYLLYI KGIFVLDFGT TFSGQPVIDV MARAFPVTIK LAIMALLFES ILGIIFGVIA

GIRRGGIFDS TVLVLSLIVI AVPTFVIGFV LQFLXGVKWG LLPVTVGSNT SITALIMPAV
 VLGAVSFAYV LRLTRQSVSE NLRADYVRTA RAKGMSGFNV MNRHVLRLNSL IPVATFLGAD
 LGALMGGAIV TEGIFGINGV GGTLYQAILK GEPTTVVSIV TVLVIVYIIA NLLVDLIYAV
 LDPRIRYA

> RXA00760 (1-1032, translated) 344 residues

MPNNEFHTNH SLGQDDQTPD QAHHFPQGRG EALVRPGQEH FIAATDETGL GAVDAVADDS
 APTSMWGEAW RDLRRRPLFW VSAVLIILAL LLAAPVQLFT STDPQFCVLA NSLDGPQSGH
 PFGFDRQGCD IFARTVYGAR ASVAVGVLT LLVALIGTVF GALAGFFGGI MDTILSRITD
 MFFAIPLVLA AIVVMQMFKE HRTIVTVVLV LGLFGWTNIA RITRGAVMTA KNEEYVTSAR
 ALGASKAKIL LSHIMPNAAL PIIVYATVAL GTFIVAEATL SFLGIGLPPS IVSWGADIAR
 AQTSLRTQPM VLFYPAMALA LTVLSFIMMG DVVRDALDPK SRKR

> RXA00761 (1-591, translated) 197 residues

MTNIPQTPN HEGEQPLLEL KDLKISFTSS TGVVDAVRGA NLTIYPGQSV AIVGESGSGK
 STTAMSIIGL LPGTGKVTEG SIMFDGQDIT GLSNKQMEKY RGSEIGLVPO DPMTNLNPVW
 RIGTQVKESL RANHVVPGE MDKRVAEVLA EAGLPDAERR AKQYPHEFSG GMRHRALIAI
 GLAARPKLLI ADEPTSA

> RXA00774 (1-654, translated) 218 residues

MDKATDALLR TSLASAESAL GNAEKLEELR TGCESQAVEL LALETPVARD LRQVVSSIIYI
 VEEITRMGAL AMHVANSVRR RYPDPVIPED MRGYFKEMAR LAADMTDHIR QILIDPEPDL
 ALEMAKSDDA VDDLHQHIMR ILTLRPWPHD TKSVDLTLL SRFYERYADH TVNVAARIYI
 LSTGLHPPEY MEKREQQRAD ADMEKRWAEL ERQFRTSE

> RXA00775 (1-771, translated) 257 residues

MSKLKLVNDVNI IYGDHFHAVQ NVNLEVPARS VTAFIGPSGC GKSTVLRSIN RMHEVTPGAY
 VKGEILLDGE NIYGSKIDPV AVRNTIGMV FQKANPFPTMS IEDNVVAGLK LSGEKNKKKL
 KEVAEKSLRG ANLWEEVKDR LDKPGGGLSG GQQQRLCIAR AIAVEPEILL MDEPCSALDP
 ISTLAVEDLI HELKEEFTIV IVTHNMQQAA RVSDQTAFYS LEATGRPGRL VEIGPTKKIF
 ENPDQKETED YISGRFG

> RXA00776 (1-921, translated) 307 residues

MTNNVVTPRM DEPLKKSSAF TDISSSRKTT NTAATVVIYG AMLIAAVPLV WVLWTVISRG
 IAPILTADWW STSQAGVMLM LPGGGAHAM IGTFMQAVVT SVISIPIGIF TAIYLVEYSN
 GNRLGRLTTF MVDILTGVPS IVAALFVYSL WIVLFGFDRS GFAVSLSLVI LMVPVIIRNT
 EEMLRVVPQD LREASYALGV PKWKTIKIV LPTALSGIVT GVMLAVARVM GESAPVLVLV
 GSSQAINWNP FGGPQASLPL MMLDMYKAGT APATLDKLWG AALTVLIIA VLNIGARIIS
 AKFSVKQ

> RXA00777 (1-1065, translated) 355 residues

MATNESVSEK QRLDTRVQA HPVAVNANSS QTKPSKKIVA EGGGSVKRPG DRIFEVLSTA
 SAAIITAIII AIAAFLIWR VPALMRNAEG IGGFFTYSGA WNTDIDAMY FGIPNLLAAT
 LLISVIALII AMPIALGIAI FLSNYSKRL VKPLGYMVDL LAAVPSIVYG LWGWQVLGPA
 LSGFYTWIES WGGSFLLFAT YQNSPSFATG RNMLTGIVL AVMLPVEIA TAREVFIQTP
 KGHIESALAL GATRWEVRL TVLPFGMSGY VSGAMLGLR ALGETMALYM VVSPSSAFRF
 SLFDGGTTFA TAIANAPEF NDNTRAGAYI SAGLVLFALT FIVNAGARAM VNRGK

> RXA00828 (1-369, translated) 123 residues

EHQFVARTVR DELEIGPKIM KVDASERIEE LLDRLRLRHL ENANPFTLSG GEKRRLSVAT
 ALVAAPKLLI LDEPTFGQDP ETFTELVTML RELTDNGISI VSVTHDPDFI AALGDHHIEV
 SAK

> RXA00832 (1-555, translated) 185 residues

TLTAVVYGGF LFRQMGAG EFQEEVEAEK ADDAAKWEVP FRGLILITV LPIVLLSHDM
 ATVMDEVLAS LGAPVAMAGL IIATIVFLPE TITSLKAAWT GEIQRVSNLA HGAQVSTVGL
 TIPAVLVIGV ITQDQVVLGE TPINLLLLGT TIAVTAIAFS SKKVS AVHGS VLLMLFGVYM
 MSMFA

> RXA00934 (1-789, translated) 263 residues

PSFSMAALPF AEGPIVATYH ASSSGSKLLK AFLPVLSPML EKVRAGIAVS EMARRWQVEQ

VGGDPVLIPN GVETSMFKAA RQIEPNPVE IVFLGRIDES RKGLDILLRA LTRLDPRPFTC
TVIGGGTPRE VAGINFGVRV SDEEKAAILG RADIYVAPNT GGESFGIVLV EAMAAGCAVV
ASDLEAFSLV TDSEAAQPAQ VLFKGTGSAD LAKKLQALID DPSSRSTLIA AGLKRANAYD
WSTVSTQVMA VYETIAIDKV RLG

> RXA00939 (1-168, translated) 56 residues
GVLLGGVTMS IGMLVHEASV LLVIAIAMLL LRPTLKEDKD KADVSTADAA KETLSA

> RXA00942 (1-204, translated) 68 residues
LSTKNYHVEG LTCANGVASV EDEIGIVAGT QGVDIDIETG RVTVTGEGFT DEEIIIEAVAN
AGYKVSGR

> RXA00950 (1-906, translated) 302 residues
MNTPAVQVQN LSLSEGSFTA VNGLSLTVEQ GSIHGFLGPN GAGKSTTIRA LIGVLKPQTG
SVAILGQDPV AHPDVLRRVG YVPGDATLWD NLTGAEVFRA LESLRKTPSN RALENELIDA
FQLDPSKKIR EYSTGNRRKV SLIAALSHEP ELLIVDEPTA GLDPIMEQVF VTYVRKARTN
GASVLLSSHI LSEVEQLCDY VTVLKEGRAV ASNEVSYLRK ISAHRITATI PAVPQHLAGR
GEVDFDAGHL SITCDASEVP DILRIIIDAG GQDIISTAAS LEEIFLRHYG ETVSGSESKA
SQ

> RXA00960 (1-459, translated) 153 residues
LKNDVDVNVA GFVVPLCATI HLAGSMMKIG LFTFAVVMY DMEVGVGLSI GFLMLGITM
IAAPGVPGGA IMAATGMLAS MLGFNTEQVA LMIAAYIAID SFGTAANVTG DGAIIVIVNK
FAKGQLHTTS PDEIEEDDRV AFDITPSDVE HHK

> RXA00980 (1-639, translated) 213 residues
MFVGVNGHAI GIVAVADAVR SDSASAIESL HKAGIQVMA TGDHRVAQN VASKLGVDEV
YSELLPEQKL ELVRDLQAAG KTVAMVG DG V NDTPALAAAD IGVAMGVAGS PAAIETADIA
LMADRLPRLA HAVTLAKRTV RTMRINILIA LATVMVLLAG VLFGGVTMSV GMLVHEASVL
LVISIAMLLL RPTLKEDAAQ ASDIKRSEIQ QIA

> RXA01000 (1-540, translated) 180 residues
MLAARGVGPY WLRTVLRVFE AVIRAFPEVV IAIILLTVTG LTPFTGALAL GISGIGQQA
WTYEAIESTP TGPSEAVRAA GGTTPPEVLRW ALWPQVAPSI ASFALYRFEI NIRTSAVLGI
VGAGGIGSML ANYTNYRQWD TVGMILLIVVV VATMIVDLIS GTIRRRIMKG ASDRVVAPSN

> RXA01002 (1-417, translated) 139 residues
PTEHDKQIAF HALESVGILD KVVTRAGALS GGQKQVAIA RALSQDPSVM LADEPVASLD
PPTAHSMVRD LENINNVEGL TVLVNLHLID LARQYTTRLV GLRAGKLVYD GPISEATDKD
FEAIYGRPIQ AKDLLGDRA

> RXA01003 (1-804, translated) 268 residues
MTTPSSTLIP QKPRAGVKTY LIIGAIVFT VATATPALGG IELDFASIAA NWRNGANKLL
QMLQPNFAFL PRTWLPMLET LQMALVGAVL SAAVSVPLTL WAAQATNTSA IGRGIVRTII
NVVRSVPDLV YATILVAMVG VGALPGILT FLFNLGIVVK LVSEAIIDSTE HPYMEAGRAA
GGSQFQINRV SALPEVMPLF ANQWLYTLEL NVRISAILGI VGAGGIGRLL DERRAFYAYA
DVSVIILEIL INVIVIEVIS NALRKRLV

> RXA01006 (1-858, translated) 286 residues
MTTSQILRRI QGAVLVLLVT FTAFIMLSA LPGDAVSARY SSPDLGLSPE QIAQIRESYG
ADESLIAQYF STLGGFLVGN FGYSVQTGTA VATQLAEALP GTLTLAILAF LLAAILALVI
SILATMDRFA WIKGIFQALP PFFVSLPSEW LGIILIQIVS FRLGWVPVIG TTPAQGLILP
TITLSIPITA PLAQVLIRSI EEVKAQPFIA AVRARGAGEM WIFFRNIIRN ALLPTLTIA
ILFGELVGGA VVTEAVFGRA GLGQMTVNAV ANRDMPVMLA IVVIAA

> RXA01012 (1-1641, translated) 547 residues
MTTPLLEIND LVVSYQTAKG LVHAVNNVSL EVHPGQITAI VGESGSGKST TAQAVIGLLA
DNAEVDSGRI SFNGRSLVGL NAREWKVNRG TKIGLIPQDP NNSLNPVKTI GASVGEGLAI
HKRGTA AERK KKVIELLERV GIDNPEVRYD QYPHELSSGM KQRALIAAAI ALEPELIIAD
EPTSALDVTV QKIILDLED MQRELGMGIL FITHDLAVAG DRADRIVVMQ KGEVRESGYA
ASVLTDPQHE YSKKLLADAP SLTIGEIPTR VPAVDPEVAQ AKGPLLVVDK FRKEHQRGKE

GAFVAANDIS FEVLPGTTHA IVGESGSGKT TLGRAIAMFN TPTSGSISVS GKDITNLSKA
 QQRELRRQIQ LVYQNPYSSL DPRQTIGSTI AEPLRNFTKV SKQEADEKVA HYLELVALDP
 ALATRRPREL SGGQRQRVAI ARAMILEPEL VVFDEAVSAL DVTVQAQILR LLDDLQRELG
 LTYVFISHDL AVVREISDTV SVMSRGNQVE LGKTAIEVFNN PQTDFTRRLI DAIPGSRYRG
 GELNLGL

> RXA01013 (1-795, translated) 265 residues
 LGNPWTRPAA VISIVVLAVA VLMALVPGLF TSQDPFTGDD VALLGPSTGTH WFGTDSVGRD
 LYSRVVYGAR ETLLGALIAV LVGLIVGTLI GLLAGAQRGW VDTVLMRFVD VLLSIPALLL
 SLTVIILLGF GTMNAAIAVG ITSVATFARL ARSQVMTVAG SDFVEAAYGS GGTQAQVLFER
 HILPNSLTPV FALAALQFGS AILQLSVLGF LGYGAPAPTP EWGLLISDAR DYMATSWWLT
 VLPGFVIIAV VMSANYLSRI IQKEA

> RXA01070 (1-1386, translated) 462 residues
 MANATAQKGR FGLPGWMTGF GAQVIAGLIL GLILGLVARG MDSGAADGEA SWLTGLLSGV
 GSAYVSLLKV MPPPLVFAAV VTSVAKLREV ANAARLAVST LVWFAITAFF SVLAGIAVAL
 IMQPGVGSTV DASNAADPSR VGSWLGFIS VIPSNIILGS GSYSENSGVN LSFNVLQILV
 ISIAIGVAAL KAGKSAEPFL KFTESFLKII QIVLWWIIRL APIGSAALIG NAVATYGWSA
 LGSGLKFLVA IYVGLAIVMF VIYPVVLKLN GIPVLGFFKR VWPVTSIGFV TRSSMGVMPV
 TQRVTEQSLG VPSAYASFAI PLGATSKMDG CAAVYPVAAA IFVAQFYGID LSIMDYVLIM
 IVSVLGSAAAT AGTTGATVML TLTLSTLGLP LAGVGLLLAI EPIIDMGRTA TNVTGQALVP
 AIVAKREGIL DQDVWDAAEK GGAAIEMATV SEKETEPAEV RS

> RXA01094 (1-948, translated) 316 residues
 MTLATIPSPQ QGVWYLGPIR IRAYAMCIIA GIIIVAIWLTR KRYAARGGNP EIVLDAAIVA
 VPAGIIGGRI YHVIDNQKY FCDTCNPVDA FKITNGGLGI WGAIVLGGIA VAVFFRYKKL
 PLAPFADAVA PAVILAQGIG RLGNWFNQEL YGAETTVPPWA LEIYYRVDEN GKFAVPTGTS
 TGEVMATVHP TFLYELLWNL LIFALLMWAD KRFKLEHGRV FALYVAGYTL GRFWIEQMRV
 DEATLIGGIR INTIVSAVVF AGAIIIVFLL KKGRETPEEV DPTFAASVAA DAVASPDRKP
 LPKAGEGIDG ETPSTR

> RXA01135 (1-324, translated) 108 residues
 VTHILFDSRR FLQLGAFASL STALAGAARY VTSTSNNEPA DNTPLTIGYV PIAGSAPIAI
 ADALGLFKKH GNVNVLKKYS GWSDLWTAYA TEQLDVAHML SPMTVAIN

> RXA01141 (1-462, translated) 154 residues
 VNSAADLKGM VLGIPEFYSV HALLLRDYL V SNAVDPIADL ELRLLRPADM VAQLTVEGID
 GFIGPGPFNE RAISNGSGRI WLLTKQLWDK HPCCAVAMAK EWKAEHPTAA QGVNLALEEA
 SAILSNPQF DSSARTLSQE KYLNQPATLL DGPS

> RXA01142 (1-420, translated) 140 residues
 TRTHLEQVGL TDAAERRPAR LSGGMQQRVG IARAFIDPP IMLLDEPFGA LDALTREELQ
 LQLLNIWEAS RRTVVMVTHD VDEAILLSDR VLVMSKSPEA TIITDIPVNL PRPRHELSED
 ASVEAETAL RKRMLHLLH

> RXA01164 (1-1575, translated) 525 residues
 VTLFVRLALA AVGGFLVFAS NEPIGWVAG IVGTALFFIS LAPWDLGVPQ KRRKKNEPVP
 FLQQMSTGPT VVQGMLLGFV HGLVTYLQLL PWIGEFVGS PYVALSVVEA LYSIALGAFG
 VLIARWRDWK VLLFPAMYVA VEYLRSSWPF DGFVAVRLAW GQINGPLANL AALGGVAFVT
 FSTVLAAGV AMVIISKRL AGAIIITASVI AIGAVSSLYV DRNGTSDESI EVAIIQGNVP
 RMGLDFNAQR RAVLANHARE TLKLDEQVDL VIWPNSSDV NPFSDAQARA IIDGAVEHVQ
 APILVGTITV DEVGPRNTMQ VFDPVEGAEE YHNKKFLQPF GEYMPFREFL RIFSPYVDSA
 GNFQPGDGTG VVEMNAANLG RAVTVGVMT C YEVI FDRAGR DAIANGAEFL TTPTNNATFG
 FTDMTYQQLA MSRMRAIEFD RAVVVAATSG VSAIVNPDGS ISQNTIRFEA ATLTESIPLK
 DVTIAARVG FYVELLLVII GVLGLFAIR MNSRSKSAK SARPA

> RXA01168 (1-720, translated) 240 residues
 RTATPDVHVL IVDDNSPDGT GERADKLAAD DDHIFVLHRE GKGGCAEYM AGFQWGLERD
 YQVLCMDAD GSHAPEQLHL LLAEITNGAD LVIGSRYVPG GRVNVNPKNR WLLSKGGNVY
 ISVALGAGLT DMTAGYRAFR REVLEALPLD ELSNAGYIFQ VEIAYRAVEA GFDVREVPIIT
 FTEREIGESK LDGSFVKDSL LEVTKWGLKH RGGQAKELSK EMVGLLLNYEW KHFKKRNTWL

> RXA01185 (1-858, translated) 286 residues
 MTDPENSQGT PQICPTDPTT QALAVRGLTK SYGDATVVNN INLDIPKGAI YGIVGPNAG
 KTTMLSMATG LLRPKNKGTAW ISGFNVWEEP NDAKRSMLL ADGLPIFDRL TGKELLTYVG
 ALRELDEGIV DQRSEELLEA LGLKEAAGKR VVDYSAGMTK KILLAQUALIH NPKVLILDEP
 LEAVDPVSGR LIQQILKNFA QTGGTVVLSS HVMELVEGLC DHVAIINRGV VEIAGHVNEV
 RRGRSYRMSS LMRLKALLFK RGHYLGWVRP KAIKAKIIRT RIGLSK

> RXA01188 (1-1104, translated) 368 residues
 MMNGVVQPQE HLDATLIAAD FHGNPENS GD RKERLNFQGW KYALNRTVRD VFPDGLLDLA
 ALLTFFSILS IAPAVLLGYS VITIFLASDS TEILNLVRDE VNQYVPEDQS HVVNGVIDSI
 AGSAAAGQVG VAVGVITALW TSSAYVRAFS RCANAVYGRS EGRTLIKRW A MLLFLNLALL
 LGIIIIILVSW VLNETLVMGI FAPIAEPLHL TNVLSFLTDR FMPIWIWVRF PVIVGVLMIF
 VATLYYWAPN ARPWKFRWLS LGSFLAIVGI LLAGVGLNFY FTLFAAFSSY GAVGSL LAVF
 IALWVFENICL IIGLKIDVEI SRAKQLQAGM PAEDYSLVPP RSIEKVAKMK QRQQLMDQA
 AATREESN

> RXA01245 (1-1767, translated) 589 residues
 ASWVTTLGLG GFHLDFFWEL ALLVTIMLLG HWLEMRALGA ASSALDALAA LLPDEAEKV
 DGTTRTVAIS ELAVDDVVLV RAGARVPADG TIMDGAAEFD EAMITGESRP VYRDTGETV
 AGTVATDNTV RIRVEATGGD TALAGIQRMV ADAQASSSRA QALADRAAAL LFWFALITAL
 ITAVVWTIIG SPDDAVVRAV TVLIIACPHA LGLAIPLVIA ISSERAAKSG VLIKDRMALE
 HMRTIDVVLV LKRTGTLTEGA HAVTGVPAT GIAEGELLAL AAAAEADSEH PVARAIVTAA
 AAHPEASQRQ LRATGFTAAS QRGIRATVDG AEILVGGPNM LREFNLTPPG ELADITGSWA
 QRGAGVLHV V RDGEIIGAVA VEDKIRPESR AAVRALQARG VKVAMITGDA TQVAQAVGKD
 LGIDEVFAEV LPQDKDTKVT QLQERGLSVA MVGDCVNDAP ALARA EVGIA IGAGTDVAME
 SAGVVLASDD PRAVLSMIEL SHASYRKMVQ NLVWATGYNI VAVPLAAGVL APIGVLLPPA
 AAAILMSLST IIVALNAQLL RRIDLDPAHL APTDGKEEKA AVSSAAPVR

> RXA01247 (1-234, translated) 78 residues
 VAAATDATPE GPTTYQVTGM TCGHCADNVT EAVSALPQVD DVQVDLIAGG VSIVTVTGSV
 PLETVHRAIE ETGYTVLS

> RXA01285 (1-543, translated) 181 residues
 PQTSIAPEGI RYVDLIARGR APYQSLIQW RTSDEDAVAQ ALASTNLTEL AARLVDELSG
 GQRQRVWVAM LLAQQTPIML LDEPTTFLDI AHQYELLELL RAFNEAGKTV VTVLHDLNQA
 ARYADHLIVM KDGHVHATGT PEEVLTAEMV QGVFGLPCII SPDPVTGTPT VVPLSRSRAG
 A

> RXA01289 (1-1044, translated) 348 residues
 MTAVAVEKQK ETSISKNLGR RRALGILGIV VALGALIVLS IAVGANPLSF SSVWQGFTAH
 DSSEASIIVW SMRIPRTL VG IVTGAAFGVA GALIQALTRN PLADPGILGV NAGAGFAVTV
 GVGFFGLSSV TGYIWFALG AAAATLLVYF IGASTSGSVN PVALVLAGVA LAAVLGGVTS
 FLTLIDPETF ESIRNWNLGS VARTDLSDTM TVLPFLAVGL AIALLLSGAL NSIALGDDLA
 ASLGTKVMRT RVLGIISVTL LAGGATALTG GIGFVGLMVP HVVRWVVGPD QRWIITFSAL
 CAPVLVLGAD ILGRIIARPG EIEVGIVTAV IGAPVLIALV RRRKASGL

> RXA01290 (1-1164, translated) 388 residues
 VVFNKSR TD ETPVAASEPV ESTRPVSEAS TSPALNPGYH AVSVQRRRFS FRIPARLMV
 SLILFAIALC SATWAITMGD YPLSLGQVIN ALAGTGEKFQ LLVVREWRLP VAIAAVVFGA
 LLGIGGAIFQ SITRNPLGSP DVIGFDAGSY TAVVLVILVL GNTHYWSIAF AAIVGGIVTA
 FAVYVLAWRK GVQGFRLLIIV GIGVSAMLSS VNAYLITRAD VEDAMVVGFW SAGSINRITW
 QSLPSLVIA AVIIVAAIVL ARSLRFMEMG DDVATTLGVK TNSTRALIV VGVATSALVT
 AAAGPISFIA LVAPQLARRL TKTPGVSLVA AAAMGSALLS CAHLLSLIIS SFYRTIPVGL
 LTVSIGGCYM IWLLLRETRR QYRTGTIR

> RXA01297 (1-798, translated) 266 residues
 MGYVGMVLAI LFI GLPLVFI VLTSFKQQSE IYTPVTWFP SEFNFDNYAN VFERVPFLNY
 FRNSIIITVI LCLVKIILGV ISAYALSILR FPGRNLVFLV VISAL MVPSE VTVISNYALV
 SQLGWRD TYQ GIIVPLAGIA FGTF LMRNHF MSIPSELIEA ARMDHCGHFR LLWKVLLPIS
 MPTLVAFSMI TVVNEWNQYL WPFLMAETDN SATLPIGLTM LQNEGVS NW GPVMAATIMT

MLPVLVMFLA LQEYMIKGLI SGA VKG

> RXA01298 (1-393, translated) 131 residues
FVWKNLGYSF VIYLAALQGL NKDLSEAPV DGASAWTRFW KVTLPQLRPT TFFLSITVTL
NSVQVFDIIH TMTGGPLGN GTTTLVYQVY TETFTNYRAG YGATIATILF LLLLIITVIQ
VRYMDKENKQ K

> RXA01303 (1-1335, translated) 445 residues
VTQLNTKGVV LQGWDPEDPE HWDSKIAWRT LWITTFSMII GFCVWYLVSA IAPLLNRIGF
DLSAGQLYWL ASIPGLAGGL IRLIYMFLPP ILGTRKLVGI SSGLFLIPMF GWFLAVQDSS
TPYWWLLTLA ALTGIGGGVF SGYMPSTGYF FPKAKSGTAL GIQAGIGNLG VSIIQFMGPW
VMGFGLLGIG FLTPQRTIEG TTVFVHNAAI VLVPWTILAA VLSFLFLKDV PVTANFRQQI
DIFGNKNTWI LSIIYLMTFG AFAGFAAQFG LIINNNFGIA SPMAETYPAE MLHAGATFAF
LGFLIGALVR AAWGPLCDRF GGAIWTFVGG IGMTIATAAA AIFLSRAETP DDFWPFLWSM
LALFFFTGLG NAGTFKQMPM ILPKRQAGGV IGWTGAIGAF GPFIVGVLLS FTPTVAFFWG
CVVFFIIATA LTWIIYARPN APFPG

> RXA01323 (1-2265, translated) 755 residues
MAQTPAKIPA ALNFIDVDLG VTGMTCTSCS ARVERKLNKL DGVEATVNVA TESAQVSYPD
SKVSPEQLIK TVEDTGYGAF TMAAAAEESE EDNAPADSGQ SRIDAARDHE AADLKHRVIV
SALLSVPVVL VSMIPALQFN NWQWAVLTLV TPIFFWGGSP FHKATWANLK RGSFTMNTLV
SLGTSAADLW SLWALFIENA GHGPMKMEMH LLPSASTMDE IYLETVAVVI TFLLLGRWFE
TKAKGQSSA LKLLDMGAK DAVVLRDGA E VRVPVNQLKL GDVFITRPG E KIATDGEVDE
GSSAVDESML TGESIPVEVT KGSKVTGATL NTSGRLMVKV TRIGADTTLS QMAKLVTDAQ
SKKAPVQRLV DQISQVFVPV VIVIAIATLI AHLVFTDAGL APAFTA AVAV LIIACPCALG
LATPTALLVG TGRGAQLGLL IKGPEILEST KKVDTIVLDK TGTVTTGTMS VTDVTAINYS
ETEILEFAAA VESASEHPIA QAIKAAAEHE QVTDFONTAG QEVTGVVRGH EVRVGRPSST
LIDALLHPFQ HAQKIGGTPV VVTIDGVDSG IITVRD TVKD TSAEAIRGLK ELGLTPILLT
GDNEGAAKSV AAEVGIDQVI ANVLPHEKVQ NVEALQAQ GK NVAMVG DGVN DAAALAQADL
GLAMGAGTDV AIEASDITLM NNDLRS AVDA IRLSRKTLGT IKGNLFWAFA YNVALIPVAA
IGLLNPMLAG IMAFSSSVFV VSNSLR LRGE KARSN

> RXA01338 (1-1878, translated) 626 residues
MLFIRSF DGI ITVAALVAIA IHLILWLALD LDGLAKNWPL IAIVIVGGIP LMWDVLKSAI
KTRGGADTLA AVSIITSVLL GEWLVAIIIV LMLSGGEALE EAASRRASGT LDALARRAPS
TAHRLLGATI LDGTEEI AVE EITVGD LVAV LPHELCPVDG EIVAGHG TMD ESYLTGEPYV
VSKSKGSQAM SGAVNGDTPL TIVATKLAHD SRYAQIVGVL HEAENNRPEM RRMADRLGAW
YTVIALALGG LGWIVSGDPV RFLAVVVVAT PCPLLI AVPV AIIGAISLAA RRGIVKNPG
MLENASGVKT VMFDKTGTLT YGRPVIDIH TAPGVEEDTV LALAASVERY SRHPLADAIR
EGAKARELHL PDVVEVSERP GQGLTGTVGE HLVRI TNRRS TLEIDPDSKN YIPVTSSGME
SVVLVDDKYA ALIRLRDEPR ASASEFIAHL PKKHKVDKLM IISGDRASEV RYLADKVGID
EVHAEASPED KLNIVNRHNE HGATMFLGDG INDAPAMAVA TVGVAMGADS DVTSEADAV
ILDSSLERLD DLLHISARMR RIALQSAGGG MALSVIGMIL AVFGFLTPLM GAIFQEVIDV
LAILNSARVA LPRGAISDFD TQEKVS

> RXA01395 (1-1086, translated) 362 residues
MAVMAYQPAD NRYDDMIYRR VGNSGLKLPA ISLGLWHNFG DDKPLSTQRS IIHRAFD RGV
THFDLANNY PPAGSAETNF GRILREDLKS HRDELISSK AGWDMWPGPY GFGGSRKYL V
SSLDQSLTRL GLDYVDIFYH HRPDPDTPL E ETMYALRDIV ASGKALYVGI SSGPELTAE
AAEFMAEEGC PLLIHQPSYS IINRWVEEPG DDGENLLQSA ANNGLGVI AF SPLAQGLLTD
KYLDGIPEG S RASQGSXXX XLNVNNIDX VXXXXXXSXX TGQSFXKXF CWVVAQPRKV
RRRITVTSAL IGASSVEQLD NSLDSLNNLE FSDAELEAID EISHDAGINI WAKATDSKTR
EN

> RXA01411 (1-327, translated) 109 residues
FIAQVMLGIG AVTANCVT SV MMAEVFQEV T RGTSAGITYN VTYAIFGGSA PFISTALVSW
TGSPLAPAVY MIIIALFAFT ASRFIPETSP VFVTATPAIK APKVLVNPG

> RXA01454 (1-267, translated) 89 residues
MMLIVAFLIA LVGHYLMGGI RAGNQMTGQK SFVSRGARTQ LAVTAGLWML VKVAGYWLD R
YDLLTKENST FTGASYTDIN AQLPAKIIL

> RXA01455 (1-462, translated) 154 residues
 VTWIFAIIAL VILIAPMSVG FYTDWLWFG E VDFRGVFSKV IVTRIVLFVI FALIAGFVTW
 LAGYFVTKLR PDEMSAFDTQ SPVYQYRQMI ENSLRRVMVI IPIFVALLAG LIGQRSWRTV
 QMWLNGQDFG VSDQQFGLDY GFYAFDLPLML RLIA

> RXA01625 (1-201, translated) 67 residues
 MAIKNYTVEG MTCGHCVSSV KEEVGEVAGV TAVDVTLETG AVQVTGEDFT DEAVKAAVVE
 AGYKVVA

> RXA01756 (1-1308, translated) 436 residues
 MKELELGEAR DVAATLEAMP IQEVIDQVER TSITKGAVLL RLLSKDRSLL VFDALGPRLQ
 ADLIGAFQDA EVLDYFADLD PDDRVSLLDE LPASIADELL RSLDPQEKQV TELVLGYAKG
 SVGRWMSPOV LLLFDDMSVA EVLDFVRNHA AEAETIYALP IVNRARQVMG VVSLRKLFLA
 DPTLKVSEIM VRPVSVLASA DIEETARWFL QLDLVAMPVV DESNMLLGVL TFDDAQDIVE
 QADSEDSARS GGSEPLQQPY LSTPIRKLVK SRIVWLLVLA VSAILTVQVL DIFEATLVEA
 VVLALFIPLL TGTGGNTGNQ AATTVTRALA LGDVRKSDVF RVLGREIRVG LMLGALLGAV
 GFVIASLVYG MPVGTVIGLT LLAVCTMAAS VGGVMPIIAK AIGADPAVFS NPFISTFCDA
 TGLIIFYAIA KLVLGI

> RXA01808 (1-1119, translated) 373 residues
 MRGGAPARTS KPGFRLEAAE ALIAEVPAPR DKVELMAFSK SRQGRVVIEL EDATVATPDD
 RILVEDLTWR LAPGERIGLV GVNGSGKTTL LRTLAGEQPL QAGKRIEGQT VKLGWLRQEL
 DDLDSLRLI DVEDVASV MMGDKQVSAS QLAERLGFSP KRQRTPVGDL SGGERRRLQL
 TRVLMAEPNV LLLDEPTNDL DIDTLQELLES LLDGWPGTMV VISHDRYLIE RVTSTWALF
 GDGKLTNLP GIEEYLQRA AMAAEDSGV LNLGAATQAG TESAATEQAA TSVESGSISS
 QERHRITKEM NALERKMGKL DQQMDKLNQ LADAAEAMDT IKLTELDTKL RAVQEEHGE
 EMQWLELGE IEG

> RXA01822 (1-582, translated) 194 residues
 MARQNSNTGG LRLVLVGIGT GAFLGAARDF FMVRADITGA STVQLWSAGS LSGRDWNHAL
 LVLISCIVIV PALCIIVRRL RLMEMGDAA GALGISVERT RLIAILLAVL LVGIATAAAG
 PIAFIALAAP QIARALARE GVLVAASISI GSGLLVAADC LEQHVDTLH TPVGLVTSLL
 GGVYLMWLLS RKEA

> RXA01890 (1-720, translated) 240 residues
 MASIVFENV T RKYSPGARPA VDKLNLEIAD GEFLVLVGPS GCGKSTSLRM LAGLEPIDEG
 RLLIDGKDAT ELRPQDRDIA MVFQSYALP NMTVRDNMGF ALKNQKVAKA EIEKRVAAES
 RILQLDPYLD RKPAALSGGQ RQRVAMGRAI VREPSVFCMD EPLSNLDAKL RVSTRAEISG
 LQRRMGVTTV YVTHDQVEAM TMGDRVAVLL LGVLQQVDTP QNLYDYPANA FVASFIGSLP

> RXA01900 (1-1299, translated) 433 residues
 MTTAVDQNSP PKQQLNKRVL LGSLSGSVIE WFDFLVYGTV AALVFNKMYF PSGNEFLSTI
 LAYASFSLTF FFRPIGGVIF AHIGDRIGRK KTLFITLMLM GGGTVAIGLL PDYNAIGIWA
 PILLMFLRIL QGIGIGGEWG GALLAYEYA PKKQRGLYGA VPQMGISLGM LLAAGVISLL
 TLMPEQFLT WGWRIPFVGS ILLVFIGLFI RNGLDETPEF KRIRDSGQQV KMPLEKVLTK
 YWPAVLVSIG AKAAETGPFY IFGTIIVAYA TNFLNIRDNI VLLAVACAAL VATIWMPLFG
 SFSDRVNRV LYRICASATI VLIVPYLV L NTGEIWFALFI TTVIGFGILW GSVNAILGTV
 IAENFAPEVR YTGATLGYQV GAALFGGTAP IIAAWLFEIS GGQWWPIAVY VAACCLLSVI
 ASFFIQRVAH QEN

> RXA01939 (1-603, translated) 201 residues
 STSGTDLTSL SHKEIFQMRR KLQVVFQNPY GSLDPMYSIY RCIEEPLTIH KVGGRKARE
 ARVVELLDV SMRSTMMRY PNELSGGQRO RIAIARALAL NPEVIVLDEA VSALDVLVQN
 QILTLLAELQ QELKLTYLFI THDLAVVRQT ADDVVVMQKG RIVEKGRDDE IFNDPQQHYT
 RDLINAVPGL GIELGTGENL V

> RXA01972 (1-594, translated) 198 residues
 VATGLLSAIG LFIATNIDDI IVLSLFFARG AGQKGTTLRI LAGQYLGFMG ILAAAVLVTL
 GAGAFLPAEA IPYFGLIPLA LGLWAAWQAW RSDDDDDDDA EIAGKKVGV L TVAGVTFANG
 GDNIGVYVPV FLNVDATAVI IYCIVFLVLV AGLVLLAKFV ATRPPIAEVL ERWEHVLFP

VLIGLGIFIL VSGGAFGL

> RXA01986 (1-618, translated) 206 residues
 MASTFIQADS PEKSKKLPL TEGPYRKRLF YVALVATFGG LLFGYDTGVI NGALNPMTRE
 LGLTAFTEGV VTSSLLFGAA AGAMFFGRIS DNWGRRTII SLAVAFFVGT MICVFAPSFA
 VMVVGRVLLG LAVGGASTVV PVYLAELAPF EIRGSLAGRN ELMIVVGQLA AFVINAIGN
 VFGHHDGVWR YMLAIAAIPA IALFFG

> RXA01995 (1-654, translated) 218 residues
 MDIRQTINDT AMSRYQWFIV FIAVLLNALD GFDVLAMSFT ANAVTEEFGL SGSQLGVLLS
 SALFGMTAGS LLFGPIGDRF GRKNALMIAL LFNVVGLVLS ATAQSAGQLG VWRLITGIGI
 GGILACITVV ISEFSNNKNR GMAMSIYAAG YGIGASLGGF GAAQLIPTFG WRSVFAAGAI
 ATGIATITATF FFLPESVDWL STRRPAGARD KINYIARR

> RXA02033 (1-789, translated) 263 residues
 MPLSGKIGGF IVAVVFLAA LSFIWTPFDP VQAFPQERLE GSSLRHLLGT DRYGRDVLSQ
 IMVGSRVTL VGIIVAIAA LIGTPLGIAA GMRRGMVETF VMRGADLMLA FPALLLAIIS
 GAVFGASTWS AMVAIGIAGI PSFARVARAG TLQVTSQDFI AAARLSKVSS ARIALRHILP
 NITSMLIVQA SVAFALAILA EAALSFLGLG TTPPDPSWGR MLQTAQASIG VTPMLAVWPG
 AAIALTVLGF NLEFGDGLRDA IDP

> RXA02034 (1-966, translated) 322 residues
 VSKTIAWTVL RYTLTFVIAS IIFVLIRVI PGDPAVALG ITATPEAIAA LQSQLGTDQP
 LFQQYFSWIG GMLTGDFGTS LSSGQDLSP IFDRLQVSLI LVGCSIVLSL LIAIPLGVLS
 ARRGGVIISG ISQIGIAIPS FLAGILLVAV FAVGLGWLP NGWIPPSINF GGFLARLILP
 VLALTAVQAA ILTRYVRSV MDVMGQDFMR TARSKGMSFN RALIIHGLRN AALPVLTVTG
 LQLTTLVIGA VVIEQVFVIP GIGSMLESV SNRDLIQVQS IVMLLVAFSL LVNLVVDLLY
 QVVDPRVGAV GVASTKVP GS VA

> RXA02035 (1-1509, translated) 503 residues
 MKITRGLLPS LLLASTIVVS SCSAGSTAYQ QPPAVDQSSI VIATTAAAAA LDFTNAAGAA
 IPQAMMSNIY EGLVRIDAEG EIQLLATSW DISDDRTEYI FHLREGVLFS NGDPFNADSA
 KFSIDRVKTD WTNGLKSGMD VVESTVIDD HTLVKSLVRP SNQWLWSMGT AIGAMMTEGG
 VDKLATDPVG TGPYTVTHWA PGRAIGFGAR ADYWGQKPLN DAATIRYFSD ATASTNALQS
 GDVDVIWAMQ APEQLATLQE YTVEVGTNG EMLLSMNNQR APFDDVRVRQ AVMFADIRQA
 VIDTALEGYG TDTGGVPVPP TDPWYEKSTM YPYDPDRARA LLEEAGAEGT RITMSIPSLP
 YAQAASEILY SQLRDVGFDP VIESTEFPV WLAQVMGQKD YDMSLIAHVE PRDIPTLFSP
 NYYLGFDDTE TQALLAEADS SANEVELMQQ AVDRIMEQAV ADNLNMVANI VVMSPEITGI
 DPNVVSAGLE LSLIGRKESG VAQ

> RXA02062 (1-1170, translated) 390 residues
 MRVGMTREY PPEVYGGAGV HVTETLRFMR EIAEVDVHCM GAPRDMEGVF VHGVDPALLES
 ANPAIKTLST GLRMAEAANN VDVVHSHTWY AGLGGHLAAR LHGIPHVATA HSLEPDRPWK
 REQLGGGYDV SSWSEKNAME YADAVIAVSA RMKDSILAAY PRIEPDNVRV VLNGIDTELW
 QPRPTFDDAE DSVLRSLGVD PQRPIVAFVG RITRQKGVEH LIKAAALFDE SVQLVLCAGA
 PDTPEIAART TALVEELQAK REGIFWVQDM LGKDKIQEIL TAADTFVCPS IYEPLGIVNL
 EAMACNTAVV ASDVGGIPEV VVDGTTGALV HYDENDVETF ERDIAEAVNK MVADRETAAK
 FGLAGRERAI NDFSATIAQ QTIDVYKSLM

> RXA02068 (1-1119, translated) 373 residues
 IFVPMLRIAA IEPKDITLVT GSVSLRTFRV RTGELQVMGD IVGAKVHTDD PELQQFHGRA
 VEIADVELEL SRTRDWIITR VAVLGERPKF GRRPVLHTVP WSHIHGITAG GVGESNHTAE
 LIAGFEDMRP ADVAKQLYQL PTAQRTEVTE ELDDEKLADI LQELSEDRQA ELIEELDIER
 AADILEEMDP DDAADLLGEL PDDKADVLLD LMDPEESAPV RRLMDFSPDT VGALMTPEPL
 IMPDSTTVAE ALAMARNPDL PTSLASLIFV VRPPTATPTG KYLGCVHLQK LLREPPSSLI
 GGILDPDLPP LYADDSQETA ARFFATYNLV CGPVLDENRH LLGAVAVDDL LDHMLPEDWR
 DAGIRPGKEH THG

> RXA02079 (1-615, translated) 205 residues
 MSEAFDATKV RKAULTVALL NFAYFFVEFF IALSAGSVSL LADSVDFLED TSINLLIFIA
 LGWPLARRAV MGKLMAIVIL APAFAAWAA IQRFSAQAP EVFPIIVASL GAVVINGASA

IIISVRQHG GSLGQAAFLS ARNDVLINIA IIMMALITAW TTSGWPDIL GCFIILLALH
AAHEVWEVSE EERLASKALA GEAI

> RXA02096 (1-1317, translated) 439 residues

MGLDVSDEQI EHAARLAQAH DFIDRLPNKY EEVIGERGLT LSGGQRQRIA LARAFLAHPK
VLVLDDATSA IDASTEDRIF QALREELHDV TILIIAHRHS TLELGDRVGL VEDGRVTALG
PLSEMRDHAR FSHLMALDFQ DSHDPEFTLD NGSLPSQEQ L WPEVSTKQY KILAPAPGRG
RGMSMPATPE LLAQIEALPA ATEETRVDAG RLRTSTSGFK LLSLFKQVRW LVVAVIALLL
VGVAADLAFP TLMRAAIDNG VQAQSTSTLW WIAIAGSVV LLSWAAAAIN TIITARTGER
LLYGLRLRSF VHLLRLSMSY FERTMSGRIM TRMTTIDIDL SSFLQSGLAQ TVVSVGTLLG
VVTMLAITDA QLALVALSVV PIIIVLTLIF RRISSRLYTA SREQASQVNA VFHESIAGLR
TAQMHRMEDQ VFDNYAGEA

> RXA02119 (1-1641, translated) 547 residues

MTETLVVNGI AGGYGHRTLF NDVNLTVAAG DVVGVVGVNG AGKSTFLKIL AGVEKPLAGT
IALSPADAFV GYLPQEHTRT SGETIAVYIA RRTGCQAATT AMDDTAEAFG ADPDNAALAD
AYAEALDRWM ASGAADLDER IPIVLADLGF ELPTSTLMEG LSGGQAARVG LAALLLSRFD
IVLLDEPTND LDLDGLEQLE NFVQGLRGGV VLVSHDREFL SRCVTTVLEL DLHQNSHHVY
GGGYDSYLEE RAVLRQHARD QYEEFAEKKK DLVARARTQR EWSSHGVRNA IKRAPDNNDK
RKAAAAESSE KQAQKVRQME SRIARLEEVE EPRKEWKLOF SVGKASRSSH VVSTLNDASF
TQGDFTLGPV SIQVNAGDRI GITGPNAGK STLLRGLLGN QEPTSGTATM GTSVAIGEID
QARALLDPQL PLISAFEKHV PDLPISEVRT LLAKFGLNDN HVERDVEKLS PGERTRAGLA
LLQVRGVNVL VLDEPTNHL D LEAIEQLEQA LASYDGVLLL VTHDRRLDA VQTNRRWHVE
AGEVREL

> RXA02220 (1-2676, translated) 892 residues

VSSPLPAAVT SKPAHALSSD EVLENLGVQD TGLTSAEATQ RLEANGPNEL PQTPPETVWQ
RLFRQVNDPM IYVLIAAVAL TAFLGHWTDT IVIGAVVIIN MMVGFIQEGK AADALASIRN
MLSPESAALR DGVFHKIDAA ELVVGDVVKL SAGDKVPADL RMLAATNLHI EESALTGEAE
AVVKGTDPE ADAGIGDRS MAFSGTLVLT GSGTGVVTAT GAGTEIGHT TMLADVDSVD
TPLTRSMKKF SSALAIVCVF LAILMLVAG LVHHTPLEEL ILSAIGFAVA AIPEGLPAVI
AITLALGVQK MAARNAITRR LNSVETLGSV TTICTDKTGT LTRNEMTVRA IATGTSLYDV
SGAGYEPLGE IRLKDGEQVS KQDFPDLYAM ALVAANVND EIQEDGMWR LSSEPTDGGI
RAFAMKTNAE ILTRTAEVPF DSAYKMATL HTIDGANTML VKGAPDRLLD RSAQQRNGEP
LDRPYWEQLI EDLASQGLRV LAAAYKELPH STSTITPEDV DQGELTFLGL YGIMDPPREE
VIEAMKVVQS AGVRVRMITG DHSSTARAIA REVGIRGQNV LTGAETIAT DEELQGLVDN
ADLFVRTSPE HKLRVVRALQ ANGEVASMTG DGVNDAPALK QADVGVAMGI KGTEATKDA
DIVLADDNFA TIAGAVEMGR TIYDNLKAV VFMLPTNGAQ GLVIFIAMLL GWELPITALQ
VLWINLITAI TSLALSFEPA AEPGIMNRKP RNPKSGLIDA PSVLRIYVVS LLLGGATFWA
FLGARDAGID IDTARTIAVT TLAVSQVFYL LSSRYFEVSA LRKELETTNP ISWLCIALML
ILQLAFVYLP FMQSTFDATA LTLRDWVMP VEGVVVFAVV ETEKFIRRLK AS

> RXA02222 (1-375, translated) 125 residues

LGRPPPGDVH TLLDDIGAEE SEADKVPIEW QNALTKADRY ANRQHMSQAR LYRQLTSDVG
EGFTEEAQY AIENVNADWN ANALVKARNY QERQAMSVDR IYRQLTSEHG EGFTPEQAQY
AIDNL

> RXA02312 (1-1359, translated) 453 residues

LSNRHLQLIA IGGAIGTGLF MSGKTISVA GPSVILVYAI IGFMFFVVR AMGELLLANL
NYKSLRDAVS DILGPGAGFV TGWTYWF CWI ATGMADIVAI TGYTQYWWPE IPLWLPGLVT
IALLFALNLA AVRLFGEF WFALIKIVAI VSLIVVGLFM VVTAFESPNG TTAQFNNLIE
HGGFFPNGIT GFLAGFQIAI FAFVGIELAG TAAAEETENPT KTLPRAINSI PIRIVVFYVL
ALAVIMMVTP WDQVRADNSP FVQMFALAGI PAAAGIINFV VITSAASSAN SGIFSTSRML
YGLSLEGAAP KRWSRLSKNL VPARGLTFSV ICLIPAVGLL YAGGTVIEAF TLITTVSSVL
FMVWVSYILV AYIVYRRNSP ELHKKSIFKM PGGVVMVAVV LVFFAAMLV LSLEPDTRAA
LIATPVWFII LGIGWLSIGG AKGAKHRSQI TSH

> RXA02313 (1-1221, translated) 407 residues

MRVAIVAESF LPNVNGVTNS VLRVLEHLKA NGHDALVIAP GARDFEEIEG HYLGFIEVRV
PTVRVPLIDS LPIGVPLPSV TSVLREYNPD IIHLASPFVL GGAAFAARQ LRIPAIYQ
TDVAGFSQRY HLAPLATASW EWIKTVHNM C QRTLAPSSMS IDELRDHGIN DIFHWARGVD

SKRFHPGKRS VALRKSWDPS GAKKIVGFVG RLASEKGVVER LAGLSGRSDI QLVIVGDGPE
 AKYLQEMMPD AIFTGALGGE ELATTYASLD LFVHPGEFET FCQAIQEAQA SGVPTIGPRA
 GGPIDLINEG VNGLLLDVVD FKETLPAAAE WILDDSRHSE MCAAWEQVK DKTWEALCTQ
 LLQHYADVIA LSQRIPLTFF GPSAEVAKLP LWVARALGVR TRISIEA

> RXA02344 (1-678, translated) 226 residues
 MLNRMKSARP KSVAPKSGQA LLTLGALGVV FGDIGTSPLY SLHTAFSMQH NKVEVTQENV
 YGIISMVLWT ITLIVTVKYV MLVTRADNQG QGGILALVAL LKNRGHWGKF VAVAGMLGAA
 LFYGDVVITP AISVLSATEG LTVISPSFER FILPVSLAVL IAIFAIQPLG TEKVGKAFGP
 IMLLWFVTLA GLGIPQIIGH PEILQSLSPH WALRLIVAEP FQAFVL

> RXA02348 (1-1134, translated) 378 residues
 PIRVAWFCVV MPALILTYLG QGALVINQPE AVRNPWFYLA PEGLRIPLVI LATIATVIAS
 QAVISGAYSL TKQAVNLKLL PRMVIRHTSR KEEGQIYMPL VNGLLFVSVM VVVLVFRSSE
 SLASAYGLAV TGTLLVLSVL YLIYVHTTWW KTALFIVLIG IPEVLLFASN TTKIHDGGWL
 PLLIAAVLIV VMRTWEWGSD RVNQERAELE LPMDKFLEKL DQPHNIGLRK VAEVAVFPHG
 TSDTVPLSLV RCVKDLKLLY REIVIVRIVQ EHVPHVPPEE RAEMEVLHHA PIRVVRVDLH
 LGYFDEQNLP EHLHAIDPTW DNATYFLSAL TLRSLRPGKI AGWRDRLYLS MERNQASRTE
 SFKLQPSKTI TVGTELHL

> RXA02353 (1-468, translated) 156 residues
 MALLILAGLQ MIPKETYEAA RVDGATAWQQ FTKITLPLVR PALMVAVLFR TLDALRMYDL
 PVIMISSSSN SPTAVISQLV VEDMRQNNFN SASALSTLIF LLIFFVAFIM IRFLGADVSG
 QRGIKKKKLG GTKDEKPTAK DAVVKADSAV KEAAKP

> RXA02354 (1-789, translated) 263 residues
 MTKRTKGLIL NYAGVVFILE WGLAPFYWMV ITALRDSKHT FDTTPWPTHV TLDNFRDALA
 TDKGNNFLAA IGNSLVISVT TTAIAVLVGV FTAYALARLE FPGKGIVTGI ILAASMFPGI
 ALVTPLFQLF GDLNWIGTYQ ALIIPNISFA LPLTIYTLVS FFRQLPWELE ESARVDGATR
 GQAFRMILLP LAAPALFTTA ILAFIATWNE FMLARQLSNT STEPVTVAIA RFTGPSSFEY
 PYASVMAAGA LVTIPLIIMV LIF

> RXA02394 (1-1311, translated) 437 residues
 MLSPAABAAL ILVIGIVVLI IASVPVAIAI GLPSLFAAMA VLGPENAAQA VAQRMFTGTN
 SFTLLAIPFF VLAGLLMNSG GIATRLIDAA KVLVGRMPAS MANTNIAANG LFGAVSGAAV
 ASASAVGTVM TPKMKKEEGYS RAYAAVNVA SAPAGMLIPP SNTFIVYSLV SSTSIAALFM
 AGVGPGLLWI LACVIVGTWL ARKENYKREQ IHPTFKQSLV VLWRALPSLL MIVIVVGGIL
 LGWFTPTESA AIAVVYCLVL GFIYRTIKVG DLADILLKAT RTTSIVMLLI AVSAALSWVM
 AFAKIPQMIS DALLSVSDSK VVILLIMFI LLLIGTVMDP TPAILIFVPI FLPVVTELGV
 DPVHFGAMVV MNLSVGVITP PVGNVLFVGS QVAGLRVETV IRRLWPYLIA IIVALFVVVF
 VPQISIWLP TMLMGG

> RXA02402 (1-744, translated) 248 residues
 VSKTEEGRSA AIIIIYAFPTF ILLGAIIAFI FPEPFIPLTN YINIFLTIIM FTMGLTLTVP
 DFQMVLRPL PILIGVVAQF VIMPFLAIV AKMFNLNPAL AVGLMLGSV PGGTSSNVIA
 FLARGDVALS VTMTSVSTIV SPIMTPFLML MLAGTETAVD GGGMAWTLVQ TVLLPVIIGL
 VLRVFLNKWI DKILPILPYL SILGIGGVVF GAVAANAERL VSVGLIVFVA VIVHNVLGXY
 VGYLTGRV

> RXA02422 (1-435, translated) 145 residues
 VSTLISEPEV DKLRKRAKRS RTEWWLAAA LLAPNLLLLA IFTYRPLLDN FRLSFFNWN
 SSPTSTFIGF DNYVEFFTRS DTLQVVLNTV IFTACAVIGS MVLGLLLAML LDQKLFGRNF
 VRSMVFAPFV ISGAAIGGAF QFVFD

> RXA02438 (1-759, translated) 253 residues
 MTDLIQLREV SKKYGAQAL NDINLNVRAE EVTCVLGDNG AGKSTLIKIL SGLHPATSGE
 VIVAGDVVNF GSPRDALDAG IATVYQDLAV VGQMSVWRNF FLGQELTGRF GVLKQEMMRR
 ITDEQLREMG IELRDVDVPV ASLGGQRQV VAIARAIYFG ARVLILDEPT AALGVKQSGM
 VLRFIAAARD RGIGVIFITH NPHHAYLVGD HFILLNLGKQ VMDKSRAEVE LEELTLAMSG
 GGELDSLSE LKR

> RXA02439 (1-1023, translated) 341 residues

MTKIKSGEAS TSIVERALKR PELTSLLGAV LVFTLFMVVA PAFRSWDSMA TVLYASSTIG
IMAVAVGLLM IADEFDLSTG VAVTTAALAA SMFSYNLWLN TWVGALIALV ISLAIGFFNG
FLVVVKTKIAS FLITLATFLM LQGINLAVTK LISGTVATPT IADMEGFPSA RAVFASSIPI
FGVNIRITVF WWLLFVIVGT FVLFKTRIGN WIFAVGGDEE AARAVGVPVR GVKIGLFMFV
GFAAWFVGMH NLFLFDSIQA GQGVGNEFLY IIAAVIGGIS MTGGRGTVVG TMIGALIFGM
TNQGIVYAGW NPDWFMFFLG GTLLLAVLLN HRFERFNKER S

> RXA02441 (1-657, translated) 219 residues

MAELSVRNLT CTYGNHIALN NITARFPTGK ITALIGSNGS GKSTLLETLA GMLAPRSGSI
NNLVPEIAFV PQRSHVSHNL PITIRQTVSM GRWSAKKNWQ RLTAADCNIV DSCLDRLAIS
GLADRPLGEV SGGQRQRALI AQGLAQQAAPL LLLDEPLAAV DSHAASLIED VINQQRNQGT
TIILATHDLD QAHQADQIIA LEKGIKPKR KATESIKKR

> RXA02442 (1-849, translated) 283 residues

MKFFTDALIV PFDVSFISRA LVAGCLAAIL CSLIGTWVIL RRLTFFGDAM SHGLLPGVAT
ASLLGGNLMF GAAISALIMS AGVVWTSRKS SLSQDVSIGL QFITMLSLGV VIVSHSDSHA
VDLTSFLFGD ILGVRPSDIF IIAIATVLGG LTIFLFHRQF TALAFDERKA HTLGLNPRFA
HLLMLALIAL ATVVVSFQVVG TLLVFGLLIG PPATAALLVQ DKASISLIMI VASLLGCAEI
YLGLLISWHA STAAGATITL LSAAIFFATL LTKSAISRLN FTA

> RXA02447 (1-270, translated) 90 residues

WWWLAEIFPV RMKGIGTGIS VFCGWINGV LALFFPALVS GVGITFSFLI FAVVGVIALLA
FVTKEVPETR GRSLEELDHA AFTGQIFKKA

> RXA02451 (1-1524, translated) 508 residues

MNTDTTQDGV SPEPSDPHLG SEVAETHREK KFFGQPWGLA NLFGVEMWER FSFYGMQSIL
AFYLYYSVTD GGLGMNQTAAL LSIVGAYGGF VYMTSLVASF IADRVLGSR TLFYSIIIVM
LGHIALALIP GYTGLSIGLV LIGLGGSGVK TAAQVVLGQL YSRDTRRDA GFSIFYMGVN
LGGLFGPLIT NALWGWWGFH WGFIAAVGM ALGLIQYVAM RKTITIGAAGH TVPNPLPKNE
YARWIIIGAV VVAAVVALIA TGIKLEWLS NITAAIALIA AIALLAQMYV SPLTTAAEKS
RLLGFIPIFI GGVLFFAIFQ TQFTVLAVYS DTRLDRNFFG IDLPPGLINS FNPIFIIIFS
GIFATLWTKL GAKQWSTAVK FGVANIVIGC ALFFFLPFAG GAENSTPMAL IIWVYFLFTI
AELLSPVGN SLATKVAPEA FQSRMFAVWL MAVSMGTSLS GTLGGYYDPT DAGSEKVVFI
TVGVAAIVLG AIVIAAKGWV LKKFIDVR

> RXA02491 (1-1254, translated) 418 residues

MRVAMISMHT SPLQQPGTGD SGGMNVIYLS TATELAKQGI EVDIYTRATR PSQGEIVRVA
ENLRVINIAA GPYELGSKEE LPTQLAAFTG GMLSTRREK VTYDLIHSY WLSQGVGWLL
RDLWRIPLIH TAHTLAAVKN SYRDDSPTPE SEARRICEQQ LVDNADVLAV NTQEEMQDLM
HHYDADPDRI SVVSPGADVE LYSFGNDRAT ERSRRELGIP LHTKVAVFVG RLQPFKGPQV
LIKAVAALFD RDPDRNLRI ICGGPSGPN TPDYRHMAL ELGVEKRIRF LDPRPPSELV
AVYRAADIVA VPSFNFESFGL VAMEAQASGT PVIAARVGGL PIAVAEGETG LLVDGHSPPH
WADALATLLD DDETRIRMGE DAVEHARTFS WAATAAQLSS LYNDALIANEN VDGETHHG

> RXA02507 (1-1401, translated) 467 residues

MSEQLQGVTH SESTPGKTPK RAALSSWIGS ALEYDFAVY GTAAALVLNH LFFPADTSPG
IAILAAMGTG GVAYVVRPLG ALIMGPLGDR YGRKFVLMC LFLIGASTFA VGCLPTFDQV
GYLAPALLVL CRVIQGLSAS GEQSSAISVS LEHADERHRA FTASWTLHGT QFGTLLATGV
FIPFTLFLSE DALMSWGWRV PFWLSAAVVL VAFLIRRGLE EPPAFRENKE AVAGAASPLA
MTLRYHKAAY ARVAIAAMIN SVNIVFTVWA LSFATNIVGL DRSTVLLVPV VANLVALIAI
PLSGMLADRI GRRPVFIMGA IGGGLAMNGY LGAIYSGNWT MIFFMGVIMS GLLYSMGNAV
WPAFYAEMFP TSVRVTGLAL GTQIGFAVSG GFVPVIASAL AGDQGDQWMK VSIFVGVVVCV
ISALVAMTAK ETKALTLEI DALHTAGGEA ADLAAASKAS EAQLAAQ

> RXA02515 (1-756, translated) 252 residues

MSTLEIRNLH AQVLPSESA EPKEILKGVN LTINSGEIHA IMGPNGSGKS TLAYTLGGHP
RYEVTAGEVL LDGENILEME VDERARAGLF LAMQYPTIIP GVSANFLRS AATAIRGEAP
KLREWVKEVR TAQEALADP EFSNRSVNEG FSGGEKKRHE VLQDLLKPK FAIMDETDSG
LDVDALRIVS EGINSYKQET EGGILMITHY KRILNYVKPD FIHVFANGQI VTTGGAEALAD
KLEADGYDQF IK

> RXA02562 (1-720, translated) 240 residues
MFLTQVSLLD HPESLPGYLS SLAIVEYLHE QPLEFRAPIT VITGENGVGK STLVEALAVG
MRLNPSGGSR HANFGREGDI VSSLHQSLKL VRRENPRDAF FFRGETMYNV ASYEEELMGE
KNMHDHLHKMS HGESVFAVID RRFNNQGGFFV LDEPEAGLSM LRQLELLGKL GNLARGGAQI
IMATHSPILL AIPGAIELEI TSSGVAKVNF EDAAEAVRAAR EFVADPRGTA AFLTAEEDHQ

> RXA02595 (1-651, translated) 217 residues
VIVVAMASIM ACLKAARLNN PMKILLLLCWR DTTHPQGGGS ERYLERVGEF LADQGHEVVF
RTAGHTDAPR RSFRDGVRY SSGGKFSVYP KAWVAMMLGR VGIGTFSKVD VVVDTQNGIP
FFGKFFSFGKP TVLLTHHCHK EQWPVVGRL AKVGWLVESQ IAPRAYKTAP YVTVSEPSAE
ELIALGVDQQ RIHIVRNGVD PVPLHTPKLD RDGQHAV

> RXA02597 (1-1788, translated) 596 residues
LPEQDLTTLA NDWLQAFKA TASSSPDEAA TAVVQLFEDE GYWRDLLAFT WNLTTAEGAD
EIAEMIRNTW PSSIFRNVEL KGEPADEGDG VTRVHFSCS ADFKCTGIVR LRNGKAWTLL
TSARELLEHP EPKGRNREMG VVHGQNEEDR NWTDRKNDRQ AALGVTEQPY TLIIGGGQGG
IALGARLKRLL GVPALIIDKA SRPGDQWRSR YHSLCLHDPV WYDHLPIYIF PDHWPVFTPK
DKMGDWLEHY VGIMDLDYWT NTECLRASYN EDTKQWDVTV NRDGAESTLH PTQLVMATGM
SGSPNKPTLP GQDKFQGEIR HSSEHPGGDV DRDKNVVVLG ANNSAHDICA DLYSNGAKPV
MIQRSSSTHIV RSDSLMREVF GLYSEDVAE AGIDTDTADL LFASWPKYKVL PGVQKQAFDK
IREDDKEFYD KLENAGFLLD FGDDDSGLFL KYLRRGSGYY IDVGASELVA DGKIPVRSNV
SIEDVKENSV VLTDTGTELP DVIVLATGYG NMNNWVAQLV DQETADKVGW CWGLGSETTK
DPGPWEGELR NMWKPTNVDS LWFHGGNLHQ SRHYSRYLSM QLKARYEGMN TPVYSK

> RXA02605 (1-495, translated) 165 residues
VACPWAGTAA LNLAAKHPDQ FRQAMSWSGY LNTTAPGMQT LLRVAMLDTG GFNVNAMYGS
IINPRREFEND PFWNMGGLAN TDVYISAASG LWSPQDDGVR VDHRLTGSVL EFVAMTSTRI
WEAKARLQGL NPTADYPMYG IHGWAQFNSQ LERTQGRVLD VMNAW

> RXA02614 (1-729, translated) 243 residues
MTATLSLKPA ATVRGLRKS YGTKEVLQID LTINCGEVTA LIGRSGSGKS TILRVLAGLS
KEHSGSVEIS GNPVAFQEP RLLPWKTVD NVTFGLNRTD ISWSEAQERA SALLAEVKLP
DSDAAWPLTL SGGQAQRVSL ARALISEPEL LLLDEPFGAL DALTRLTAQD LLLKTVNTRN
LGVLLVTHDV SEAIALADHV LLLDDGAITH SLTVDIPGDR RTHPSFASYT AQLLEWLEIT
TPA

> RXA02616 (1-711, translated) 237 residues
LQKHTRGGKH RKQTTSPVTK GGVAFFAVAT GAVSTAGAGG AVAAQASNQP VEVNFELTAN
DTTDLVAGSS APQILSIAEF KPVVNLGDQI VKTIQYNADR IQADLDARGP SVVRPAEGSY
TSGFGARWGT NHNGVDIANA IGTPILAAMD GTVIDAGPAS GFGNWVRLQH EDGTITVYGH
METVEVTVGQ TVKAGERIAG MGSRGFSTGS HLHFEVYPAG GGAVIDPAPWL AERGITL

> RXA02627 (1-843, translated) 281 residues
DVTVESQPER VVALGWGDAE AALEFGVQPV GASDWLAFGG EGVGPWIEDS AYDEAPEIIG
TMEPEYEKIA ALEPDLILDV RSSGDQERYD KLSSIALTIG VPEGGDSYLT PRAEQVTMIA
TALGQAERGE EVNAEYEQLT ADIRAAHPGW PEKTAAAVSA TATSWGAYIK GSNRVDTLDD
LGFQENPELA KQPGDGTGFS IKFSEETFGV VSDLVVGFA IGMTPEEMAE QVPWQMLTAT
RDGRSFVMRPR EISNAFSLGS PQSTRFALDA LVPLLEEHA E

> RXA02628 (1-405, translated) 135 residues
MLEGFRDFVL RGNVIELAVA VVIGTAFTAI VTAFSESIIN PLIASIGSTE VEGLGPHIRA
GNAATFVDFG AVITAAINFL IIAAIVYFVL VAPMNKLSET LAKRKGVEED ETPASIEAEL
LTEIRDLLQE QKRLQ

> RXA02650 (1-579, translated) 193 residues
MVNVTSKDG ANVTPMSKKE KRRTVKQVVA LMAAIVVVIA SLDQIVKQIM LSWLEPGVPV
PIIGDWFRFY LLFNPGAASF MGENSTWIF TTIQLSFVIG IAIYAPRIKH KWIAAGLALV
AGGALGNVLD RLFRDPSFFF GHVVDYISVG NFAVFNIAA SISCVVVFL IGMFLEDREN
AQHAKATDEK DEA

> RXA02660 (1-639, translated) 213 residues
 MIIGVTLLVF IVMSFSPADP ARLALGESAS PEALEAYREA NGLNDPMMVR YDFDILGMLK
 GDLGTSSGGV AVTDIVARAF PITLQLTFWG LIIAVVVALI LGVIAALYRD RWPDQLIRVV
 SIAALATPSF WLAILLIQWL GTIPGAWGFF PALVTRWVPF SEDPATYFNN IALQRLRWQS
 PLQVLWPALF VPPWWKNWTR TTSAQQSVQD PQN

> RXA02661 (1-219, translated) 73 residues
 VIGLRVGSML GGAVIIEIIF NIQAMGQLIL DGVTRNDVYL VQGVTLTVAI AFIIIVNIAVD
 LLYVLVNPRI RSI

> RXA02663 (1-1395, translated) 465 residues
 MAPILVFATV LVADAIVFEA SLSFINAGVK PPSPSWGNI L ADGKALLLSG AWWPTFFPG
 MILLTVLCLN ILSEGLTDTL ASPKPKPVSA SAKKALKKEE SGEKEGSGIV LGHTTREETAN
 ASLLASLAAL STSENNNNR LIFDGNPTPL LEVRDLKISF PNAHGDINIV DGVNFTVAPG
 QTMGLVGESG CGKSITAMSI MGLLPPTAKI EGEILFDGKN LLDLKPDELN ALRGHEIAMI
 YQDALSSLNP SMLISAQMKQ LTRRGGRSA EELLELVGLD PKRTLQSYPH ELGGGQRQV
 LIAMALTRNP RLLIADEPTT ALDVTVQQQV VDLLNELREK LGFAMIFVSH DLALVARLVH
 KLTVMYAGQV VEQGTREIL IDPRHEYTRG LLGSVLSIEA GVDRLYQVPG TVPSPKEFVA
 GDRFAPRSEF PELGLDQKPV LRPITGTEHA YAATDELLAA KGEQR

> RXA02664 (1-660, translated) 220 residues
 VGESGCGKST LARVMVGLQP VTSGEVLFGK KPMKPRGAQR KELGSSSVSV FQDPATSLNP
 RMTVREQLLD PLRVHKVGE ASRNQWVSEL ISMVGLPQSA LEVLPRQVSG GQRQVARIAR
 ALALKPDIIV ADEPTALDV SVRAQVLNLL LDLKTELGLG LVFISHDINT VRYVSDRIAV
 MLAGEIIEEN TTSEIFNNAQ QDYTRTLLEA TPSSLNKTRL

> RXA02684 (1-864, translated) 288 residues
 VLAVGLVLF VVTLWADSKL NRVDATPATQ VANTAGTNWL LVGSDSRQGL SDEDIERLGT
 GGDIGVGRD TIMVLHMPRT GEPTLLSIPR DSYVNVPGWG MDKANAAFTV GGPELLTQTV
 EEATGLRIDH YAEIGMGGLA NMVDAVGGVE MCPAEPMYDP LANLDIQAGC QEFDGAAALG
 YVRTRATALG DLDRVVRQRE FFSALLSTAT SPGTLLNPF TFPMISNAVG TFTVGEGDHV
 WHLARLALAM RGGIVTETVP IASFADYDVG NVAIWDEAGA EALFSSMR

> RXA02728 (1-813, translated) 271 residues
 MAIVSLDNT VSIEGKKLLD AVSLKAYPGE VLGLIGPNGA GKSTLLSVLS GDRLPDSGEV
 NVGGLDPATA AASDMARVRA VMLQDVSVAF SFLVWDVEM GRRPWQKAST PEEDHEIIEA
 ALAATSVSHL AEREITTLTG GERARVALSR VLAQQTPIVL LDEPTAAMDI SHQEQTGLTA
 RALAAAGAAV IVVLHDLNAA AAYCDSIVCL SDGRVIASGS VDQVYSTETL SRVYGWPIRV
 DMSGKYVRVE PDRSEANLPS VLQVKNTVSP A

> RXA02750 (1-816, translated) 272 residues
 MAVLFSIMGA LILLVLYLF LGKLQIDGLM VDLPSARD D VEGFVFNWVF SGILITSAIT
 VPQAALGVLV EDRTRGGIKD FLVAPVSRTT LTVSYIFAAV IVAMTILIFE IVVGSIGLAI
 LGHFSMSIAR VLELVVALL LTLVFSIAIA FLITLVKSQG GMSALSSLVG TLAGFLSAAY
 IPPIALPEAV TNVLNFLPFT PAGMLIRQIV VAPALDAISL PPEAFDIFQF GYGLKLEMF
 EPVSTWVAVG IVASWGVVFG LIAAFKMKSV VR

> RXA02761 (1-201, translated) 67 residues
 MMDGINRRTT LITGYSLTTI SHVLIGIASV AFPVGDPLRP YVILTLVVVF VGSMQTFNLG
 SYLGYAL

> RXA02762 (1-285, translated) 95 residues
 MLSELFPLAM RGFAIGISVF FLWIANAFGL LFFPTIMEAV GLTGTFMFMA GIGVVALIFI
 YTQVPETRGR TLEEIDEDVT SGVIFNKDIR KGKVH

> RXA02769 (1-711, translated) 237 residues
 TVVPVYLAEL APLEIRGSLT GRNELAIVTG QLLAFVINAL IAVTLHGVID GIWRIMFAVC
 ALPAVALFLG MLRMPESPRW LVNQGRYDDA RRVMETVRTP ERAKAEMDEI IAVHSENNAA
 LPGVKQSSGQ ASGQVSSKHT HMSIGEVLSN KWLVRLLIAG IGVAVAQQLT GINAIMYYGT
 RVLEESGMSA EMAVVANIAF GAVAVIGGLI ALRNMRLDR RTTFIIGLSL TTFHLL

> RXA02795 (1-1095, translated) 365 residues

IDVSLPERTA SAYPHELSSG QRQRALIAM LANDPDLLIC DEPTTALDVV VQKQIVDLLL
RLTKERGTL LFITHDLGLI ARTCERLLVM KSGETVERGD TEAILRSPAH SYTQQLLDAS
ILDQPEIASD SGAPVVVIDVE EASKSFKETT ALHKVSLAVR KGDLLGIVGG SGSGKTTLLK
LIAGLDKPTT GTVAVTGGVQ MVFQDPQSSL NPRMKIKDIV AEPLLGWNAA EKTTRVAEVI
TQVGLSPDVL DRYPHEFSGG QRQRISIARA LAIKPAILLA DEPVSALDVS VRKQVLDLLQ
QLVEEYGITL VEVSHDLAVV RHLCTTVWVM EQGRVLEQGP IDSVYDHPQT EYTKELLDV
PRLSL

> RXA02808 (1-258, translated) 86 residues

FYFGILPVLA ESASHFGIEP VEMARASITG QPVHMQSPLV PAILLLVSLA NVNLGDHKK
VLWRACIVSI AMLAVALFIG VVPLSA

> RXA02863 (1-975, translated) 325 residues

MKKSIIAIVA SALVLSGCTS DSSDSSGTSG TVETTSITTS VAAADGAFPR TVTLDDSSIT
LESKPERIAV LTPEAASLVL PITGADRVVM TAEMDTADEE TAALASQVEY QVKNNGSLDP
EQVVAGDPDL VIVSARFDE QGTIDILEGL NVPVNFDS AWGDIDAITK HLEIVGELVG
EEDKAAEAIA EIDANRIDID KPATSPTVLT LMQRGPRQMV MPESAMLNGL IREAGGTPVV
DSLGAVGIT ADPEQVAMA PEIIIIQDFQ GKGRENFANF LSNPALANVP AIENDKIFYA
DTVTTGVTAG TDITTGLOQV AEMLS

> RXA02864 (1-780, translated) 260 residues

MPQLVEIRD L NVEFPSRHAV KNVSFSAPAG KVTALIGPNG AGKSTALSAI AGLVESTGEV
MVGSGVASK SAKARARLLS LVPQNTLRI GFSARDVAM GRYPHRGRFA VETDADRRAT
DDALRAINAL DIAEQPVNEL SGGQQQLIHI GRALAQDTAV VLLDEPVSA DLRHQVEVLQ
LLRARANSCT TVIVVLHDLN HVARWCDHAV LMADGEVVSQ GDIREVLEPA TLSTVYGLPI
AVRDDPETSS LRVIPHPNPF

>RXN00001 TRANSLATE of: rxn00001.seq check: 7420 from: 1 to: 1128

MATVTFKDALSYPGAKEPTVKKFNLEIADGEFLVLVGPSCGKSTTLRMLAGLENVTDG
AIFIGDKDVTHVAPRDRDIAMVFQNYALYPHMTVGENMGFALKIAGKSQDEINKRVDEAA
ATLGLTEFLERKPKALSGGQRQVRVAMGRAIVRNQVFLMDEPLSNLDAKLRVQTRTQIAA
LQRKLGVTTVYVTHDQTEALTMGDRIAVLKDGYLQVVGAPRELYDRPANVFVAGFIGSPA
MNLGTFSVKGDATSGHARIKLSPETLAAMTPEDNGRITIGRPEALEIIPGESTDLSI
PIKLDVEELGSDSFLYGLVGEGLGSSSEDVPESQIVVRAAPNAAPAGSVFARIV
EGGQHNFSASTGKRLP

>RXN00099 TRANSLATE of: rxn00099.seq check: 3872 from: 1 to: 1173

VKNPRLIALAAIILTSFNLRTAITALAPLVSEIRDDLGVSASLIGVLGMIPTAMFADAAAF
ALPSLKRKFTTSQLLMFAMLLTAAGQIIRVAGPASLLMVGTVFAMFAIGVTNVLPIAVR
EYFPRHVGGMSTTYLVSFQIVQALAPTLAVPISQWATHVGLTGWRVSLGSWALLGLVAAI
SWIPLLSLQGARVVAAPSKVSLPVWKSSVGVGLGLMFGFTSFATYILMGFMPQMVGDVQ
GAVLLGWWSILGLPLNILGPWLVTFTNCFPMVVIASVMFLIGNGGFCLAPDVAPWLWAT
LSGLGPLAFPMALTLINIRAETSAGASALSSFGQGLGYTIACFGPLLTGFIVDATGSFRT
IFVLFVATLTVIRGGYFATRQVYVEKLLNR

>RXN00193 TRANSLATE of: rxn00193.seq check: 1918 from: 1 to: 594

KAFXQREGFISAFGFTVLVIVSVITVNIFAFLAWLLTRKLRGTNFFRTVFFMPNLIGG
IVLGYTWQTMINAVLSHYATTISADWKFGYAGLIMLLNWQLIGYMMIYYIAGLQNVPEL
IEAAELDGVNKWEMLRHVTIPVMPSITICLFLTLSNSFKLFDQNLALTNGAPGGQTEMV
ALNIINTLFNRMNVEGVG

>RXN00378 TRANSLATE of: rxn00378.seq check: 9591 from: 1 to: 2610

VDAVNTAISDAKTAALKAGVGLNRATASEEEEDLSSSIKVSLAFELEGLSNAPSLMVVE
KALEKIPGVSADLIYPSQTAWITATDRVHPETLIEVFEQFGIKAHLSNSSLLRRHQQLSA
EVNREARLDYRSRMDAKRISPRVRRHNRQEMVHAVRARESGWIKRRNHTTSQHEDPMSG
DVLFTARALITPKRLWVSLPFALIVLALSLSNPWQFDYQWLSAVLAIPVVVWGAWPFHR
AAAGGIIRGISALDATSSIAIAAYAWSIAMLLFETPGGKSWRSYPSWFAFDHGTLTQNE
IYFDVACGITVLLLAGRLLTRRRSQSSLLAELGRLQIDPQRIVTVVRKHLKRVVQELNI
PVQEVVRNDDVKVPPNTTIPVDGTVIGGGSRIAASIIMGQDQDVKVNDKVFAGSLNLES
EIKVRVIRTGHRTRIAAVHRWVKEATLKENRHNRAAIRSAGNLVPITFTLAVVDFCLWAL

ISGNINAAFTTTTAVLACVAPVALALSAPLATRNSIEAAARHGILVRSGEIFRVLDDVDT
 AVFNRVGTLTDGEMTVETVTADKGEDPELVLRVAGALAMESHHAISKALVKASREARDTG
 AGGEDVPHWIEVGNVEITEAGSFQATIELPLIKPSGEKIMRTTEALLWRPRSMTEVREHL
 SPRLVAAATSGGAPLIVRWKKGKDRGVITLSDHVRSDSSDAI IAIEEQGIETMMLSRDTYP
 VARRYADSLGITHVLGAIAPGKKAQVVRVHTRGSTVAMIGDESVMDCLVADVGVLMGV
 DRPSDLRDDSDPAADVVMREEVMSVPTLFKLARRYAKLVNGNIALAWIYNGVAMVLAV
 SGLLHPMAATVAMLASSLLIEWRSGRARKY

>RXN00412 TRANSLATE of: rxn00412.seq check: 7568 from: 1 to: 1080
 VSHTASTPTPEEYSAQQPSTQGTRVEFRGITKVFSSNNKSAKTALDNVTLTVEPGEVIGI
 IGYSAGKSTLVRLINGLDSPTSGSLLLNGTDIVGMPESKLRKLRNIGMIFQQFNLFQS
 RTAAGNVEYPLEVAKMDKAARKARVQEMLEFVGLGDKGKNYPEQLSGGQKQRVGIARALA
 TNPTLLLADAEATSALDPETTHEVLELLRKVNRELGITIVVITHEMEVVRSIADKVAVMES
 GKVVEYGSVYEVFSNPQTQVQKQFVATALRNTPDQVESEDLLSHEGRLFTIDLTETSGFF
 AATARAAEQGAFVNIVHGGVTTLQQRQSFGKMTVRLTGNTAAIEEFYQTLTKTTTIKEITR

>RXN00431 TRANSLATE of: rxn00431.seq check: 340 from: 1 to: 789
 MVSIDTYNACVDFPIFDAKSRSMKKAFLGAAGGAIGRNQDNVTVVVEALKNVNLHLREGDR
 VGLVGHNGAGKSTLLRLLSGIYEPTRGSA DIRGRVAPVFDLGVMGMDPEISGYENIIIRGL
 FLGQTRKQMKAKMEEIADFTELGEYLSMPLRTYSTGMRIRLALGVVTSIEPEILLDEGI
 GAVDAAFAKARDRLQALVERSGILVFASHSNDFLAQLCNTALWVDHGQIREAGLVPDVV
 EAYEGKGAGDHVRRLLTRMEEEEK

>RXN00444 TRANSLATE of: rxn00444.seq check: 7535 from: 1 to: 837
 MVLAQTKKARRSENHILPGWLLIPATLAMLLIIGPIFALLLQIPWDRSWELLTAPESLGT
 ARLSIGTALFSTALCAIVGFPLALALHLYERSHPRVTSVLTVLVYAPLVLSPVVSGLALT
 FLWGRRGFLGSWLDQVGLPIAFTTTAVVFAQVFVALPFFISTVTTALRGIPKQFEEIAAT
 EGATRWEIMHKMIIPLAMPGIFTGMILGFARALGEYGATLTFAGNIAGVTRTIPLHIELG
 LSSNDMDKALGAVIMLLAVVYVLIIGAIGALRLFSKVRKV

>RXN00466 TRANSLATE of: rxn00466.seq check: 8825 from: 1 to: 996
 VQSRLSKILRSSVVGVAVLALLAGCSNNADDDTADSTSTGNSAFFVSIEHEFGTTTIDDV
 PERVVTLGVTDA DIVLALGTVPVGNTGYKFFENGLGPWTDDELVEGKELTLLDSDSTPDLE
 QVAALEPDLIIGVSAGFDDVVEYQLSDIAPVVARPAGTAAYAVAREEATNLVARAMQSE
 KGQELNEETDALIQAARDENPSFDGKTGTVILPYQKGAYLPGDARGQFLDSLGLSPE
 AVLSRDTGDSFFVDVPAESVKDVGDLVLLVLSNDENLDITAENPLFETLNVVQKDAVIVA
 TTEERGAITYNSVLSVPFALEHLAPRIAEALK

>RXN00523 TRANSLATE of: rxn00523.seq check: 9218 from: 1 to: 1026
 MSLSHQLKRQRASRNSRRWLIVAALGVVTLGIFAFSLMWGEVIFYGPAQVLKVLSSGQQVPG
 ASYSGVLRPLPRAVMGLTAGLAFGAAGVIFQTVLRNQLASPDIIIGISSGASAAGVICIVF
 FGMSQSAVSAISLCASLAVALLIYLVAIRGGFSATRLILTIGIGIAAMLNSLVSYSLSKAD
 SWDLPTATRWLTGSLNGATWDRAMPLIVTTVVLIPLLVANARNVDLMRLGNDSSAVGLGVA
 TNRTRVIAIIAAVALIAVATAACGPFAFVAFVSGPIAARILGSGGSLIIPSALIGGLIVL
 IADLIGQYFLGTRYPGVVGTAFGAPFLIYLLIRSNRAGVTL

>RXN00525 TRANSLATE of: rxn00525.seq check: 5915 from: 1 to: 1263
 MSLAESILLALTSLRSNKMRAALLTLGVIIGIASVIGILTIGKALQDQTLNSLESIGAND
 LSAQVEERPDEDSPEPDMFAFSGAANSSGNLIPEETVDTLRDRFAGSITGISVGGMGTOG
 TLIGDTADLKSDDLGVNEDYMMWNGVEMNYGRAITQDDVAAQRPVAVIAPDTFNTLFDAN
 PNLALGSEVAFELNGQETFLRVIGVYKEAAAGGLVGSNPTVHTYTPYTVANDITHTEDGL
 NTLSIRAAQGVQDQSLKGSQTYFDALYANNDSHHVAMLD FRKQIEEFNTILGAMSLGIS
 AIGGISLLVGGIGVMNIMLVSVTERTREIGVRKALGARRRDIRLQFVVEAMICFIGGIL
 GVLLGGILGLIMSSAIGYISLPPSLSGIVIALVFSMAIGLFFGYYPANKAAKLDPIDALRY
 E

>RXN00702 TRANSLATE of: rxn00702.seq check: 9529 from: 1 to: 1707
 MSAPFSARTAWSTDVPLELESVAASYDDERTLAAPQISDVNLTLFEIGEILLVVGRTGSG
 KSTLLNAMSGAMPHATGGRLDGRVRVVGDRDTRDFPPRMLSDVVGVGQDPAAASFITNTVE
 EELAYSMEQLGLPPAVMRKRVEETDLLGIAELRYVPLAELSGGEQQRVAIGAVLTTRPA
 LIILDEPTSALDPNGAEDVLATVTKLAHDLAMTVVLAEHRIERVLYVDRVAHVAGADGHV

TVGTPEEIMADSDVAPPVELGRWAGWAPLPLSIRDARAHSADMRKRLYQRGLVNVKLHN
 HAVQPLLLIAEDIMVDFPEIRAVDGVNLLNLSGEITVLMGRNGCGKSSLLWALQSGSTRNQ
 GSVQVLDEAAGFSWTDPKTLKPAKRRNLVSMVPQTPTDILYESTVHAELARSDKDAAPA
 GTTREILDSLVPNIPDHLHPRDLSEGGKLSLALSIQLAAKPRVVFDEPTRGLDYDGKKS
 LARSFQQADDGHAILVVTHDVEFSALCADRVLFMASGKIISDGTAVEILPASPAYAPQV
 AKITAGIQEESHWLTVSAVKAALGHGEIS

>RXN00726 TRANSLATE of: rxn00726.seq check: 2288 from: 1 to: 591
 NAGRLYVDGDLIGYRERDGVLYEISEKDAAKQRSIDIGMVFQNFNLFPHRTVIENIIEAPI
 HVKKQPESKARARAMELLEQVGLAHKADAYPVQLSGGQQORVAIARAVAMEPKMLMFDEP
 TSALDPELVGEVLRVMKQLADDGMTMLVVTHEMGFAHEVADQVVFVFMADGVVVEAGTPEQV
 LDNPKEQRTKDFLSSLL

>RXN00732 TRANSLATE of: rxn00732.seq check: 6509 from: 1 to: 1647
 NHLLLLPTVKADIIDNGVVTGDIGYIWHHTGGIMLALTLVQVACAIAGVYFGSKLSMRVGR
 DLRSALFGKVVNFSEEMGQFGAPSLITRNTNDVQQVQMLVQMTSTLMISAPMLAIGGII
 MAVRQDLGLSWLMVVSIPVLIIVVALIIVRMVPLFQTMQKRIDRINQIIREQLTGIRVIR
 AFVREDVERERFTTASDKVDIGVRTGNLMALMFPVAVMLIMNLSAVAVIWFAGAFQVESGE
 TQIGTLFAFLQYIMQILMGVMAAFMFVMPRAAVSADRIGEVLTPSVQAPETPAQPS
 TSAGEIVFNATFAYPGADDPVLNNVSFRVAPGSTTAIGSTGSGKTTLIGLVPRLFDVT
 EGDVTVDGTDVREFEPLKLWDRIGLVPQKSFSGTIANLRYGNEDATETQLWQALAI
 QAADFVREMPEGLDSEIAQGGTNVSGGQRQLAIARALLKQPEIYIFDSSFSALDVSTDA
 ALRRALSTNLPDATKLIVAQRVSTIRDADQIVVLDNGEVVGIGTHTNLLNTCGTYREIVE
 SQETAQAQS

>RXN00759 TRANSLATE of: rxn00759.seq check: 3116 from: 1 to: 924
 MLRYVGRRLQMPVFFGATLLIYALVFLMPGDPVQALGGDRGLTEAAAEKIRQEYNLDK
 PFIVQYLLYIKGIFVLDFGTTFSGQPVIVDMARAFVPTIKLAIMALLFESILGIIFGVIA
 GIRRGGIFDSTVLVLSLIVIAVPTFVIGFVLQFLVGKWLGLLPVTVGSNTSITALIMPAV
 VLGAVSFAYVLRRLTRQSVSENLRADYVRTARAKGMSGFNVNMRHVLNRSLIPVATFLGAD
 LGALMGGAIVTEGIFGINGVGGLTYQAILKGEPTTVVSIVTVLVIVYIIANLLVDLIYAV
 LDPRIRYA

>RXN00808 TRANSLATE of: rxn00808.seq check: 7354 from: 1 to: 1458
 VLGTNVFGALAVMLFVRFLIPQPDASNFNAEISYLPVAGFAYLAFAIVAGMLVTFLMFRP
 VLDWQRSPEDHNRNMVRNLVMRIPIYQAILCAVWVLIGIAIATLISASVSTSLALVAFS
 TLMAAAIVVLLTYLEAERLVRPVAASALARREFDSTLEPPVSQRLRMTWLLTLGIPVMGI
 LLLIWGYSQGI FGSDASGIMPAIAALAFASLVGTGLGNRLVSSVVDPIRELQEAIRNVR
 RGENDVQVDIYDGSEIGVLQAGFNEMMRGLRERQVRDLFGRYVGAEVAKRALEERPTLG
 GEDRKVAVLFVDVIGSTTFVAVNHTPEEVEALNEFFEHVVEVVHRNKGVINKEFGQDAALA
 IFGAPLPLSDATGHALAAARELRAELKDLQLKAGIGVAAGHVAVAGHIGGHARFEYTVIGD
 AVNQAARLTEIAKTTPGRTVTNASTLREANEAEQARWTLMKSVELRGRSQMTQIARPIRP
 TLADRS

>RXN00828 TRANSLATE of: rxn00828.seq check: 8544 from: 1 to: 453
 VRGGLNTPPHKWRSDLAARIGTVFQDPEHQFVARTVRDELEIGPKIMKVDASERIEELL
 DRLRLRHLENANPFTLSGGEKRRLSVATALVAAPKLLILDEPTFGQDPETFTTELVTMLRE
 LTDNGISIVSVTHDPDFIAALGDHHEVSAK

>RXN00832 TRANSLATE of: rxn00832.seq check: 2297 from: 1 to: 1050
 MPFSWLKPIDYARIFVGWASIFIPLITLPSIIEALIVAVILFCAFGVVKMAERLAHIL
 GDFPGSLILTLISIVIEVILICAVMLGPADSTTAGRDSVMAVSMIIMGLVVGLCLLIGGL
 RHGSMFPHNGVGTPTYLVLIAVFAVPAFRGEYSTGQALVISTLTAVVYGFFLFRQM
 GAQAGEFQEVEVAEKADDAKWEVPFRGLILITVLPVILLSHDMATVMDEVLASLGAPV
 AMAGLIATIVFLPETITSLKAAWTGEIQRVSNLAHGAQVSTVGLTIPAVLVIGVITGQD
 VVLGETPINLLLLGTTIAVTAIAFSSKKVSAVHGSVLLMLFGVYMMSMFA

>RXN00934 TRANSLATE of: rxn00934.seq check: 9723 from: 1 to: 1083
 VRIGMVCPYSFDEPGGVQAHILDLARTFIAQGHVQVLGPCSADTQVPDFVVRGGGSIPI
 PYNGSVARLSFGPKMFKAVRTFLREGNFDVLHIHEPNSPSFSMAALRFAEGPIVATYHAS
 SSGSKLLKAFLPVLSPMLEKVRAGIAVSEMARRWQVEQVGGDPVLIPNGVETSMFKAARQ

IEPNDPVEIVFLGRLEDSRKGLDILLRALTRLDPRFTCTVIGGGTPREVAGIN FVGRVSD
 EEKAAILGRADIYVAPNTGGESFGIVLVEAMAAGCAVVASDLEAFSLVTDSEAAQFAGVL
 FKTGSDADLAKKLQALIDDPSSRSTLIAAGLKRANAYDWSTVSTQVMAVYETIAIDKVR
 LG

>RXN00939 TRANSLATE of: rxn00939.seq check: 3908 from: 1 to: 1236
 MTRQKTQPFLEKFSKYTPGVMIAALAVGLITLNVELALTLLVIACPGALVISIPVSIVA
 GIGRSKADGVLIKGGEYLETSAKVDTVVVDKGTGLTNGRPELTNVDVLDPAYSDDEVLT
 AARAETASEHPLAEAIIRGAENRGLTVAMVEKAEPVAGRGIRADVDGATVAVGSADLLDH
 TPDNTRILELNEQGRRTAMYVGINGKAVGIVAVADTIRDDAPAAIRSLHNKGIRVVMATGD
 AERVARNVAAELGVDEVRAELMPEDKLEIVKELQAQGRVAMVGDGVNDTPALATADIGV
 AMGAAGSPAAIETADIALMADKLPRLPYALGLAQRTVRTMRVNIGIALLTVTILLAGVLL
 GGVMTSIGMLVHEASVLLVIAIAMLLLRPTLKEDKDKADVSTADAAKETLSA

>RXN00960 TRANSLATE of: rxn00960.seq check: 4118 from: 1 to: 1035
 MARHCCSNRYASTVFSGLIAYGASQALYPWLLKDHQSVTEIDL DAGALQPYFNIEMPPPF
 EVMTALLLAFCLGLGMAVIKSDTLFKVTRELERVVMKTITAFVIPLPLFI FGIFLGMGM
 NGGLLEIMSAFGKVLILAVVGTLLFLAIQFIIAGAVSKKNPWKLFKNMLPAYFTALGTSS
 SAATIPVTYQQTLKNDVDVNVAGFVPLCATIHLA GMMKIGLFTFAVVFMYDMEVGVGL
 SIGFLLMLGITMIAAPGVPGGAIMAATGMLASMLGFNTEQVALMIAAYIAIDSFGTAANV
 TGDGAIAVIVNKFAGKQLHTTSPDEIEEDDRVAFDITPSDVEHHK

>RXN00980 TRANSLATE of: rxn00980.seq check: 2367 from: 1 to: 1794
 MLADAFMIAAAIVAGWP IASQALRIRMVSIDLLVVVAAV GAMFINNYWESA AVTFLF
 ALGKALERATMNTRKALSDLVDAAPETATRLNADDSTEVVELWELEPGDIVLVRNGEQI
 PVDGNIAGVGGIDESNITGESMPAEKGQGS D VYAGTWLRSGVLRVEATGIGSDSTLAKI
 IHRVEDAQDDKARTQTFLEKFSKYTPGVMIAAAVGLITWDVELALTLLVIGCPGALVI
 SIPVSVIAGIGRAARDGVLIKGGEYLETA AKVDVVVDKGTGLTTGRPELTDVEVIEPAY
 SQGEVLELAARAETASEHPLADAIIRGAQDRGLSTTLVEAAENITGRGIIANVDGQAVAV
 GSAELLDHEPDSTRILELNAEGKTAMFVG VNGHAIGIVAVADAVRSDSASAIESLHKAGI
 QVVMATGDAHRVAQNASKLGVDEVYSELLPEQKLELVRDLQAAGKTVAMVGDGVNDTPA
 LAAADIGVAMGVAGSPAAIETADIALMADRLPRLAHAVTLAKRTVRTMRINILIALATVM
 VLLAGVLFGGVTMSVGMVHEASVLLVISIAMLLLRPTLKEDAAQASDIKRSEIQQIA

>RXN01000 TRANSLATE of: rxn01000.seq check: 4854 from: 1 to: 846
 MSTLTSHRTVPAPSSPPARPNKLARNIVAIVAALIVLIATGTLKIEWNELPQMPAQVWHY
 LELMFSDPDWSKFGRVQEMWRSIAMAWLGAILCVVVSVP LGM LAARGVGPYWLRTVLR
 VFAVIRAFPEVVI AIIILLTVTGLTPFTGALALGISGIGQQA KWTYEAIESTPTGPSEAVR
 AAGGTTPEVLRWALWPQVAPSIASFALYREFEINIRTSAVLGIVGAGGIGSMLANYTNYRQ
 WDTVGMILLIVVVVATMIVDLISGTIRRRIMKGASDRVVAPSN

>RXN01002 TRANSLATE of: rxn01002.seq check: 1757 from: 1 to: 804
 MNSDASATTNSWAINFDHVSVTYPNGTKALDDVSLTINPGEMVAIVGLSGSGKSTLIRTI
 NGLVRATEGTVTVGPHQINTLKGKALRDARGQIGMIFQGFNLSSRSVFQNVLVGRFAHT
 AWRNLLGFPTHEHDKQIAFHAE SVGILHKVWTRAGALSGGQKQ RVAIARALSQDPSVML
 ADEPVASLDPPTAHSV MRDLENINNVEGLTVLVNLHLIDLARQYTTRLVGLRAGKLVDG
 PISEATDKDFEAIYGRPIQAKDLLGDRA

>RXN01141 TRANSLATE of: rxn01141.seq check: 9956 from: 1 to: 825
 LSTALAGAARYVTSTSNNEPADNTPLTIGYVPIAGSAPIAIA DALGLFKKHGVNVTLLKKY
 SGWSDLWTAYATEQLDVAHMLSPMTVAINAGVTNASRPTELSFTQNTNGQAITLASKHYG
 SVN SAADLKG MVLGIPFEYSVHALLR DYLVSNVADPIADLELRLLRPADMVAQLTVEGI
 DGFIGPGPFNERAISNGSGRIWLLTKQLWDKHPCCAVAMAKEWKA EHPTAAQGV LNALEE
 ASAILS NPAQFDSSARTLSQE KYNQPATLLDGPS

>RXN01142 TRANSLATE of: rxn01142.seq check: 3960 from: 1 to: 498
 LTARGNIDFGLRSARPSLSKTERADITRTHLEQVGLTDAAERRPARLSGGMQQRVGIARA
 FAIDPPIMLLDEPFGALDALTRRELQLQLLNIWEASRR TVVMVTHDVDEAILLSDRVLVM
 SKSPEATIITDIPVNLPRPRHELSEDASVEAETTALRK RMLHLLH

>RXN01164 TRANSLATE of: rxn01164.seq check: 868 from: 1 to: 1635

VTLFVRLALAAVGGFLVFASNEPIGWVAGIVGTALFFISLAPWDLGVPQKRRKKNEPVP
 FLOQMSTGPTVVQGMLLGFVHGLVTYLQLLPWIGEFVGS LPYVALSVVEALYSIALGAFG
 VLIARWRDWKVLFFPAMYVAVEYLRSSWPFDFGFAWVRLAWGQINGPLANLAALGGVAFVT
 FSTVLAAVGVAMV IISKRLAGAIITASVIAIGAVSSLYVDRNGTSDESIEVAAIQGNVP
 RMGLDFNAQRRRAVLNHAHARETLKLDEQVDLVIWPNSSDVNPFSDAQARAIIDGAVEHVQ
 APILVGTITVDEVGPRNTMQVDFPVEGAAEYHNKKFLQPFGEYMPFREFLRIFSPYVDSA
 GNFQPGDGTGVVEMNAANLGRAVTGVMTCEYEVIFDRAGRDAIANGAEFLTPTNNATFG
 FTDMTYQQLAMSRMRAIEFDRAVVVAATSGVSAIVNPDGSISQNTRIFEAATLTESIPLK
 DTVTIAARVGFYVELLLVIIGVLAGLFAIRMNSRSKSAKGSARPAQVRVKKVPAKKAATN
 RRKVK

>RXN01168 TRANSLATE of: rxn01168.seq check: 6703 from: 1 to: 810
 MSSEAVDATTLLVIPTTYNELENLPLIVDRVRTATPDVHVLIVDDNSPDGTGERADKLAAD
 DDHIFVLHREGKGGCAEYMAQFQWGLERDYQVLCEMDADGSHAPEQLHLLLAETNGAD
 LVIGSRYPVGGRRVWNWPKNRWLLSKGGNVYISVALGAGLTDMTAGYRAFRREVLEALPLD
 ELSNAGYIFQVEIAYRAVEAGFDVREVPITFTEREIGESKLDGSFVKDSLLEVTKWGLKH
 RGGQAKELSKEMVGLLNYEWHFKKRNTWL

>RXN01285 TRANSLATE of: rxn01285.seq check: 1049 from: 1 to: 726
 LNVITIPDNTFTAIIGPNGCGKSTLLRGFSRVLNPQHGVLLDGRQLDSFKPKIEIARELGL
 LPQTSIAPEGIRVYDLIARGRAPYQSLIQQWRTSDEDAVAQALASTNLTELAARLVDELS
 GGQRQVRVWAMLLAQQTPIMLLDEPTTFDLIAHQYELLELLRAFNEAGKTVVTVLHDLNQ
 AARYADHLIVMKDGHVHATGTPEEVLTAEMVQGVFGLPCIISPDPVTGTPTVVPLSRRA
 GA

>RXN01298 TRANSLATE of: rxn01298.seq check: 8940 from: 1 to: 930
 VSTLISEPEVDKLRKRAKRSRRTTEWWLAAALLAPNLLLLAIFTYRPLLDNFRLSFFNWN
 SSPTSTFIGFDNYVEFFTRSDTLQVVLNTVIFTACAVIGSMVLGLLLAMLLDQKLFGRNF
 VRSMVFAPFVISGAAIGVAFQFVDFPNFGLVQDLLGRIGVDS PQFYQNPWALFMVTF
 VWKNLGYSFVIYLAALQGLNKDLSEAAPVDGASAWTRFWKVTLPQLRPTTFFLSITVTLN
 SVQVFDIHTMTRGGPLGNGTTTLVYQVYTETFTNYRAGYGATITILFLLLLIITVIQV
 RYMDKENKQK

>RXN01323 TRANSLATE of: rxn01323.seq check: 658 from: 1 to: 2265
 MAQTPAKIPAAINFIDVDLGVGTGMTCTSCSARVERKLNKLDGVEATVNYATESAQVSYDP
 SKVSPEQLIKTVEDTGYGAFTMASAAAESEEDNAPADSGQSRIDAARDHEAADLKHRVIV
 SALLSPVVLVSMIPALQFNWQWAVLTLVTPIFFWGGSPFHKATWANLKRGSFTMNTLV
 SLGTSAADLWSLWALFIENAGHPGMMEMHLLPSASTMDEIYLETVAVVITFLLLGRWFE
 TKAKGQSSEALRKLLDMGAKDAVVLRDGAEVVRVPVNLKLGDFVITRPGEKIATDGEVDE
 GSSAVDESMLTGESIPVEVTGKSKVTGATLNTSGRLMVKVTRIGADTTLSQMAKLVTDQ
 SKKAPVQRLVDQISQVFVPVIVIAIATLIAHLVFTDAGLAPAFATAAVAVLIIACPCALG
 LATPTALLVGTGRGAQLGLLIKGEILESTKKVDTIVLDKTGTVTGTMSVTDVTAINYS
 ETEILEFAAAVESASEHPAQIAIAKAAEHEQVDFQNTAGQEVTVGVRGHEVRVGRPSST
 LIDALLHPFQHAQKIGGTPVVVTIDGVDSGIITVRDVTVKDTSAEAIRGLKELGLTPILLT
 GDNEGAAKSVAAEVGIDQVIANVLPHEKVQNVLEALQAQGNVAMVGDGVNDAAALAQADL
 GLAMGAGTDVAIEASDITLMNNDLRSVDAIRLSRKTGLTIKGNLFWAFAYNVALIPVAA
 IGLLNPMLAGIAMAFSSVFVVSNSLRRLRGFKARSN

>RXN01338 TRANSLATE of: rxn01338.seq check: 9102 from: 1 to: 1902
 KTYTPNPWMLFIRSF DGIIITVAALVAIAIHLILWLALDLDGLAKNWPLIAIVIVGGIPLM
 WDVLSAIAKTRGGADTLAAVSIITSVLLGEWLVAIIIVLMLSGGEALEEAAASRRASGTL
 ALARRAPSTAHRLLGATILDGTEEIAVEEITVGDVAVLPHELCPVDGEIVAGHGTMD
 YLTGEPYVVS KSKGSQAMSGAVNGDTPLTIVATKLAHDSRYAQIVGVLHEAENNRPEMRR
 MADRLGAWYTVIALALGGLGWIVSGDPVRFLAVVVVATPCPLLIAPVVAIIGAISLAARR
 GIIIVKNPGMLENASGVKTVMFDTGTLTGRPVITDIHTAPGVEEDTVLALAASVERYSR
 HPLADAIREGAKARELHLPDVVEVSESRPGQGLTGTVEHLVRITNRRSTLEIDPDSKNYI
 PVTSSGMESVVLVDDKYAALIRLRDEPRASAEFIAHLPKKHVKDKLMIISGDRASEVRY
 LADKVGIDEVHAEASPEDKLNIVNRHNEHGATMFLGDGINDAPAMAVATVGVAMGADSDV
 TSEADAVIDLSSLERLDDLLHISARMRRIALQSAGGGMALSVIGMILAVFGFLTPLMGA
 IFQEVIDVLAILNSARVALPRGAISDFDTQEKVS

>RXN01411 TRANSLATE of: rxn01411.seq check: 3735 from: 1 to: 765
 MLGVGWRIPLFLMAVPLGLIGWWIRTGAQENVRPASERPEAPIKQALRTEWKMLRVGGFI
 SCTGLSFYIFTTYMTTFLRSTVGLGTLVLAGNIIALSMAAIVAPFVGRAIDKFPRRNM
 AFATLSTVIMAIIPAYIIAGQGTLTASLIAQVMLGIGAVTANCVTSVMMAEVFQEVTRGTS
 AGITYNVTYAIFGGSAPFISTALVSWTGSPLAPAVYMIIIALFAFTASRFIPETSPVFVT
 ATPAIKAPKVLVNP

>RXN01808 TRANSLATE of: rxn01808.seq check: 4151 from: 1 to: 1149
 QSLACKELAWMRGGAPARTSKPGFRLEAAEALIAEVPAPRDKVELMAFSKSRQGRVIEL
 EDATVATPDDRILVEDLTWRAPGERIGLVGVNGSGKTTLLRTLAGEQPLQAGKRIEQGT
 VKLGWLRQELDDLDLSRRLIDCVEDVASVYMMGDKQVSASQLAERLGFSPKRQRTFVGDL
 SGGERRRLQLTRVLMAEPNVLLDDEPTNDLDIDTLQELSLDGGWPGTMVVISHDRLIE
 RVTDSWTALFGDGKLTNLPGGIEEYLQRRAMAAEDSGVLNLGAATQAGTFSAAEQAA
 TSVESSGISSQERHRITKEMNALERKMGKLDQQMDKLNQQLADAAEAMDTIKLTELDTKL
 RAVQEEHGELEMQWLELGEIEG

>RXN01939 TRANSLATE of: rxn01939.seq check: 574 from: 1 to: 1731
 MTTNIPQTPNHEGEQPLLELKDLKISFTSSTGVVDAVRGANLTIYPGQSVIAVGESGSGK
 STTAMSIIGLLPGTGKVTESIMFDGQDITGLSNKQMEKYRGSEIGLVPQDPMTNLNPVW
 RIGTQVKESLRANHVVPVPGSEMDKRAEVLAEAGLPDAERRAKQYPHEFSGGMRQALIAI
 GLAARPKLLIADSEPTALDVTVQQRILDHLETLTKDLGTAVLFITHDLGLAAERAHLV
 MHRGRIVESGSPSLKILRNPHQPYTQRLVKAAPSLASARIQSAQEQQIESAELLSATAVAE
 GTIPEMEEKVIEVKNLTREDFIRGARGDKKKLKAVDVVSFFVRKGTTLVGVESGSGKST
 VANMVLNLLLEPTSGEVLYNGTDLTSLSHKEIFQMRRKLQVVFQNPYGSGLDPMYSIYRCIE
 EPLTIHKVGGDRKAREARVAELDMVSMRSTMRYPNELSGGQRQRIAIARALALNPEV
 IVLDEAVSALDVLVQNQILTLAELQQELKLTLYLFITHDLAVVRQTADDVVMQKGRIVE
 KGRTDIDFNDPQQHYTRDLINAVPGLGIELGTGENLV

>RXN01995 TRANSLATE of: rxn01995.seq check: 3763 from: 1 to: 1338
 MDIRQTINDTAMSRYQWFIVFIAVLLNALDGFVDLAMSFTANAVTEEFGLSGSQLGVLLS
 SALFGMTAGSLLFGPIGDRFGRKNALMIALLENVVLVLSATAQSAGQLGVWRLITGIGI
 GGILACITVVISEFSNNKNRGMAMSIYAAGYGIGASLGGFGAAQLIPTFGWRSVFAAGAI
 ATGIATITATFFFLPESVDWLSTRRPAGARDKINYIARRLGKVGTFELPGEQSLSTKKAGL
 QSYAVLVNKENRGTSIKLWVAFGIVMFGFYFANTWTPKLLVETGMSEQQGIIGGLMLSMG
 GAFGSLLYGFLTTFKSSRNTLMTFMVLSGLTLILFISSTSVPSIAFASGVVVGMLINGCV
 AGLYTLSPQLYSAEVRRTTGVGAAIGMGRVGAISAPLLVGGLLDGWSPTQLYVGVAIVVI
 AGATALIGMRTQAVAVEKQPEALATK

>RXN02062 TRANSLATE of: rxn02062.seq check: 5414 from: 1 to: 1170
 MRVGMMTREYPPEVYGGAGVHVTETLRFMREIAEVDVHMGAPRDMEGVFVHGVDPALES
 ANPAIKTLSTGLRMAEAAANNVDVHSHSTWYAGLGHLAARLHGIPHVATAHSLEPDRPWK
 REQLGGGYDVSSWSEKNAMEYADAVIAVSARMKDSILAAYPRIEPDNVRVVLNGIDTELW
 QPRPTFDDAEDSVLRSGLVDPQRPIVAFVGRITRQKGVEHLIKAAALFDESQVLVLCAGA
 PDTPEIAARTTALVEELQAKREGIFWVQDMLGDKIQEILTAADTFVCPSIYEPLGIVNL
 EAMACNTAVVASDVGGIPEVVVDGTTGALVHYDENDVETFERDIAEAVNKMVADRETAAK
 FGLAGRERAINDFSWATIAQQTIDVYKSLM

>RXN02096 TRANSLATE of: rxn02096.seq check: 3261 from: 1 to: 1692
 MGLDVSDEQIEHAARLAQAHDFIDRLPNKYEEVIGERGLTSLGGQRQRIALARAFLAHPK
 VLVLDDATSAIDASTEDRIFQALREELHDVTILIIAHRHSTLELGDRLVGLVEDGRVTALG
 PLSEMRDHARFSLMALDFQDSHDPEFTLDNGSLPSQEQLWPEVSTEKQYKILAPAPGRG
 RGMSPATPELLAQIEALPAATEETRVDAAGRLRTSTSGFKLLSLFKQVRWLVVAVIALLL
 VGVAADLAFPTLMRAAIDNGVQAQSTSTLWWIAIAGSVVLLSWAAAAINTIITARTGER
 LLYGLRLRSFVHLLRLSMSYFERTMSGRIMTRMTTIDNLSSFLQSGLAQTVVSVGTIG
 VVTMLAITDAQLALVALSVVPIIIVLTILFIRRISSRLYTASREQASQVNAVHESIAGLR
 TAQMHRMEDQVFDNYAGEAEFRRLRVKSQTALAIYFPGLGALSEIAQALVLGFGALQVT
 RGDISTGVLVAFVLYMGLMFGPIQQLSQIFDSYQQAAGVFRITELLATQPSVQIWAPTG
 TLGRLPRSLYCLTTSPSAIQTIRS

>RXN02348 TRANSLATE of: rxn02348.seq check: 8038 from: 1 to: 1884
 MLNRMKSARPKSVAPKSGQALLTLGALGVVFGDIGTSPLYSLHTAFSMQHNVKVEVTQENV

YGIISMVLWTITLIVTVKYVMLVTRADNQGQGGILALVALLKNRGHWGKFVAVAGMLGAA
 LFYGDVVTITPAISVLSATEGLTVISPSFERFILPVSLAVLIAIFAIQPLGTEKVGKAFGP
 IMLLWFVTLTAGLGIPQIIGHPEILQSLSPHWALRLIVAEPFQAFVLLGAVVLTVTGAEAL
 YADMGHFGARPIRVAVFCVMPALILTYLGQGALVINQPEAVRNPWFYLAPEGLRIPLVI
 LATIATVIASQAVISGAYSLTKQAVNLKLLPRMVIRHTSRKEEGQIYMPLVNGLLFVSVM
 VVVLVFRSSESLASAYGLAVTGTLLVLSVLYLIYVHTTWKKTALFIVLIGIPEVLLFASN
 TTKIHDGGWLPPLIAAVLIVVMRTWEWGS DRVNQERAELELPMDFLEKLDQPHNIGLRK
 VAEVAVFPHGTSDTVPLSLVRCVKDLKLLYREIVIVRIVQEHVPHVPPEERAEMEVLHHA
 PIRVVRVDLHLGYFDEQNLPEHLHAIDPTWDNATYFLSALTLSRLPGKIAGWRDRLYLS
 MERNQASRTESFKLQPSKTITVGTTELHL

>RXN02354 TRANSLATE of: rxn02354.seq check: 8723 from: 1 to: 834
 MTKRTKGLILNYAGVVFILFWGLAPFYWMVITALRDSKHTFDTTPWPTHVTLDNFRDALA
 TDKGNFLAAGNSLVISVTTTATIAVLVGVFTAYALARLEFPKGIVTGIILAASMFPGI
 ALVTPFLFQLFGDLNWIGTYQALIIPNISFALPLTIYTLVSFFRQLPWELEESARVDGATR
 GQAFRMILLPLAAPALFTTAILAFIATWNEFMLARQLSNTSTEPVTVAIARFTGPSSFEY
 PYASVMAAGALVTIPLIIMVLIFQRRIVSGLTAGGVKA

>RXN02356 TRANSLATE of: rxn02356.seq check: 7192 from: 1 to: 996
 MATVTFDKVTIRYPGAERATVHELDLDIADGEFLVLVGPSCGKSTTLRALAGLEGVESG
 VIKIDGKDVGTQEPADRDIAVFQNYALYPHMTVAKNMGFALKLAKLPQAQIDAKVNEAA
 EILGLTEFLDRKPKDLSGGQQRQVRVAMGRALVRDPKVFLMDEPLSNLDAKLRVQTRAEVAA
 LQRRLGTTTVYVTHDQVEAMTMGDRVAVLKDGLLQQVAPPRELYDAPVNEFVAGFIGSPS
 MNLFPPANGHKMGVRPEKMLVNETPEGFTSIDAVVDIVEELGSESIVYATWEGHRLVARVW
 EGPVPAPGTPVTFSDAAQAHHFDLESGERIA

>RXN02391 TRANSLATE of: rxn02391.seq check: 7541 from: 1 to: 399
 MTQSDLPDDVQELVTKIFGLARDGGAESAATLGAYVDNGVDVNLNQNQDGNLTLLMLAAYAG
 HADVQALIERGADVDRVNNRNQTPLAGAIFKKEEAVIEALLAGGADPYAGTPTAVDTAK
 MFGREDLVARFES

>RXN02442 TRANSLATE of: rxn02442.seq check: 5164 from: 1 to: 849
 MKFFTDALIVPFDVSFISRALVAGCLAAILCSLIGTWVILRRLTFFGDAMSHGLLPGVAT
 ASLLGGNLMFGAAISALIMSAGVWVTSRKSSLSQDVSIGLQFITMLSLGVVIVSHSDSHA
 VDLTSFLFGDILGVRPSDIFIIATATVLGGTLTIFLFHRQFTALAFDERKAHTLGLNPRFA
 HLLMLALIALATVVVSFQVVGTLVLFGLLIGPPATAALLVQDKASISLIMIVASLLGCAEI
 YLGLLISWHASTAAGATITLLSAAIFFATLLTKSAISRNLNFTA

>RXN02447 TRANSLATE of: rxn02447.seq check: 8454 from: 1 to: 1095
 TVVPVYLAELAPLEIRGSLTGRNELAIVTGQLLAFVINALIAVTLHGVIDGIWRIMFAVC
 ALPAVALFLGMLRMPESPRWLVNQGRYDDARRVMETVRTPERAKAEMDEIIAVHSENNAA
 LPGVKQSSGQASGVVSSKHTHMSIGEVLSNKWLVRLLIAGIGVAVAQQLTGINAIMYYGT
 RVLEESGMSAEMAVVANIAFGAVAVIGGLIALRNMDRLDRRTTFIIGLSLTTFHLLIAA
 AGTLLPEGNSIRPFAIMILVVGFLVSMQTFNLVAVVWVLAEIFPVRMKGIGTGISVFCGW
 GINGVLALFFPALVSGVGITFSFLIFAVVGVIALAFVTKFVPETRGRSLEELDHAFTGQ
 IFKKA

>RXN02455 TRANSLATE of: rxn02455.seq check: 2559 from: 1 to: 1269
 LKRLTRIASISMASMLAAASLVACSGSTDEEGDVYFLNFKPEQDVAYQEIAYTEETGV
 KVKVVTAASGSYEQTLKAEIGKDEAPTFLFQVNGPAGFITWQDYMDMSDTEVAKQLTDDI
 PPLTTEDGEVRGVPFVEGFGIINYDEIFDKYIATSGAKIKSTDEITSYQKLKEVAEDMQ
 AKKDELGIEGAFASTSLTSSDWRWQTHLANAPIWQYEQDKGVEDTNEIEFSYNKEYKNL
 FDLYLENSTVEKSLAPSKTVSDSMAEFAQGKAAMVQNGNWAWSQISETSGNVVKEDKIKF
 LPMYMGLPDEEKHGINVG TENYLGVNSEASEVDQQATKDFVDWLF TSEAGKEHVVKDLGF
 IAPFESYTAENTPNDPLSEQVAEAIANKDLTTYPNWFQYFPSQQFKDDFGQDLSQYASGK
 LKW

>RXN02515 TRANSLATE of: rxn02515.seq check: 4857 from: 1 to: 756
 MSTLEIRNLHAQVLPDESAPKEILKGVNLTINSGEIHAIMGPNSGKSTLAYTLGGHP
 RYEVTAGEVLLDGENILEMEVDERARAGLFLAMQYPTIIPGVSVANFLRSAATAIRGEAP
 KLREWVKEVRTAQEALAIIDPEFSNRSVNEGFSGGEKKRHEVLQDLCLKPKFAIMDETDSG

LDVDALRIVSEGINSYKQETEGGILMITHYKRILNYVKPDFIHVFANGQIVTTGGAEALAD
KLEADGYDQFIK

>RXN02549 TRANSLATE of: rxn02549.seq check: 8075 from: 1 to: 2703
MVHAKQTKKPLPRFLHSAHFYVWIVLGFVVFAQPYGQVAADTKLDLLNLPAGFLTALHA
WTDFTTLGQLQNAQYGYLFPQGFFFLITDFLPDWIAQRLWWVLVLGLGFSGFYALVARLG
IGNPAFRVIAALLFALSPTLTTLTAISSETWPIMLAPWVCLPILLSRNVDARAIALSLLP
AACMGAVNATATMAALIPAALILLYRGLFLRLLLWGMGVLAVNSWWIGPLLVLGKYAPPF
TEFIESSSVTTSWLNPEILRGTTSWTPFVDTERQAGYLLVNDALFVTLVSVLVAALGLIG
LTLMKHGRGLWAFMLAIGLLILGSAHLTAVQEFLDGPGAALRNHKKFDLLVRMPLMVGVA
LGSHISLPLLGTTALTSGQGKHHTIPLPLQKRQAAGLLVVIIVAGALAPAWSARLLPQGT
WDEVDPDYWEATEFLNQATGTRTLIWPSSPFARQDWGWTRDEPAQPLLDVPWAVRDAIP
LVPPEAIRGLDGLDDLTGLTGLNDEALKRLGIGAVLVRHDEADPDIEVDLPGEKHTFG
SQGQVDVYLTDPRNMWITSGETSKQLPTVAGGGEILSLDITINGYSPRTLVSENAQIVTD
TPQLVGNTYGDGTSSAALASLDETEVKNRIVDYPASAGPMTQVVQEGSITASSSGSDATSF
GGADPDRSLNSLLDHYNTAWYPTPGDTSWLEVSFGTGTLSISPRSTVTATITSGDSVM
VREFEKGRTTTVTLAEPEARIEFDGFGVIGISELSLEGLSRTITVPETSPDVQQFVFQRLTV
PTSFLDRFTTVPRHMSVTVEAQSCVTLLELDGDRIDCGPSNSPPEPTRCAPNRNGSPSPNP
LRSPFLFSQQQTSRQHPPTACSSPRALSIQVPARLSTPPPPQSNSTPPPKVSSSPRTPPA
S

>RXN02570 TRANSLATE of: rxn02570.seq check: 2673 from: 1 to: 642
MNPLTWIIGAFSMWIVVLGVNKLGLSIAVIIAQVVMIRVRNVSVLASTALLSVPALAS
MALIHMPYSSDGWLIALTLTARFSALMSIFLLAATAITIPELVKSLYRWPKLAYIVGSAL
QMIPQKGQTLALVRDANALRGRSVKGPVRAVKYVGLPLITHLLSAGAARAIPLEVAGLDR
PGPRTVLVEVVEGRVEKHCRWLLPLLAVGMAWWL

>RXN02595 TRANSLATE of: rxn02595.seq check: 5016 from: 1 to: 1164
VIVVAMASIMACLAARLNNPMKILLLCWRDTHPQGGGSERYLERVGEFLADQGHEVVF
RTAGHTDAPRRSFRDVRYSRSGGKFSVYPKAWVAMMLGRVIGITFSKVDVVVDVTQNGIP
FFGKFFSGKPTVLLTHHCHKEQWPVVGRLAKVGWLIESQIAPRAYKTAPYVTVSEPSAE
ELIALGVDDQRIHIVRNGVDPVPLHTPKLDRDGGHAVTSLRSLVPHKQIEHAMDVVAALDG
VVLDDVESGWWQKELVDYARTLGVS DRVVFHGGQVAEDHKHALLERATIHLMPSRKEGWGL
AVTEAAQHGVPTIGYRSSGGLRDSVVDGETGLLVDSKAELISATKTLIDASLRSKLGAS
AKQRAENYKWDTAGAQFEELLLGLASKK

>RXN02614 TRANSLATE of: rxn02614.seq check: 5216 from: 1 to: 729
MTATLSLKPAAATVRGLRKS YGTKEVLQGIDLTINCGEVTALIGRSGSGKSTILRVLAGLS
KEHSGSVEISGNPAVAFAQEPRLLPWKTVLDNVTFGNRTDISWSEAQERASALLAEVKLP
DSDAAWPLTSLGGQAQRVSLARALISEPELLLLDEPFGALDALTRLTAQDLLLLKTVNTRN
LGVLLVTHDVSEAIADHVLDDGAIHSLTVDPIDGDRRTHPSFASYTAQLLEWLEIT
TPA

>RXN02795 TRANSLATE of: rxn02795.seq check: 7318 from: 1 to: 1437
VLKVSDLTVGNNFVHNVSFEVNPGERVGIIGESGSGKSLTALSIMGLTDLPTTGQITFNG
KPSATFRGTRIAMVFEPMASALNPLMRIGRQIEEMMTLHGASKKDARARLKSLLIDVSLP
ERTASAYPHELSSGQQRALIAMALANDPDLLICDEPTTALDVVVQKQIVDLLLLRLTKER
GTALLFITHDLGLIARTCERLLVMKSGETVERGDTEAILRSPAHSYTQQLLDASILDQPE
IASDSGAPVVIDVEEASKSFKETTALHKVSLAVRKGDLLGIVGSGSGKTTLKLIAGLD
KPTTGTVAVTGGVQMVFDQPSLNPMMKIKDIVAEPLLGNAAEKTTRVAEVITQVGLS
PDVLDTRYPHEFSGGQQRISIRALAIKPAILLADEPVSALDVSVRKQVLDLLQQLVEEY
GITLVFVSHDLAVVRHLCTTVWVMEQGRVLEQGPIDSVYDHPQTEYTKELLDAVPRLSL

>RXN02925 TRANSLATE of: rxn02925.seq check: 5237 from: 1 to: 2217
MSTPHHHGDHPAPETDHTHHPNHAGHEHHADAATHGQAMPHDHPHSTVDEEHQVHSHGEH
AGHSAAMFRDRFWWSLILSVPVVFFSPMFADLLGYNIPEIPGAYWIPPVLGTIIFLYGGT
PFLKGAMTELKSRQPGMMLLIAMAITVAFIASWVTTLGLGGFHLDFWWELALLVTIMLLG
HWLEMRALGAASSALDALAALLPDEAEKVVDGTTTRTVAISELAVDDVVLVRAGARVPADG
TIIDGAAEFDEAMITGESRPVYRDTGETVVAGTVATDNTVRIRVEATGGDTALAGIQRMV
ADAQASSSRAQALADRAAALLFWFALITALITAVVWTIIGSPDDAVVRAVTVLIIACPHA
LGLAIPLVIAISSERAASKSVLIKDRMALEHMRTIDVVLFDKTGTLTEGAHAVTGVAAPT

GIAEGELLALAAAAEADSEHPVARAIVTAAAAHPEASQRQLRATGFTAASGRGIRATVDG
 AEILVGGPNMLREFNLTTPEGELADITGSAQRGAGVLHVVRDGEIIGAVAVEDKIRPESR
 AAVRALQARGVKVAMITGDATQVAQAVGKDLGIDEVFAEVLDPQDKDTKVTQLQERGLSVA
 MVGDGVNDAPALARAEVGGIAIGAGTDVAMESAGVVLASDDPRAVLSMIELSHASYRKMVQ
 NLVWATGYNIVAVFLAAGVLAPIGVLLPFAAAAILMSLSTIIVALNAQLLRIDLDPAHL
 APTDGKEEKAASVSAAPVR

>RXN02933 TRANSLATE of: rxn02933.seq check: 4913 from: 1 to: 810
 MPLSGKIGGFIVAVVFLAALSFIWTFDPVQAFQERLEGSSLRHLLGTDYGRDVLQS
 IMVGSRVTLVGGIIVAVIAALIGTPLGIAAGMRRGMVETFMVARGADLMLAFPALLLAIIS
 GAVFGASTWSAMVAIGIAGIPSFARVARAGTLQVTSQDFIAAARLSKVSSARIALRHILP
 NITSMLIVQASVAFALAILAEALSFLGLGTTTPDPSPWGRMLQTAQASIGVTPMLAVWPG
 AAIALTVLGFNLFGDGLRDAIDPKREVGRA

>RXN02945 TRANSLATE of: rxn02945.seq check: 2147 from: 1 to: 933
 MTTALGTRVVARNFYRHASRENPAKLDINFEIAPGERILLTGASGAGKSTLLAALAGVL
 GGSDEGVSTGELLVDAPSIGLVLDQDPDSQVIASRIGDDVAFGCENLQIPREEIWPRVERA
 LELVGLDLPLSHPTKYLSGGQKQRLALAGVIAMGARLILLDEPTANLDPQGQKNVVAVD
 RVVQETGATLIVVEHRHELWVNIIDRIISITDGEDVQPAELIKVGQLPGAQPSTSKPILW
 ANDLLCTWGGLRSFEVPEGASTVITGPNAGKSTLALTMGGLLPRKVGSWNSLTRCAAL
 TRPRTSGVQLI

>RXN02975 TRANSLATE of: rxn02975.seq check: 5313 from: 1 to: 249
 VIVTNDLEVRVGARTLLDAPGQLLRVQPGDRIGLVGRNGAGKTTTMRILSGETKPYGGSV
 TTSGEIGYLPQDSREGNIEQTAR

>RXN02994 TRANSLATE of: rxn02994.seq check: 4127 from: 1 to: 723
 IKMTGVQKYFGDFHALTDIDLEIPRGQVVVLGPGSGKSTLCRTINRLETIEEGTIEID
 GKVLP EEGKGLANLRADVGMVFQSFNLFPHLTIKDNVTLAPIKVRKMKKSEA EKLAMSL
 ERVGIANQADKYPAQLSGGQQQORVAIARALAMNPKIMLFDEPTSA LDP EMVNEVLDMAS
 LAKEGTMVCVTHEMGEFARKAADRVLFMADGLIVEDTEPDSFFFTNPKSDRAKDFLGKILA
 H

>RXN03020 TRANSLATE of: rxn03020.seq check: 1931 from: 1 to: 603
 MTLHVSNNLNTVADGSTSRLLNNIHFWMNSQAKSSVSPAHPAPENPPYSPSSAASKAPD
 SGTATLGDDIDLLNPQNRAALRRNHLGIVFQQPNLLPSLTVLDQLLLIPRLGRILPPSRSA
 RTQHKDKALSLLNSIGLDLAKRKVSELSSGQQQARVNLARALMNSPKLLLVDDEPTAALDQ
 HSASEVTELIVSMAHQYNAPT

>RXN03080 TRANSLATE of: rxn03080.seq check: 3725 from: 1 to: 780
 MPQVLEIRDLNVEFSPSRHAVKNVSFSAPAGKVTALIGPNGAGKSTALSAIAGLVESTGEV
 MVGGSGVASKSAKARARLLSLVPQNTRELIGFSARDVVAMGRYPHRGRFAVETDADRRAT
 DDALRAINALDIAEQPVNELSGGQQQLIHIGRALAQDTAVVLLDEPVSALDLRHQVEVLQ
 LLRARANSGETTVIVVLHDLNHVARWCDHAVLMADGEVVSQGDIREVLEPATLSTVYGLPI
 AVRDDPETSSLRVIPHPNPF

>RXN03081 TRANSLATE of: rxn03081.seq check: 3848 from: 1 to: 459
 MKKSLIAIVASALVLSGCTSDSSDSSGTSGETVETTSITTSVAAADGAFFRTVTLDSSIT
 LESKPERIAVLTPAASLVLPITGADRVMTAEMDTADEETAALASQVEYQVKNNGRLDP
 EQVVAGDPDLVIVSARFDTEQGTIDILEGLNVP

>RXN03108 TRANSLATE of: rxn03108.seq check: 138 from: 1 to: 267
 MTKPNASVELNTITKSYGSTTIIGDTSITINDGEFVSLDPSGCGKSTILKMIAGLASPS
 TGTVSAGNEEIKGPGPDGRGMVFDHALLP

>RXN03116 TRANSLATE of: rxn03116.seq check: 7423 from: 1 to: 609
 MGEDVVEKHFAFGLKAAKQRRFFARTVALMPQNPTIPAGLSVFDYVLLGRHPSYAPGRA
 DDEIVKRCLADLKHLEHFSRGLDELSSGGERQVRVSLARALAQEPRIVLLDEPTSA LDIGHA
 QETLELIDAIRHRLGLTVIAAMHDLTLTAQYGDRVLMNNGGRKVFEGTAAEVLTAQRIS
 IYDATVIVEVIDGRPVVIPQRSH

>RXN03129 TRANSLATE of: rxn03129.seq check: 210 from: 1 to: 1224
 MASIVFENVTRKYSFGARPAVDKLNLEIADGEFLVLVGPSCGKSTSLRMLAGLEPIDEG
 RLLIDGKDATELRPQDRDIAMVFQSYALYPNMTVRDNMGFALKNQKVAKEIEKRVAEAS
 RILQLDPYLDKPAALSGGQRQVRVAMGRAIVREPSVFCMDEPLSNLDAKLRVSTRAEISG
 LQRRMGVTTVYVTHDQVEAMTMGDRVAVLLLGVLQQVDTQPONLYDYPANAFVASFIGSPS
 MNLIEGTIRGDKVTLGTGIQISVPDEVAEVRNPNDRFEGRFPVIVGARPEHMYLTANES
 GAVLGEVSHIDELGADSMVYVLASGVKNPNTDLLGEGIPEDMRVTVVGAEETDKARLGIR
 VERHHGLKAGDKVHVVAAPKDVHLFDGLDGRRIGASVLAPAHTVQSGH

>RXN03164 TRANSLATE of: rxn03164.seq check: 9986 from: 1 to: 870
 MIYRRVGNISGLKLPALISLGLWHNFGDDKPLSTQRSIIHRAFDGRVTHFDLANNYGPPAGS
 AETNFRGRILREDLKSHRDELISSKAGWDMWPGPYGFGSRKYLVSLLDQSLTRLGLDYV
 DIFYHHRPDPDTPLEETMYALRDIVASGKALYVGISSYGPETAEEAEFMAEEGCPLLIH
 QPSYSIINRWVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLDKYLDGIPEGSRASQG
 KSLSEGMLNVNIDMVRKLNDAQERGQSLAQMALAWVLREQREYAGGLP

>RXS00088 TRANSLATE OF: RXS00088.seq check: 1389 from: 1 to: 876
 IEDNHGTEGISLPIEGVAATDNRAFELLDRWGVELVAAPLQLVPFTVTGYTEEGGVANLGSHREPDLEA
 LAAQPSLIINGQRFQYQYDDIIALNPDATVVELDPRDGEPLDQELIRQAETLGEIFGEEEDAQIVAD
 FESALERAKTAYAAISDQTVMAVNVSGGNIGYIAPSVGRTYGPIFDLVGLTPALEVGNASSDHEGDDIN
 VEAIAAANPDLLVMDRDGGTSTRNEADYVPAEQIVSDNEALANVKAVTDGYVYAPADTYTNENIITY
 TEILNGMADMFEKAAQ

>RXS00372 TRANSLATE OF: RXS00372.seq check: 2326 from: 1 to: 1077
 MSSKHPLKRTAVTVFALGASAAALLVACSEPSDEVSTAETTTASSSANASDAAGEKVTITVYTSEPEEKV
 DEINKAFMEANPDIEVEYRAGTGDLTARIEAEKASGSIEADVLWAADAATFETYAAQGDLELEDVET
 SDIEEALDAENFYVGTRIIPTVIAYNTEVVDDQAEPLTSWADLTDPKYAGQLVMPDPAVSGAAAFNASV
 WKNDPALGEAWITALGENQPMIAQNSNGPTSQEIAGGGHPVGIVVDYLVRDLAAAGSPIDTIYASEGSPY
 ITEPAGVFADSEKKEAAERYINFLLSVEGQEIAVEQAYLPVREDVGTPEGTPELADIELMTPDLEVVT
 DKAAAVEFFQNAMN

>RXS00453 TRANSLATE OF: RXS00453.seq check: 3260 from: 1 to: 2349
 VISAWLLILAIVGGLALTMQKGFSNSFTIEDTPSIDATVSLVENFPDQTNPVTAAGVNVVQSPGTTL
 DDPQMMTAMDAVDYIEDNLPDFGGGERFGNPVEVSPALEEMVIEQMTSMGLPEETAAKDAANLAVLSE
 DKTIGYTSFNIDVEAAEYVEQKHRDVINEAMQIGEDLGVVEAGGPAFGDPPIQIETTSEIIGIGIAFIV
 LIFTFGSLIAAGLPLITAVIGVGIGALAIVLATAFTDLNNVTPVLAVMIGLAVGIDYALFILSRYAEY
 KRMPRADAAGMAVGTAGSAVVAFAGATVIAIALVALIADIGFLTAMGISAAFTVFVAVLIALTFIPALLG
 VFGGHAFKGIPIGIGGNPTPKQTWEQALNRRSKGRSWVKLVQKAPGLVAVVVLGLGALTIPAMNLQLS
 LPSDSTSNIIDTTQRQSADLMAEGFGAGVNAFFLVIVDTHVNADSTALQPLIEAQEPEEGEFDRQQAAR
 FATYMYVTQTYSNIDVKNQAIISVNDDFTAAQILVTPYTGPKADKETPELMHVLRAQEAQIEDVTGTTEL
 GTTGFTAVQLDITEQLEDAMPVYLAVVVGLAIFLLILVFRSLVPLVAGLGFLLSVGAAGFATVVLVWQE
 GFGGFVNTPGPLISFMPIFLIGVTFGLAMDYQVFLVTRMREHYTHNGKGQPGSKYTPVEQSVIEGFTQ
 GSRVVTAAALIMIAVFVAFIDQPLPFIKIFGFALGAGVFFDAFFIRMGLVPASMFLMGKATWMPKWL
 RILPSLDIEGTALEKEWEEKQAAR

>RXS00479 TRANSLATE OF: RXS00479.seq check: 9191 from: 1 to: 2190
 MSTSIITTENKKKSGPPRLMRIFLPALLILVWLVGAGVGGPYFGKVSEVSSNSQTTYLPESADATQVQEQ
 LGDFTDSESIPIAVVMVSDPLTQQDITQLNEVVAGLSELDIVSDEVSPAIPSEDGRAVQVFPVLPNPSA
 ELTESVEKLSETLTQQTPDYVSTYVTGPAGFTADLSAAAFAGIDGLLLAVALAAVLVILVIVYRSFILPI
 AVLATSLFALTVALLVVWVLAKWDILLSGQTQGILFILVIGATDYSLLYVARFREELRVQQDKGIAT
 GKAIASVEPILASGSTVIAGLLCLLFSDLKSNSTLGPVASVGIIIFAMLSALTLLPALLFVFGVAFWP
 KRPKYEPEKARAKNDIPASGIWSKVADLVEQHPRAIWVSTLIVLLLGAAFVPTLKADGVSQSDLVLGSS
 EARDGQQALGEHFPGGSGSPAYIIVDETQAAQAADVVLNNDNFETVTVTSDSPSGSAPITADGIVPLG
 SGTAPGPVVVEGQVLLQATLVEAPDSEEAQKAIRSIRQTFADENISAVVGGVTATSVDTNDASIHDRNL
 IIPIVLLVILVILMLLLRSIVAPLLLVVTTTVVSFATALGVAALLFNHVFSFPGADPAVPLYGFVFLVAL
 GIDYNI FLVTRIREETKTHGTRLGILRGLTVTGGVITSAGVVLAATFAALYVIPILFLAQIAFIVAFGV
 LIDTLLVRAFLVPALFYDIGPKIWWPSKLSNQKYQKQPQL

>RXS00654 TRANSLATE OF: RXS00654.seq check: 6625 from: 1 to: 1266
 VLDILIYPVSGVMKLWHLLHNVAGLDDSLAWFFSLFGLVITIRAIIPFTWQMYKSGRTAAHIRPHRA
 ALREEYKGYDEASIRELQKRQNDLNKEYGINPLAGCVPGLIQIPIVLGLYWALLRMARPEGGLNPVF

QSIGFLTPEEVESFLAGRVSNVPLPAYVSMPTQLKYLSTTQAEVLSFVLPLFITAAILTAIINMAMSMY
RSFQTN DYASGFSNGMLKFMIVMSILAPIFPLSLGLTGFPPTAIALYVWSNNLWTLTQTIIIMMVLIERK
YPLTDDDFKVHLEQRDIYRAKQKEKRIFLWTRRKNRMLILTPWNASTLHATNVELTKTRTAEINEAKQ
ARKEIANKRRETQREMNRAMQRLKQRAAEVKAKKKGLIDASPNEDTPSENEETKLSSPQVEPTTTAEF
NREPSQED

>RXS00758 TRANSLATE OF: RXS00758.seq check: 161 from: 1 to: 1602
MTLKKSLAVTTAAALALSACSSDSSSSSSSSSGSEGGDNYVLVNGTEPQNPLVPNGTNEVGGGRIV
DSIFSGLVYYDVGSPVNDVAESIELEGDKTYRITIKDQGTFTDGTPTVAESFVNAWNNVANSTLSSY
FFESILGYEEGVESMEGLQVVDDTTFTVELTQPESDFPLRLGYSAFFPLPESAFDDMDAFGENPIGNP
YKLQEWNNHNDATIVPNADYTGGRAQNDGVKFIIFYPTFDSAYADLLSDNLDVLDALPDSAFSSFEDEL
SGRSINQPSAVFQSFTIPESLEHFSGEEGLRRQAI SLAVNRDEITQTI FEGTRTPATDFTSPVIDGHS
DSLQGADVLTYPERAQELWAQADEISPWSGEFSISYNADGGHQAWVDATANSIRNTLGLDAIGNPYPD
FKSLRDDVTNRTINGAFRTGWQADYPSLGNFLGPLYGTGAGSNDGDYSNPDFAKLAEANAADVDAST
PLYNEAQEIILLQDLPAIPTWYSNAVGYSTNVNVEFQWNSQPAYYQITKN

>RXS00912 TRANSLATE OF: RXS00912.seq check: 8141 from: 1 to: 273
MDNTLYTAGLTIAAAFFMLSFIFTIYRIIVGPNSIDRLGLDGTVSMIQCSMATYICWTLDTTVTNFMM
VIALLGFISSVSVARFRKRDGA

>RXS00932 TRANSLATE OF: RXS00932.seq check: 6704 from: 1 to: 474
MTPQKLHRFAALLEMGTWTLIIIGMILKYSGVTDVAVTPIAGGIHGFGLCFAAITITVWINNKWTFPQG
IAGLIVSVIPWAALPFALWADKKGLVAGGWRFSDPSEKPHTEFFDKILAQLVRHPIRSILILLVIIAVVF
SILLAMGPPYDPAIANTVD

>RXS01346 TRANSLATE OF: RXS01346.seq check: 3214 from: 1 to: 1575
MRTATKVIATVMASLAIGLASCSSSSSGTPDVNYVSVNGTEPQRGLIPGDTNENGGGRVDMLYSGLVY
FDEAGVAQNDLAASIDQETDTTYKITLRDGIKFSDGSDITATDFVDTWNVVENGLLNTSFFSPIKGYE
EGVETLEGLNVVDDRTFTIELAQPDSEFTQIRIGYYGFAPMPASARDDIDAFGENPVSSGPYKLEQWDHN
AELKVVANEHYDGPRAANNDGLKYVFYAQNDAAYSDDLGNLDVLDLIPPSAYTTYEELSGRSINQPA
ASYLELSIRMESPNFEGQQQLRRQAI SMAINREEIAEQIFAGTYTPALDFTAPVLDGWRDDLNGNDVL
TFQPDKARELWEDAEETAPFEGELQISYNADVPNREWVDVANSISNELDVNATGNPFPDFKSFRD TYR
TTGLDGAYRTAWFADYPSIGNFLGPNYTSVGASNDKAYENPEFDQLIADAAAATKEETFQAYAQAQEM
LLRDLPAIPLWYPNVVGGYSESVDNVSVNWKAIPVYWAITKQ

>RXS01425 TRANSLATE OF: RXS01425.seq check: 9957 from: 1 to: 885
VLSPDSGITWALSIMFLTFTVRMVLVKPMVNTMRSQRKMQDMAPKMQAIREKYKNDQOKMMEETRKLQK
EVGVNPIAGCLPMLVQIPVFLGLFHVLRFSNRTGSGVGQLEMTVEQNANTPNYIFGVDEVQSFLRADLF
GAPLSSYITMPADAFDAFLGLDVSRLNIALVAAPMILLIVVATHMNARLSVNRQEARKAAGKQQAASSD
QMAMQMOMNMKMLWFMPATILFTGFIWTIGLLVYMSNNVWTFQQRYYIFAKMDAEAEAEKRAAK
RTTAPKPGVKPENPKKRKK

>RXS01658 TRANSLATE OF: RXS01658.seq check: 7999 from: 1 to: 1833
DPQILSPTFTQQQLRNFGYFPDQLAMDRFEVDGKLRFVVAARELDPNALQQNQDWINRHTVYTHGN
GFIAAQANQVDEVARDVGSTRGGYPVYTVSDLQSNARAAESEDAAELGIKVDEPRVYGYPLIASATDGA
DYAIVGDTGDGPVEYD TDTSSYTYEGAGGV DIGNMVN RAMFALRYQEMNMLLSDRVGSSEKILFERDPR
SRVEKVAPWLTTDSKTYPTVIDGRIKWIVDGYTTLDLSPYSTRTSLEATQDAVMPDGTPOPLITDRVG
YIRNSVKAVVDAYDGTVELYEFDTEDPVLKAWRGVFPD TVKDGSEISDELRAHLRYPEDLFKVQORDMLA
KYNVDDSGTFFTNDAFWSVPGDPTAAEGRQELKQPPYYVVAADPETGESSFQLITPFRGLQREYLSAHM
SASSDPVTYGEITVRVLPDTSVTQGPQAQDAMSSDQVAQDQTLWRGSNDLHNGNLLTLPVGGGEILY
VEPIYSQRKDQASAFPKLLRVLFYKGVGYAPTIAEALSQVGIDPKEAQDIEEVDGTATTPSTDETDT
DTDQPATETPTAPVSEAGIAAINDALSNLEAARDSSFEEYGRALDALDRAVDSYQSAQ

>RXS01677 TRANSLATE OF: RXS01677.seq check: 5194 from: 1 to: 744
VNQQSKKWLVP TLVVI IAVLLI AVVLLMYRGNASDTAEGVSAAATSDSAAASTAASGSASGAADSDLTS
VEARDPSDPVAVGDVDAPVGLVVFSDYQCPFCAKWSDETLPQMMKHVEDGNLRIEWREVNIFGEPSERG
ARAAAYAAGLQDAYLEYHNALFANGEKPSEDLLSEGLIKLAGDLGLDESKFTADFPQSPETAVAI AQHQQ
LGIDL GAYSTPAFL LGGPIMGAQPASVFEEAFEQALAAKE

>RXS02586 TRANSLATE OF: RXS02586.seq check: 4914 from: 1 to: 270

MHLLRDDNWWAPGFVKKAYTVMGHGSEVEEAPRPTTRRLNDDEEVTVHEAVVAGDTVASRGGLSTQENR
DLVSFVELKARLEKRRLEDLD

>RXS02587 TRANSLATE OF: RXS02587.seq check: 637 from: 1 to: 2091
VFSKWGHFAYRFRRIVPLVVIAAILALFVIFGTLGDRMSQEGWDDPGSSSTAAARIELETFGRDNDGD
VVLLFTAPEGTSFDDAEVFSSISGYLDGLIENNPDEVSHINSYFDTRNQNLSSKDGTTQFAALGLKGDG
EQTLKDFREIEDQLHPDNLGGVTTEVAGATAVADALDEGMAGDISRAEVFALPFVAILLLIVFGSVVA
AAMPLIVGILSILGSLGILAILAGFFQVNVFAQSVVTLGLGLAIDYGLFMVSRFREEMDKGTPVEQAV
ATTTATAGKTVVFSAMVAVALSGLFVFPQAFKSVAFGAISAVGLAALMSVTVLPSLFSMLGKNIDKW
SLRRTARTARRLEDTIWYRVPWAMRHAKAVTVGVVLLLLALTVPVLTGVKFGGINETYLPANDTRVAQ
ERFDEAFPAFRTEPVKLVVTGADNNQLIDIYVQANEVEGLTDRFTAGATDDGTTVLSTGIQDRSLNEQ
VVEQLRAISVPEGVEVQIGGTPAMEIESIEALFEKLLWMALYIVLATFILMALVFGSVILPAKAIIMTI
LGMGATLGLITLTMFVDGVGASALNFSPLMSPVLVIMAIYGLSTDYEVFLVSRMVEARDKGESTDD
AIRYGTATHGSIITAAALIMIVVCGAFGFSEIVMMKYIAFGMIAALILDATIIRMMLVPRRDAPASRRQ
LVGTRLR

>RXS02590 TRANSLATE OF: RXS02590.seq check: 3473 from: 1 to: 936
MGISLLSSLLKIHGFPVVADFFFALAVVVAIVIIIGWLIYRSPSFKTEVMPAWAMLSMGLIALGTASPV
VLGDDLWGFMFVCWSIGTAVGLVAYSLEYITAILRSKAGTPTFAWGLPLVTPMVASTSAAQLHEHFELPA
MLWVSFGLFLLTLASAPAVFTRVYFYFYFGPKAQGIPLMATPTSWIPLGMVGQSTAAAQLIGASFGSKTA
ITMGIIYGIIMGIFTIPLGAIAHFVYRAVFKGATYSPTWWASTFPVGTLSLGAHFLSQSTGVEWFNYF
SLYLIALMLFHVIVSTIAGTIAVMRRIVGKLKSQLA

>RXS02932 TRANSLATE OF: RXS02932.seq check: 938 from: 1 to: 972
VSKTEEGRSAIIIIYAFPTFILLGAIIFAFIFPEPFPIPLTNYINIFLTIIIMFTMGLTLTVPDFQMVLRP
LPILIGVVAQFVIMPFLAIVVAKMFNLNPAVAGLLMLGSPVGGTSSNVIAFLARGDVALSVTMTSVST
IVSPIMTPFLMLLAGTETAVDGGMAWTLVQTVLLPVIIIGLVLRVFLNKWIDKILPILPYLSILGIGG
VVFGAVAANAERLVSGLIVFVAVIVHNVGLGYVVGYLTVGRVFKFPEAANRTMAIEIGTQSAGLASGMAG
RFFTPEAALPGAVAALVHNITGAVYVGLVRNRPLTKASRKESVAVSS

>RXS03042 TRANSLATE OF: RXS03042.seq check: 1569 from: 1 to: 606
LVLAFLVLLLVSRSIWVPLIAALGFGLSVLATFGATVAIFQEGAFGIIDDPQPLLSFLPIMLIGLVFGL
AMDYQIFLVTRMREGFTKKGKTAGNATSNGFKHGARVVTAAALIMVSVFAAFIAQDMAFIKTMGFALAVA
VFFDAFVVRMMIIPATMFLDLDKAWWLKPKWLDKILPNVDVEGEGLSELHEARTEELKENVGVA

>RXS03075 TRANSLATE OF: RXS03075.seq check: 8649 from: 1 to: 726
VAKFLYKLGSTAYQKKWPFLAVWLVLIGITTLAGLYAKPTSSSFISIPGLDSVTTMEKMQERFPGSDDA
TSAPTGSVVIQAPGKTLTDPEVGAENVQMLDEVTRATGVLKDADSVVDPVLAAQGVAAQMTPALEAQGV
PAEKIAADIESISPLSADETTGIIISMTFDADSAMDISAEDREKVTNILDYDDGDLTVVYNGNVFGAAA
TSLDMTSELIGLLVAAVVLIVTFGSFIAAGMPLIS

>RXS03124 TRANSLATE OF: RXS03124.seq check: 3878 from: 1 to: 960
MTPTLASMIGLAVGIDYALFIVSRFRNELISQTGANDLEPKELAERLRTMPLAARAHAMGMAVGTAGSA
VVFAGTTVLIALVALSIINIPFLTVMIAAAITVAIAVLVALSFLPALLGLLGTRIFAARVPGPKVPDP
EDEKPTMGLKWVRLVRKMPVAYLLVGVLGAIAPATNMRLAMPTDGTSTLGTAPRTGYDMTADAFGP
GRNAPMIALIDATDVPEERPLVFGQAVEQFLNTDGVKNAQITQTTENFDTAQILLPQNLMSMSAPLR
LSQLFVQMLRPSLMTFARRMALLASPOFTMTSLLASATSWFLTF

>RXS03125 TRANSLATE OF: RXS03125.seq check: 4701 from: 1 to: 171
LVLAFLVLLLVSRSIWVPLIAALGFGLSVLATFGATVAIFQEGAFGIIDDPQPLLCF

>RXS03220 TRANSLATE OF: RXS03220.seq check: 3878 from: 1 to: 960
MGLREILSSKWLVRILLVGIGLGVAQQLTGINSIMYYGQVVLIEAGFSENAALIANVAPGVIAVVGAFI
ALWMDGINRRTTLITGYSLTTISHVLIGIASVAFVPGDPLRPYVILTLLVVVFGVSMQTFLNVATWVML
SELFPLAMRGFAIGISVFFLWIANAFGLFFPTIMEAVGLTGTFFMFAGIGVVALIFIYQVPETRGRT
LEEIDEDVTSGVIFNKDIRKGVH

>RXS03221 TRANSLATE OF: RXS03221.seq check: 3878 from: 1 to: 960
MFRDPAPPSKGTTNLGDKMASTFIQADSPEKSKLPPLTEGPYRKRLFYVALVATFGGLLFGYDTGVIN
GALNPMTRELGLTAFTEGVVTSLLFGAAAGAMFFGRISDNWGRRTIISLAVAFFVGTMICVFAPSFA

